

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 8, 2005, 23:18:52 ; Search time 171 seconds  
(without alignments)  
1146.711 Million cell updates/sec

Title: US-10-036-342-57  
Perfect score: 2623  
Sequence: 1 MDPKIGRMAASLLAVLLLLL.....NYIEGTKLFRAFFLEMAQLH 507

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2623	100.0	507	5	AAU72908 Human met
2	2623	100.0	507	5	ABB07950 Human met
3	2623	100.0	507	6	ABU69115 Human PRO
4	2623	100.0	507	6	ABO19431 Human sec
5	2623	100.0	507	6	ABU69092 Human PRO
6	2623	100.0	507	6	ABU81556 Human sec
7	2623	100.0	507	6	ADA76582 Novel hum
8	2623	100.0	507	7	ABO25139 Human sec
9	2623	100.0	507	7	AAE39109 Human PRO
10	2623	100.0	507	7	AAE39046 Human PRO
11	2623	100.0	507	7	ADC29813 Novel hum
12	2623	100.0	507	8	ADF09256 Human sec
13	2621	99.9	507	3	AAE18921 A novel p
14	2612.5	99.6	508	4	AAE39109 Human car
15	2612.5	99.6	508	4	AAE39109 Human sec
16	2612.5	99.6	508	6	ABR47759 Human sec
17	2612.5	99.6	508	6	ABR00082 Human gen
18	2612.5	99.6	508	7	ADB91551 Human sec
19	2612.5	99.6	508	7	ADC74152 Human sec
20	2612.5	99.6	508	7	ADE11767 Human sec
21	2612.5	99.6	509	3	AAE76144 Human sec
22	2585.5	98.6	508	7	ADC77691 Human 550
23	2566.5	97.8	501	4	AAU28396 Amino aci
24	2566.5	97.8	501	4	AAU25426 Human Sch
25	2566.5	97.8	501	4	AAU15115 Schizophr



99	180	6.9	428	6	ABM70853	Abm70853 Staphyloc	172	133	5.1	366	8	ABM83690	Abm83690 Human dia
100	176	6.7	318	2	AAY08759	Aay08759 L. monocy	173	132	5.0	383	2	AAW79066	Aaw79066 N-acetyl-
101	176	6.7	432	7	ADJ33264	Adj33264 Enterococ	174	132	5.0	383	8	ADK13774	Adk13774 E. coli i
102	175	6.7	402	7	ADH87450	Adh87450 Enterococ	175	132	5.0	473	5	AAU72909	Aau72909 Human met
103	174	6.6	394	8	ADR31503	Adr31503 Succinyl	176	132	5.0	473	5	ABB98126	Abb98126 Human PMM
104	174	6.6	431	8	ADN46747	Adn46747 Thermo	177	131.5	5.0	351	7	ADM25522	Adm25522 Hyperther
105	174	6.6	439	8	ADI67226	Adi67226 Lactobaci	178	130	5.0	342	8	ABM83694	Abm83694 Human dia
106	172	6.6	331	5	ABP61032	Abp61032 Lactobaci	179	130	5.0	400	4	ABB66170	Abb66170 Drosophil
107	172	6.6	331	7	ADE12747	Adel2747 L. rhamno	180	130	5.0	443	6	ABU02677	Abu02677 S. pneumo
108	172	6.6	425	7	ADH85976	Adh85976 Enterococ	181	128.5	4.9	258	7	ADH87006	Adh87006 Enterococ
109	172	6.6	465	8	ADI67225	Adi67225 Lactobaci	182	128.5	4.9	372	8	ADN46443	Adn46443 Thermo
110	171	6.5	418	5	ABP38707	Abp38707 Staphyloc	183	127.5	4.9	361	6	ABU92042	Abu92042 Human pro
111	171	6.5	418	8	ADS05236	Ads05236 Staphyloc	184	127	4.8	372	8	ABM83692	Abm83692 Human dia
112	171	6.5	468	5	ABP26705	Abp26705 Streptoco	185	127	4.8	378	8	ABM83691	Abm83691 Human dia
113	168.5	6.4	372	8	ADK17043	Adk17043 Nanoarcha	186	126.5	4.8	339	3	AAG43832	Aag43832 Arabidops
114	166	6.3	469	6	ABU46620	Abu46620 Protein e	187	126	4.8	203	5	ABU51393	Abu51393 Helicobac
115	166	6.3	486	5	ABP26706	Abp26706 Streptoco	188	126	4.8	373	8	ADP43682	Adp43682 Human PMM
116	165	6.3	469	6	ABU43262	Abu43262 Protein e	189	126	4.8	418	4	AAG81643	Aag81643 S. epider
117	164.5	6.3	386	6	ABM68627	Abm68627 Photorhab	190	126	4.8	449	4	AAU33879	Aau33879 Staphyloc
118	164.5	6.3	470	6	ABU44150	Abu44150 Protein e	191	125.5	4.8	359	4	ABB62632	Abb62632 Drosophil
119	164	6.3	467	6	ADB09472	Adb09472 Alloiococ	192	125.5	4.8	430	5	ABP39457	Abp39457 Staphyloc
120	164	6.3	489	6	ADB09474	Adb09474 Alloiococ	193	125.5	4.8	430	8	ADS05305	Ads05305 Staphyloc
121	162.5	6.2	450	7	ADC96907	Adc96907 E. faeciu	194	125.5	4.8	432	7	ADG73059	Adg73059 Pseudomon
122	161	6.1	469	6	ABU43726	Abu43726 Protein e	195	125.5	4.8	432	7	ADL12114	Adl12114 Pseudomon
123	160	6.1	471	8	ADS06743	Ads06743 Staphyloc	196	125	4.8	373	5	ABB08102	Abb08102 Enzyme si
124	158.5	6.0	466	4	AAU37944	Aau37944 Streptoco	197	125	4.8	373	6	ABU07744	Abu07744 Human ami
125	158	6.0	402	8	ADL04999	Adl04999 M. catarr	198	125	4.8	373	7	ADE79014	Ade79014 Human pro
126	157.5	6.0	466	3	AAY81712	Aay81712 Streptoco	199	124.5	4.7	401	4	ABB62639	Abb62639 Drosophil
127	157.5	6.0	466	6	ABU00999	Abu00999 S. pneumo	200	124	4.7	381	7	ADM26975	Adm26975 Hyperther
128	157.5	6.0	466	8	ADK48781	Adk48781 Streptoco	201	124	4.7	616	6	ABM72146	Abm72146 Staphyloc
129	157.5	6.0	470	8	ADR94981	Adr94981 Novel S.	202	123.5	4.7	441	7	ABO65647	Abo65647 Klebsiell
130	156	5.9	410	8	ADS43035	Ads43035 Bacterial	204	122	4.7	2291	4	ABB61876	Abb61876 Drosophil
131	155.5	5.9	466	4	AAU37801	Aau37801 Streptoco	205	120.5	4.6	409	2	AAR24528	Aar24528 Arginine
132	155.5	5.9	466	6	ABU45932	Abu45932 Protein e	206	119.5	4.6	361	6	ADA55384	Ada55384 Human pro
133	155	5.9	465	6	ABU17872	Abu17872 Protein e	207	119.5	4.6	361	7	ADN38883	Adn38883 Cancer/an
134	153	5.8	451	3	AAG50166	Aag50166 Arabidops	208	119.5	4.6	361	8	ADN05662	Adn05662 Antipsori
135	152	5.8	446	3	AAG06549	Aag06549 Arabidops	209	119.5	4.6	361	8	ADS10651	Ads10651 Human the
136	151	5.8	391	2	AAW21016	Aaw21016 H. pylori	210	118.5	4.5	1433	8	ADJ67954	Adj67954 G. stearo
137	151	5.8	469	6	ABU16179	Abu16179 Protein e	211	118.5	4.5	1433	8	ADJ68166	Adj68166 G. stearo
138	151	5.8	469	6	ABM71197	Abm71197 Staphyloc	212	118.5	4.5	1433	8	ADK01244	Adk01244 DNA polym
139	150.5	5.7	419	8	ADS30510	Ads30510 Bacterial	213	118.5	4.5	1433	8	ADJ79463	Adj79463 G. stearo
140	150.5	5.7	472	5	ABB54156	Abb54156 Lactococc	214	118.5	4.5	1433	8	ADJ84903	Adj84903 B. steart
141	150	5.7	388	2	AAW62863	Aaw62863 Helicobac	215	118.5	4.5	1433	8	ADM77691	Adm77691 DNA polym
142	149	5.7	396	7	ADF08023	Adf08023 Bacterial	216	118.5	4.5	1433	8	ADM66358	Adm66358 G. stearo
143	149	5.7	440	3	AAG06550	Aag06550 Arabidops	217	118.5	4.5	1433	8	ADO04411	Ado04411 B. steart
144	149	5.7	469	4	AAU36697	Aau36697 Staphyloc	218	118.5	4.5	1433	8	ADP82488	Adp82488 B. stearo
145	148.5	5.7	430	3	AAG50167	Aag50167 Arabidops	219	118	4.5	336	8	ABM83688	Abm83688 Human dia
146	143.5	5.5	407	2	AAR30458	Aar30458 Pig amino	220	117	4.5	1846	8	ADQ39531	Adq39531 Human myo
147	141.5	5.4	450	3	AAG06511	Aag06511 Arabidops	221	116.5	4.4	343	7	ADE79013	Ade79013 Human pro
148	141	5.4	408	2	AAR30459	Aar30459 Human ami	222	116.5	4.4	343	8	ABM83695	Abm83695 Human dia
149	141	5.4	408	5	ABB08103	Abb08103 Human pep	223	116	4.4	329	6	ABU30098	Abu30098 Protein e
150	141	5.4	408	7	ADE59755	Ade59755 Human Pro	224	116	4.4	334	7	ADC96959	Adc96959 E. faeciu
151	141	5.4	408	8	ADQ30527	Adq30527 Pancreas	225	114.5	4.4	636	6	ABU41842	Abu41842 Protein e
152	141	5.4	408	8	ADR40173	Adr40173 Human ami	226	114	4.3	265	7	ADH88574	Adh88574 Enterococ
153	141	5.4	408	8	ABM80467	Abm80467 Tumour-as	227	114	4.3	803	7	ADF04338	Adf04338 Bacterial
154	140.5	5.4	401	3	AAG43830	Aag43830 Arabidops	228	113.5	4.3	116	5	ABP09238	Abp09238 Human ORF
155	140.5	5.4	401	5	ABB92971	Abb92971 Herbicida	229	113	4.3	409	2	AAW89440	Aaw89440 Mycoplasm
156	140.5	5.4	441	8	ABM83687	Abm83687 Human dia	230	113	4.3	410	5	ABG31994	Abg31994 M. argini
157	139.5	5.3	443	8	ADK47763	Adk47763 Streptoco	231	113	4.3	410	8	ADP79612	Adp79612 Mycoplasm
158	139.5	5.3	446	8	ADR96040	Adr96040 Novel S.	232	113	4.3	441	4	ADP79611	Adp79611 Mycoplasm
159	139	5.3	474	4	AAB96247	Aab96247 Putative	233	113	4.3	441	8	AAG92859	Aag92859 C glutami
160	138.5	5.3	341	3	AAG06551	Aag06551 Arabidops	234	112.5	4.3	337	4	AAB96136	Aab96136 Putative
161	137.5	5.2	393	7	ABO74129	AbO74129 Pseudomon	235	112	4.3	166	3	AAB40345	Aab40345 Human ORF
162	137	5.2	215	4	AAU37468	Aau37468 Staphyloc	236	112	4.3	409	2	AAW89441	Aaw89441 Mycoplasm
163	137	5.2	408	4	ABB66172	Abb66172 Drosophil	237	112	4.3	410	5	ABB76127	Abb76127 Mycoplasm
164	137	5.2	429	3	AAG06512	Aag06512 Arabidops	238	112	4.3	410	5	ABG31995	Abg31995 M. arthri
165	137	5.2	576	6	ABU40289	Abu40289 Protein e	239	111.5	4.3	597	2	AAU73944	Aay73944 Human pro
166	136.5	5.2	446	5	ABP40280	Abp40280 Staphyloc	240	111.5	4.3	597	2	AAU73944	Aay73944 Human pro
167	136	5.2	190	4	AAU34381	Aau34381 Staphyloc	241	111.5	4.3	616	3	AAW83325	Aab58325 Lung canc
168	135	5.1	442	8	ADN47750	Adn47750 Thermo	242	111.5	4.3	630	4	AAW93651	Aam93651 Human pol
169	134.5	5.1	341	3	AAG43831	Aag43831 Arabidops	243	111.5	4.3	630	8	ADL31483	Adl31483 Human pro
170	134	5.1	391	8	ADS21973	Ads21973 Bacterial	244	111.5	4.3	770	5	ABB89615	Abb89615 Human pol
171	133.5	5.1	434	7	ABO72302	Abo72302 Pseudomon							

245	111.5	4.3	1163	8	ADO08105	Ado08105 Mouse pol	318	103.5	3.9	1435	4	AAB31934	Aab31934 Amino aci
246	111.5	4.3	1447	4	AAM39304	Aam39304 Human pol	319	103.5	3.9	1435	7	ABW01647	Abw01647 Staphyloc
247	111.5	4.3	1466	4	AAM39303	Aam39303 Human pol	320	103.5	3.9	1436	4	AAU34070	Aau34070 Staphyloc
248	111.5	4.3	1798	6	ABJ37072	Abj37072 Human bre	321	103.5	3.9	1438	6	ABU15873	Abu15873 Protein e
249	111.5	4.3	1811	4	ABG09031	Abg09031 Novel hum	322	103.5	3.9	1442	4	AAU36728	Aau36728 Staphyloc
250	111.5	4.3	2000	8	ADP23277	Adp23277 PRO polyp	323	103.5	3.9	1442	6	ABM73132	Abm73132 Staphyloc
251	111.5	4.3	2061	5	ABP68628	Abp68628 Human pan	324	103	3.9	330	6	ABU29050	Abu29050 Protein e
252	111.5	4.3	2061	7	ABM85357	Abm85357 Human pro	325	103	3.9	385	7	ADH87067	Adh87067 Enterococ
253	111.5	4.3	2061	8	ADR37739	Adr37739 Human fer	326	103	3.9	809	7	ADF06401	Adf06401 Bacterial
254	111.5	4.3	2061	8	ABM81166	Abm81166 Tumour-as	327	102.5	3.9	887	8	ADS30607	Ads30607 Bacterial
255	111	4.2	422	4	AAB79819	Aab79819 Corynebac	328	102.5	3.9	1118	4	AAB48264	Aab48264 Rice magn
256	111	4.2	422	4	AAB79123	Aab79123 Corynebac	329	102	3.9	539	3	AAB13586	Aab13586 Streptom
257	111	4.2	1231	8	ADN20850	Adn20850 Bacterial	330	102	3.9	1738	7	ADE47738	Ade47738 Human NOV
258	110.5	4.2	401	4	ABB62394	Abb62394 Drosophil	331	102	3.9	1738	8	ADJ79008	Adj79008 Human NOV
259	110.5	4.2	1478	5	AAU10540	Aau10540 Rat CIRL-	332	101.5	3.9	337	6	ABM69342	Abm69342 Photorhab
260	110.5	4.2	1478	7	ADD46680	Add46680 Rat Prote	333	101	3.9	353	6	ADA33943	Ada33943 Acinetoba
261	110.5	4.2	1488	7	ADE55162	Ade55162 Rat Prote	334	101	3.9	656	6	AAE35497	Aae35497 Streptom
262	110.5	4.2	1488	7	ADE55174	Ade55174 Rat Prote	335	100.5	3.8	399	6	ABU33347	Abu33347 Protein e
263	110.5	4.2	1488	7	ADE55170	Ade55170 Rat Prote	336	100.5	3.8	623	6	ABU02013	Abu02013 S. pneumo
264	110.5	4.2	1488	7	ADE55166	Ade55166 Rat Prote	337	100.5	3.8	623	6	ABP81435	Abp81435 Streptoco
265	110	4.2	409	8	ADP79614	Adp79614 Mycoplasm	338	100.5	3.8	648	8	ADS41904	Adn41904 Bacterial
266	110	4.2	409	8	ADP79616	Adp79616 Mycoplasm	339	100.5	3.8	656	8	ADN18615	Adn18615 Bacterial
267	110	4.2	409	8	ADP79613	Adp79613 Mycoplasm	340	100.5	3.8	826	7	ADK41554	Adk41554 Anti-cell
268	110	4.2	409	8	ADP79615	Adp79615 Mycoplasm	341	100.5	3.8	861	8	ADS17671	Ads17671 Rat major
269	110	4.2	650	6	ABU48779	Abu48779 Protein e	342	100.5	3.8	872	8	ADS17743	Ads17743 HIV-Tat (
270	110	4.2	784	8	ADQ39526	Adq39526 Human myo	343	100.5	3.8	873	8	ADS17679	Ads17679 Cysteine
271	110	4.2	1104	8	ADQ39520	Adq39520 Human myo	344	100.5	3.8	877	8	ADS17737	Ads17737 Rat major
272	110	4.2	1279	8	ADQ39528	Adq39528 Human myo	345	100.5	3.8	878	8	ADS17691	Ads17691 Polylysin
273	110	4.2	1845	8	ADQ39530	Adq39530 Human myo	346	100.5	3.8	889	8	ADS17797	Ads17797 Polylysin
274	110	4.2	1845	8	ADQ39533	Adq39533 Human myo	347	100.5	3.8	892	8	ADS17689	Ads17689 Hist7 joi
275	110	4.2	1914	8	ADN03875	Adn03875 Antipsori	348	100.5	3.8	894	8	ADS17785	Ads17785 Polylysin
276	110	4.2	1914	8	ADQ39522	Adq39522 Human myo	349	100.5	3.8	917	8	ADS17755	Ads17755 Rat major
277	110	4.2	1953	5	AAU84351	Aau84351 Protein M	350	100.5	3.8	934	8	ADS17793	Ads17793 Polylysin
278	109	4.2	279	6	ADB07676	Adb07676 Alloiococ	351	100.5	3.8	957	8	ADS17697	Ads17697 GAL4 pept
279	109	4.2	290	7	ABO70609	Abo70609 Pseudomon	352	100.5	3.8	968	8	ADS17771	Ads17771 GAL4 + ra
280	109	4.2	414	6	ADB11694	Adb11694 Alloiococ	353	100.5	3.8	973	8	ADS17759	Ads17759 GAL4+ante
281	109	4.2	428	5	ABP65764	Abp65764 Bifidobac	354	100.5	3.8	992	8	ADS17703	Ads17703 RNA bindi
282	108.5	4.1	95	5	ABP63651	Abp63651 Human ORF	355	100.5	3.8	1003	8	ADS17781	Ads17781 MS2 + rat
283	108.5	4.1	1162	8	ADT89537	Adt89537 Mus muscu	356	100.5	3.8	1008	8	ADS17775	Ads17775 MS2 pepti
284	108.5	4.1	1496	4	AAM39305	Aam39305 Human pol	357	100.5	3.8	1013	8	ADS17767	Ads17767 GAL4 + ra
285	108	4.1	246	4	AAB79125	Aab79125 Corynebac	358	100.5	3.8	1040	8	ADS17749	Ads17749 Rat major
286	107.5	4.1	379	7	ADC95892	Adc95892 E. faeciu	359	100.5	3.8	1100	8	ADS17709	Ads17709 Green flu
287	107	4.1	546	8	ADN47281	Adn47281 Thermococ	360	100.5	3.8	1127	8	ADS17789	Ads17789 Polylysin
288	107	4.1	552	5	ABB97379	Abb97379 Novel hum	361	100.5	3.8	1206	8	ADS17763	Ads17763 GAL4 + ra
289	106.5	4.1	321	5	ABB49299	Abb49299 Listeria	362	100	3.8	471	7	ADF05420	Adf05420 Bacterial
290	106.5	4.1	321	6	ABU32973	Abu32973 Protein e	363	99.5	3.8	622	8	ABM84112	Abm84112 Human dia
291	106.5	4.1	553	3	AAB24225	Aab24225 Human ves	364	99.5	3.8	653	8	ADS43215	Ads43215 Bacterial
292	106.5	4.1	565	7	ADM25925	Adm25925 Hyperther	365	99.5	3.8	654	4	AAB96566	Aab96566 Putative
293	106.5	4.1	1464	4	AAM41091	Aam41091 Human pol	366	99.5	3.8	807	4	ABG14952	Abg14952 Novel hum
294	106.5	4.1	1464	4	AAM41089	Aam41089 Human pol	367	99	3.8	319	3	AAG50168	Aag50168 Arabidops
295	106.5	4.1	1464	4	AAM41090	Aam41090 Human pol	368	99	3.8	1031	4	AAB48266	Aab48266 Wheat mag
296	105.5	4.0	403	4	AAU34689	Aau34689 E. coli c	369	99	3.8	1704	4	AAU00983	Aau00983 Drosophil
297	105.5	4.0	583	4	ABG09034	Abg09034 Novel hum	370	99	3.8	1704	4	AAU00984	Aau00984 Drosophil
298	105.5	4.0	1430	4	ABG09032	Abg09032 Novel hum	371	99	3.8	1704	4	AAU00985	Aau00985 Drosophil
299	105	4.0	552	8	ADQ35180	Adq35180 Human TRI	372	99	3.8	1704	4	AAU00969	Aau00969 Drosophil
300	104.5	4.0	383	7	ADF07241	Adf07241 Bacterial	373	98.5	3.8	573	6	ADB11786	Adb11786 Alloiococ
301	104.5	4.0	851	8	ADP98924	Adp98924 C. albica	374	98.5	3.8	580	6	ADB11784	Adb11784 Alloiococ
302	104.5	4.0	1372	4	ABG14554	Abg14554 Novel hum	375	98.5	3.8	603	6	ADB11782	Adb11782 Alloiococ
303	104.5	4.0	1378	4	ABG23678	Abg23678 Novel hum	376	98.5	3.8	609	6	ADB11780	Adb11780 Alloiococ
304	104.5	4.0	1379	4	ABG10257	Abg10257 Novel hum	377	98.5	3.8	793	7	ADC01447	Adc01447 Enterohae
305	104.5	4.0	1400	4	ABG09151	Abg09151 Novel hum	378	98.5	3.8	829	8	ADN21524	Adn21524 Bacterial
306	104.5	4.0	1788	4	ABG06749	Abg06749 Novel hum	379	98.5	3.8	3418	2	AAU04356	Aay04356 Human BRC
307	104.5	4.0	2048	7	ADJ69296	Adj69296 Human hea	380	98.5	3.8	3418	2	AAU04358	Aay04358 Human BRC
308	104.5	4.0	2563	4	ABG14767	Abg14767 Novel hum	381	98	3.7	502	5	ABB93657	Abb93657 Herbicida
309	104	4.0	340	4	ABB62643	Abb62643 Drosophil	382	98	3.7	895	7	ABO65982	Abo65982 Klebsiell
310	104	4.0	458	4	AAU41311	Aau41311 Propionib	383	98	3.7	903	5	AAM49743	Aam49743 Synechoco
311	104	4.0	458	6	ABM37830	Abm37830 Propionib	384	98	3.7	1381	8	ADM57193	Adm57193 A thalian
312	104	4.0	1155	6	ABU19192	Abu19192 Protein e	385	98	3.7	1703	7	ADC10148	Adc10148 Human NOV
313	103.5	3.9	260	4	ABM00025	Abm00025 Allergen	386	98	3.7	2111	4	AAB66471	Aab66471 Protein e
314	103.5	3.9	578	5	ABR38860	Abr38860 A. niger	387	97.5	3.7	402	6	ABU31049	Abu31049 Protein e
315	103.5	3.9	805	6	ADA89636	Ada89636 Staphyloc	388	97.5	3.7	462	7	ABO79546	Abo79546 Pseudomon
316	103.5	3.9	932	6	ABU24586	Abu24586 Protein e	389	97.5	3.7	540	5	ABB76955	Abb76955 4-Hydroxy
317	103.5	3.9	1435	2	AAU49070	Aay49070 PolC gene	390	97.5	3.7	560	5	ABB76990	Abb76990 4-Hydroxy



391	97.5	3.7	581	6	ABU28069	Abu28069 Protein e	464	94	3.6	382	6	ABM38778	Abm38778 Propionib
392	97.5	3.7	674	7	ABR82629	Abr82629 Human RGS	465	94	3.6	639	5	ABP73694	Abp73694 Candida a
393	97.5	3.7	819	8	ABM81432	Abm81432 Tumour-as	466	94	3.6	817	4	AAG81478	Aag81478 S. epider
394	97.5	3.7	981	6	ADA33197	Ada33197 Acinetoba	467	94	3.6	817	4	AAG82217	Aag82217 S. epider
395	97.5	3.7	2000	6	ABR52622	Abr52622 Protein s	468	94	3.6	817	6	ABU43148	Abu43148 Protein e
396	97.5	3.7	2000	7	ADK62602	Adk62602 Disease t	469	94	3.6	823	5	ABP39236	Abp39236 Staphyloc
397	97	3.7	371	7	ADJ69524	Adj69524 Human hea	470	94	3.6	823	8	ADS05972	Ads05972 Staphyloc
398	97	3.7	4746	8	ADN17780	Adn17780 Bacterial	471	94	3.6	852	6	ABM67688	Abm67688 photorhab
399	96.5	3.7	372	5	ABB53873	Abb53873 Lactococc	472	94	3.6	876	6	ABM73510	Abm73510 Staphyloc
400	96.5	3.7	421	6	ABU23175	Abu23175 Protein e	473	94	3.6	901	6	ABU48667	Abu48667 Protein e
401	96.5	3.7	560	5	ABB76954	Abb76954 4-Hydroxy	474	94	3.6	1053	2	AAR88578	Aar88578 Chicken f
402	96.5	3.7	560	5	ABB76953	Abb76953 4-Hydroxy	475	94	3.6	1330	7	ADE61063	Ade61063 Rat Prote
403	96.5	3.7	740	6	ABM68618	Abm68618 Photorhab	476	94	3.6	1546	8	ADN17890	Adn17890 Bacterial
404	96.5	3.7	1622	5	ABU05503	Abu05503 M. tuberc	477	93.5	3.6	412	7	ADF07897	Adf07897 Bacterial
405	96.5	3.7	1622	6	ABU35909	Abu35909 Protein e	478	93.5	3.6	431	8	ADQ35183	Adq35183 Human TRI
406	96.5	3.7	4551	3	AAB18637	Aab18637 Amino aci	479	93.5	3.6	472	7	ABO74061	AbO74061 Pseudomon
407	96.5	3.7	4551	3	AY67201	Aay67201 Narbonoli	480	93.5	3.6	535	5	ABP38493	Abp38493 Staphyloc
408	96.5	3.7	4551	6	ABG71661	Abg71661 S. venezu	481	93.5	3.6	535	8	ADS04661	Ads04661 Staphyloc
409	96.5	3.7	4551	6	ADA09400	Ada09400 S. venezu	482	93.5	3.6	639	5	ABP53637	Abp53637 Maize cal
410	96.5	3.7	4551	7	ADH53444	Adh53444 Streptomy	483	93.5	3.6	655	4	AAB62031	Aab62031 Recombina
411	96.5	3.7	4613	3	AY77200	Aay77200 S. venezu	484	93.5	3.6	707	8	ADJ71961	Adj71961 Human PMM
412	96.5	3.7	4613	3	AY77192	Aay77192 S. venezu	485	93.5	3.6	763	6	ABU33126	Abu33126 Protein e
413	96.5	3.7	4613	8	ADL91916	Adl91916 Streptomy	486	93.5	3.6	1459	7	ADC26275	Adc26275 Human NOV
414	96.5	3.7	11877	8	ADL91934	Adl91934 Streptomy	487	93.5	3.6	1487	6	ABU20437	Abu20437 Protein e
415	96.5	3.7	12199	3	AY77180	Aay77180 S. venezu	488	93.5	3.6	1488	8	ADM97582	Adm97582 Human cal
416	96	3.7	485	8	ADS28138	Ads28138 Bacterial	489	93.5	3.6	1613	6	ABU49364	Abu49364 Protein e
417	96	3.7	584	4	ABG12694	Abg12694 Novel hum	490	93.5	3.6	1638	8	ADK71824	Adk71824 Human kin
418	96	3.7	584	4	ABG04938	Abg04938 Novel hum	491	93.5	3.6	1669	4	ABG13314	Abg13314 Novel hum
419	96	3.7	896	5	ABB08760	Abb08760 Synechoco	492	93.5	3.6	1719	5	AAE21707	Aae21707 Human PKI
420	96	3.7	1267	4	AAU54438	Aau54438 Propionib	493	93.5	3.6	1732	8	ADF89991	Adf89991 Human ser
421	96	3.7	1267	6	ABM50957	Abm50957 Propionib	494	93.5	3.6	1732	8	ADS93536	Ads93536 Human MRC
422	96	3.7	1448	5	ABP73615	Abp73615 Candida a	495	93.5	3.6	1770	5	AAE25099	Aae25099 Human kin
423	96	3.7	1707	6	AAE29910	Aae29910 Human tra	496	93	3.5	214	4	AAB94961	Aab94961 Human pro
424	96	3.7	1707	7	ADG17567	Adg17567 Human TRP	497	93	3.5	230	8	ADS11009	Ads11009 Human the
425	95.5	3.6	506	7	ADE34351	Ade34351 Human hyp	498	93	3.5	255	4	AAB60499	Aab60499 Human cel
426	95.5	3.6	506	8	ADK52100	Adk52100 Human ato	499	93	3.5	398	7	ADC96791	Adc96791 E. faeciu
427	95.5	3.6	506	8	ADN04834	Adn04834 Antipsori	500	93	3.5	501	2	AAW01044	Aaw01044 Y. pestis
428	95.5	3.6	506	8	ADO20065	Ado20065 Human PRO	501	93	3.5	515	8	ABM82622	Abm82622 Human dia
429	95.5	3.6	508	8	ADN25757	Adn25757 Bacterial	502	93	3.5	588	6	ABU39223	Abu39223 Protein e
430	95.5	3.6	880	8	ADR88902	Adr88902 Anopheles	503	93	3.5	646	6	ABU25463	Abu25463 Protein e
431	95.5	3.6	1029	8	ADN72299	Adn72299 Thale cre	504	93	3.5	686	4	AAU35250	Aau35250 Enterococ
432	95	3.6	408	2	AAW89442	Aaw89442 Mycoplasm	505	93	3.5	694	6	ABU28924	Abu28924 Protein e
433	95	3.6	409	5	AAE16137	Aae16137 Mycoplasm	506	93	3.5	767	6	ABR53431	Abr53431 Protein s
434	95	3.6	409	5	AAE16136	Aae16136 Mycoplasm	507	93	3.5	767	7	ADK64670	Adk64670 Disease t
435	95	3.6	409	5	AAE16134	Aae16134 Mycoplasm	508	93	3.5	768	4	AAU02405	Aau02405 Human nov
436	95	3.6	409	5	ABG31996	Abg31996 M. hominu	509	93	3.5	778	4	AAU02393	Aau02393 Human nov
437	95	3.6	409	8	ADP79608	Adp79608 Mycoplasm	510	93	3.5	788	4	AAU02406	Aau02406 Human nov
438	95	3.6	409	8	ADP79609	Adp79609 Mycoplasm	511	93	3.5	793	4	AAU02399	Aau02399 Human nov
439	95	3.6	409	8	ADP79607	Adp79607 Mycoplasm	512	93	3.5	798	4	AAU02394	Aau02394 Human nov
440	95	3.6	409	8	ADP79610	Adp79610 Mycoplasm	513	93	3.5	803	4	AAU02387	Aau02387 Human nov
441	95	3.6	506	5	AAE23112	Aae23112 Influenza	514	93	3.5	811	6	ABU20871	Abu20871 Protein e
442	95	3.6	851	8	ADQ66949	Adq66949 Novel hum	515	93	3.5	813	4	AAU02400	Aau02400 Human nov
443	95	3.6	867	6	ABU32276	Abu32276 Protein e	516	93	3.5	823	4	AAU02388	Aau02388 Human nov
444	95	3.6	876	6	ABU42445	Abu42445 Protein e	517	93	3.5	848	3	AAB43716	Aab43716 Human can
445	95	3.6	1376	4	ABB52592	Abb52592 Escherich	518	93	3.5	893	7	ADN95809	Adn95809 Human BEC
446	95	3.6	1416	5	ABU48526	Abu48526 Protein e	519	93	3.5	893	8	ABM81744	Abm81744 Tumour-as
447	94.5	3.6	172	5	ABP38582	Abp38582 Staphyloc	520	93	3.5	893	8	ABM81745	Abm81745 Tumour-as
448	94.5	3.6	172	8	ADS06312	Ads06312 Staphyloc	521	93	3.5	893	8	ADS17662	Ads17662 Human maj
449	94.5	3.6	402	4	AAU36006	Aau36006 Helicobac	522	93	3.5	896	2	AAW00733	Aaw00733 Human maj
450	94.5	3.6	478	4	AAG81837	Aag81837 S. epider	523	93	3.5	900	7	ADK40909	Adk40909 Novel hum
451	94.5	3.6	590	8	ADK60222	Adk60222 Angiogene	524	93	3.5	900	8	ADR15632	Adr15632 Kinase 39
452	94.5	3.6	590	8	ADK60523	Adk60523 Angiogene	525	93	3.5	904	8	ADS17741	Ads17741 HIV-Tat (
453	94.5	3.6	590	8	ADP73146	Adp73146 Angiogene	526	93	3.5	905	8	ADS17677	Ads17677 Cysteine
454	94.5	3.6	662	8	ADS44317	Ads44317 Bacterial	527	93	3.5	909	8	ADS17735	Ads17735 Human maj
455	94.5	3.6	787	4	AAG81127	Aag81127 Mycobacte	528	93	3.5	910	8	ADS17687	Ads17687 Polylysin
456	94.5	3.6	787	6	ABU36510	Abu36510 Protein e	529	93	3.5	913	4	AAU02407	Aau02407 Human nov
457	94.5	3.6	983	4	ABB70130	Abb70130 Drosophil	530	93	3.5	921	8	ADS17795	Ads17795 Polylysin
458	94.5	3.6	1169	6	ABU43125	Abu43125 Protein e	531	93	3.5	921	4	AAU02395	Aau02395 Human nov
459	94.5	3.6	1253	6	ABU24351	Abu24351 Protein e	532	93	3.5	923	8	ADS17685	Ads17685 Hist7 joi
460	94.5	3.6	2274	5	ABP30377	Abp30377 Streptoco	533	93	3.5	926	8	ADS17783	Ads17783 Polylysin
461	94.5	3.6	2278	5	ABP28340	Abp28340 Streptoco	534	93	3.5	938	4	AAU02401	Aau02401 Human nov
462	94	3.6	198	3	AAG33533	Aag33533 Arabidops	535	93	3.5	948	4	AAU02389	Aau02389 Human nov
463	94	3.6	382	4	AAU42259	Aau42259 Propionib	536	93	3.5	949	8	ADS17753	Ads17753 Human maj



537	93	3.5	966	8	ADS17791	Adsl17791 Polylysine	610	92	3.5	671	6	ABG72975	Abg72975 Human reg
538	93	3.5	989	8	ADS17695	Adsl17695 GAL4 pept	611	92	3.5	686	7	ADH87181	Adh87181 Enterococ
539	93	3.5	1000	8	ADS17769	Adsl17769 GAL4 + hu	612	92	3.5	687	5	ABB92504	Abb92504 Herbicida
540	93	3.5	1005	8	ADS17757	Adsl17757 GAL4+ante	613	92	3.5	879	6	ABU43686	Abu43686 Protein e
541	93	3.5	1024	8	ADS17701	Adsl17701 RNA bindi	614	92	3.5	908	5	ABP30892	Abp30892 Streptoco
542	93	3.5	1040	8	ADS17773	Adsl17773 MS2 pepti	615	92	3.5	927	5	ABP27156	Abp27156 Streptoco
543	93	3.5	1045	8	ADS17765	Adsl17765 GAL4 + hu	616	92	3.5	1059	7	ADE93714	Ade93714 Fava bean
544	93	3.5	1053	3	AAB07496	Aab07496 A T-cell	617	92	3.5	1160	8	ADS27129	Ads27129 Bacterial
545	93	3.5	1072	8	ADS17747	Adsl17747 Human maj	618	92	3.5	1160	8	ADS26746	Ads26746 Bacterial
546	93	3.5	1099	4	AAU02408	Aau02408 Human nov	619	92	3.5	1167	8	ADS26378	Ads26378 Bacterial
547	93	3.5	1109	4	AAU02396	Aau02396 Human nov	620	92	3.5	1997	4	AAU70671	Aau70671 Murine ot
548	93	3.5	1124	4	AAU02402	Aau02402 Human nov	621	92	3.5	2298	4	AAU70669	Aau70669 Murine co
549	93	3.5	1132	8	ADS17707	Adsl17707 Green flu	622	92	3.5	2371	4	AAU70670	Aau70670 Murine br
550	93	3.5	1134	4	AAU02390	Aau02390 Human nov	623	91.5	3.5	310	7	ADE12791	Adel12791 L. rhanno
551	93	3.5	1159	8	ADS17787	Adsl17787 Polylysine	624	91.5	3.5	381	4	AAG91096	Aag91096 C glutami
552	93	3.5	1162	4	AAU02409	Aau02409 Human nov	625	91.5	3.5	409	5	AAE16135	Aael16135 Mycoplasma
553	93	3.5	1172	4	AAU02397	Aau02397 Human nov	626	91.5	3.5	411	5	ABP73447	Abp73447 Candida a
554	93	3.5	1172	5	ABP74098	Abp74098 Human TRI	627	91.5	3.5	496	6	ABU27629	Abu27629 Protein e
555	93	3.5	1187	4	AAU02403	Aau02403 Human nov	628	91.5	3.5	504	8	ADS27419	Ads27419 Bacterial
556	93	3.5	1197	4	AAU02391	Aau02391 Human nov	629	91.5	3.5	514	8	ADN26350	Adn26350 Bacterial
557	93	3.5	1238	8	ADS17761	Adsl17761 GAL4 + hu	630	91.5	3.5	553	4	AAG89901	Aag89901 C glutami
558	93	3.5	1273	8	ADS17777	Adsl17777 MS2 pepti	631	91.5	3.5	553	7	ADL65923	Adl65923 C. glutam
559	93	3.5	1310	7	ADL95403	Adl95403 Rabbit en	632	91.5	3.5	679	3	AAB16685	Aab16685 Bacteriop
560	93	3.5	1544	4	AAU02410	Aau02410 Human nov	633	91.5	3.5	839	3	AAB56864	Aab56864 Human pro
561	93	3.5	1544	7	ADC83406	Adc83406 Human LTR	634	91.5	3.5	959	6	ABU49828	Abu49828 Protein e
562	93	3.5	1554	4	AAU02398	Aau02398 Human nov	635	91.5	3.5	1134	5	ABP29883	Abp29883 Streptoco
563	93	3.5	1554	7	ADC83401	Adc83401 Human LTR	636	91.5	3.5	1134	8	ADO10473	Ado10473 Group B S
564	93	3.5	1554	8	ADQ91195	Adq91195 Transient	637	91.5	3.5	1354	7	ADF74146	Adf74146 Human nov
565	93	3.5	1566	7	ADC83408	Adc83408 Human LTR	638	91.5	3.5	1416	8	ADR18229	Adr18229 Rat GOBLI
566	93	3.5	1566	7	ADC83403	Adc83403 Human LTR	639	91.5	3.5	1654	8	ADQ39529	Adq39529 Human myo
567	93	3.5	1566	7	ADC83405	Adc83405 Human LTR	640	91.5	3.5	1732	8	ADF95103	Adf95103 Rat serin
568	93	3.5	1566	8	ADQ91199	Adq91199 Rat TRPM	641	91.5	3.5	1732	8	ADF89992	Adf89992 Rat serin
569	93	3.5	1569	4	AAU02404	Aau02404 Human nov	642	91.5	3.5	2294	7	ADJ68907	Adj68907 Human hea
570	93	3.5	1579	4	AAU02392	Aau02392 Human nov	643	91.5	3.5	3418	2	AAW23287	Aaw23287 Human bre
571	93	3.5	1591	8	ADQ91197	Adq91197 MurineTRP	644	91.5	3.5	3418	2	AAW19211	Aaw19211 Human bre
572	93	3.5	1617	6	ABU33749	Abu33749 Protein e	645	91.5	3.5	3418	2	AAU04357	Aay04357 Human BRC
573	93	3.5	2773	8	ADN27223	Adn27223 Bacterial	646	91.5	3.5	3418	2	AAU04354	Aay04354 Human BRC
574	92.5	3.5	310	4	AAU17344	Aau17344 Novel sig	647	91.5	3.5	3418	2	AAU04355	Aay04355 Human BRC
575	92.5	3.5	310	7	ADB94052	Adb94052 Human nov	648	91.5	3.5	3418	2	ADJ68372	Adj68372 Human hea
576	92.5	3.5	370	2	AAU14924	Aay14924 Amino aci	649	91.5	3.5	3418	8	ADK67819	Adk67819 Human BRC
577	92.5	3.5	370	6	ABP70895	Abp70895 Mycobacte	650	91.5	3.5	3418	8	ADJ32561	Adj32561 Human BRC
578	92.5	3.5	391	5	AAG91034	Aag91034 C glutami	651	91.5	3.5	3418	8	ADL32565	Adl32565 Human BRC
579	92.5	3.5	393	5	ABB47374	Abb47374 Listeria	652	91.5	3.5	3423	4	ABG23417	Abg23417 Novel hum
580	92.5	3.5	457	6	ABM68419	Abm68419 Photorhab	653	91.5	3.5	4820	4	ABBS58592	Abbs58592 Drosophil
581	92.5	3.5	520	2	AAW36491	Aaw36491 Human TUL	654	91	3.5	246	4	AAE09045	Aae09045 Equine in
582	92.5	3.5	520	3	AAB26906	Aab26906 Human TUL	655	91	3.5	289	8	ADS41720	Ads41720 Bacterial
583	92.5	3.5	623	8	ADK46809	Adk46809 Streptoco	656	91	3.5	315	6	ABU28121	Abu28121 Protein e
584	92.5	3.5	632	7	ADC07814	Adc07814 Rice prot	657	91	3.5	478	4	ABB69816	Abb69816 Drosophil
585	92.5	3.5	633	8	ADR95456	Adr95456 Novel S.	658	91	3.5	505	6	ABU18380	Abu18380 Protein e
586	92.5	3.5	698	7	ADG47626	Adg47626 Human rib	659	91	3.5	656	7	ABO76389	AbO76389 Pseudomon
587	92.5	3.5	745	4	AAB65611	Aab65611 Novel pro	660	91	3.5	706	7	ADH87649	Adh87649 Enterococ
588	92.5	3.5	745	8	ADI29217	Adi29217 Human MAR	661	91	3.5	737	7	ADL95399	Adl95399 Rabbit te
589	92.5	3.5	968	7	ABO70179	AbO70179 Pseudomon	662	91	3.5	871	6	ABU23674	Abu23674 Protein e
590	92.5	3.5	987	4	ABG01594	Abg01594 Novel hum	663	91	3.5	917	2	AAR36821	Aar36821 PE bindin
591	92.5	3.5	1303	4	ABG12230	Abg12230 Novel hum	664	91	3.5	917	2	AAR32469	Aar32469 PE bindin
592	92.5	3.5	1501	5	ABP52140	Abp52140 Saccharom	665	91	3.5	1010	3	AAU44688	Aay44688 Partial n
593	92.5	3.5	1501	8	ADN18953	Adn18953 Bacterial	666	91	3.5	1038	4	ABG04908	Abg04908 Novel hum
594	92.5	3.5	2042	7	ADM25528	Adm25528 Hyperther	667	91	3.5	1038	4	ABG25053	Abg25053 Novel hum
595	92.5	3.5	2106	7	ADJ70287	Adj70287 Human hea	668	91	3.5	1054	7	ADB64784	Adb64784 Human pro
596	92	3.5	246	4	AAE09047	Aae09047 Equine in	669	91	3.5	1071	8	ADN23806	Adn23806 Bacterial
597	92	3.5	327	5	ABP28720	Abp28720 Streptoco	670	91	3.5	1077	3	AAB07497	Aab07497 A T-cell
598	92	3.5	423	4	AAB96331	Aab96331 Putative	671	91	3.5	1098	7	ADJ70147	Adj70147 Human hea
599	92	3.5	511	5	AAE20629	Aae20629 Human gen	672	91	3.5	1268	8	ADQ66160	Adq66160 Novel hum
600	92	3.5	511	5	ABG65261	Abg65261 Human alb	673	91	3.5	1274	4	AAB47329	Aab47329 FCTR6. 8/
601	92	3.5	511	6	ABG72986	Abg72986 Human RGS	674	91	3.5	1286	4	ABG25629	Abg25629 Novel hum
602	92	3.5	511	8	ADL78528	Adl78528 Albumin f	675	91	3.5	1286	4	ABG25994	Abg25994 Novel hum
603	92	3.5	539	6	ABG72985	Abg72985 Human RGS	676	91	3.5	1286	4	ABG25086	Abg25086 Novel hum
604	92	3.5	571	6	ABG72984	Abg72984 Human RGS	677	91	3.5	1347	8	ADP55059	Adp55059 Human PRO
605	92	3.5	588	4	AAU35412	Aau35412 Haemophil	678	91	3.5	1367	8	ADQ66090	Adq66090 Novel hum
606	92	3.5	588	6	ABU30211	Abu30211 Protein e	679	91	3.5	1680	8	ADJ35146	Adj35146 Xylanase
607	92	3.5	601	6	ABG72983	Abg72983 Human RGS	680	91	3.5	1701	5	ABB08024	Abb08024 Human Rho
608	92	3.5	624	6	ABG72982	Abg72982 Human RGS	681	91	3.5	1707	4	ABG07400	Abg07400 Novel hum
609	92	3.5	643	6	ABG72981	Abg72981 Human RGS	682	90.5	3.5	178	3	AAG33534	Aag33534 Arabidops

683	90.5	3.5	224	6	ABU18525	Abu18525 Protein e	756	89	3.4	333	5	ABG99179	Abg99179 Human end
684	90.5	3.5	500	4	AAU38171	Aau38171 Salmonell	757	89	3.4	333	8	ADJ83838	Adj83838 HERV-K HM
685	90.5	3.5	500	6	ABU47717	Abu47717 Protein e	758	89	3.4	334	8	ADJ83895	Adj83895 HERV-K HM
686	90.5	3.5	641	8	ADJ48678	Adj48678 Oil-assoc	759	89	3.4	335	8	ADJ83896	Adj83896 HERV-K HM
687	90.5	3.5	714	6	ABM68578	Abm68578 Photorhab	760	89	3.4	409	6	ABU41410	Abu41410 Protein e
688	90.5	3.5	1167	2	AAW22470	Aaw22470 Streptoco	761	89	3.4	428	4	AAU51162	Aau51162 Propionib
689	90.5	3.5	1167	3	AAB01264	Aab01264 SCPA12 pe	762	89	3.4	428	6	ABM51681	Abm51681 Propionib
690	90.5	3.5	1496	8	ADM57229	Adm57229 A thalian	763	89	3.4	453	6	ADB07082	Adb07082 Alloiococ
691	90.5	3.5	1507	8	ADI28429	Adi28429 Arabidops	764	89	3.4	467	6	ADB07084	Adb07084 Alloiococ
692	90.5	3.5	1513	6	ABU36934	Abu36934 Protein e	765	89	3.4	589	6	ABM68874	Abm68874 Photorhab
693	90.5	3.5	1679	6	ABR52863	Abr52863 Protein s	766	89	3.4	665	5	AAU10665	Aau10665 Human LiC
694	90.5	3.5	1679	7	ADK62332	Adk62332 Disease t	767	89	3.4	702	6	ABU24641	Abu24641 Protein e
695	90.5	3.5	1963	5	ABB93446	Abb93446 Herbicida	768	89	3.4	732	7	ADL95398	Adl95398 Mouse tes
696	90.5	3.5	3418	3	AAU77819	Aay77819 BRCA2 pro	769	89	3.4	764	8	ADO59889	Ado59889 Mouse ang
697	90	3.4	432	5	AAU84339	Aau84339 Protein H	770	89	3.4	790	7	ADC19720	Adc19720 H. influe
698	90	3.4	432	6	ABU56546	Abu56546 Lung canc	771	89	3.4	914	6	ABU25821	Abu25821 Protein e
699	90	3.4	432	8	ADQ35179	Adq35179 Human TRI	772	89	3.4	989	4	AAU33401	Aau33401 Enterococ
700	90	3.4	480	2	AAW01045	Aaw01045 Y. pestis	773	89	3.4	1120	6	ABU42979	Abu42979 Protein e
701	90	3.4	495	2	AAW88482	Aaw88482 Bovine pa	774	89	3.4	1312	7	ADL95401	Adl95401 Mouse end
702	90	3.4	496	7	ADG67846	Adg67846 Human TRP	775	89	3.4	1725	5	ABG91809	Abg91809 Human int
703	90	3.4	621	5	ABB49284	Abb49284 Listeria	776	89	3.4	15281	2	AAR44929	Aar44929 T. niyeum
704	90	3.4	621	6	ABU32926	Abu32926 Protein e	777	88.5	3.4	150	5	ABP02292	Abp02292 Human ORP
705	90	3.4	664	6	ADA33938	Ada33938 Acinetoba	778	88.5	3.4	245	4	AAE09051	Aae09051 Equine in
706	90	3.4	672	8	ADN26406	Adn26406 Bacterial	779	88.5	3.4	396	5	ABB48811	Abb48811 Listeria
707	90	3.4	799	5	ABP73572	Abp73572 Candida a	780	88.5	3.4	396	6	ABU32470	Abu32470 Protein e
708	90	3.4	1313	7	ADL95402	Adl95402 Rat endot	781	88.5	3.4	482	8	ADN18415	Adn18415 Bacterial
709	90	3.4	1799	5	ABB84545	Abb84545 Transient	782	88.5	3.4	500	8	ADN18857	Adn18857 Bacterial
710	90	3.4	1939	7	ADG67791	Adg67791 Human TRP	783	88.5	3.4	554	7	ADB70226	Adb70226 C. neofor
711	90	3.4	1970	7	ADG67789	Adg67789 Human TRP	784	88.5	3.4	563	6	AAO16117	Aao16117 Human can
712	90	3.4	1974	7	ADG67793	Adg67793 Human TRP	785	88.5	3.4	563	6	ABJ19253	Abj19253 Human can
713	90	3.4	2000	5	ABB84546	Abb84546 Transient	786	88.5	3.4	563	7	ADF18685	Adf18685 Human reg
714	90	3.4	2004	6	AAE32072	Aae32072 Human TRI	787	88.5	3.4	563	7	ADJ70351	Adj70351 Human hea
715	90	3.4	2017	7	ADG67787	Adg67787 Human TRP	788	88.5	3.4	603	5	ABB48333	Abb48333 Listeria
716	90	3.4	4725	4	ABG23837	Abg23837 Novel hum	789	88.5	3.4	617	3	AAG30569	Aag30569 Arabidops
717	90	3.4	4977	4	ABG17057	Abg17057 Novel hum	790	88.5	3.4	623	4	AAU37906	Aau37906 Streptoco
718	90	3.4	7201	4	ABB71136	Abb71136 Drosophil	791	88.5	3.4	623	6	ABU46161	Abu46161 Protein e
719	89.5	3.4	351	4	ABG25481	Abg25481 Novel hum	792	88.5	3.4	641	3	AAG30568	Aag30568 Arabidops
720	89.5	3.4	372	5	ABB73530	Abb73530 M vaccae	793	88.5	3.4	645	3	AAG30567	Aag30567 Arabidops
721	89.5	3.4	401	2	AAU33270	Aay33270 Plasmid p	794	88.5	3.4	718	4	AAU54939	Aau54939 Propionib
722	89.5	3.4	401	2	AAU33264	Aay33264 E. coli b	795	88.5	3.4	718	6	ABM51458	Abm51458 Propionib
723	89.5	3.4	401	2	AAU33268	Aay33268 Plasmid p	796	88.5	3.4	735	7	ADF18691	Adf18691 Human reg
724	89.5	3.4	401	2	AAW92938	Aaw92938 DE1973127	797	88.5	3.4	759	7	ABO67243	AbO67243 Klebsiell
725	89.5	3.4	401	2	AAW92934	Aaw92934 E. coli b	798	88.5	3.4	873	8	ADS42575	Ads42575 Bacterial
726	89.5	3.4	401	2	AAW92936	Aaw92936 DE1973127	799	88.5	3.4	901	6	ABM72914	Abm72914 Staphyloc
727	89.5	3.4	416	6	ABU22726	Abu22726 Protein e	800	88.5	3.4	1072	4	AAG70871	Aag70871 C albican
728	89.5	3.4	426	7	ADH88873	Adh88873 Enterococ	801	88.5	3.4	1078	6	ABM65857	Abm65857 Propionib
729	89.5	3.4	460	6	ABU48650	Abu48650 Protein e	802	88.5	3.4	1249	4	AAU02957	Aau02957 Angiotens
730	89.5	3.4	478	8	ADS41883	Ads41883 Bacterial	803	88.5	3.4	1252	4	AAU02985	Aau02985 Angiotens
731	89.5	3.4	478	8	ADN18593	Adn18593 Bacterial	804	88.5	3.4	1266	6	ABU25979	Abu25979 Protein e
732	89.5	3.4	512	8	ADS17779	Ads17779 MS2 + hum	805	88.5	3.4	1606	6	ABR41651	AbR41651 Human DIT
733	89.5	3.4	530	4	AAG99947	Aag99947 ERA bindi	806	88.5	3.4	1648	5	ADI39480	Adi39480 Arabidops
734	89.5	3.4	695	5	ABP65706	Abp65706 Bifidobac	807	88.5	3.4	1752	3	AAG50492	Aag50492 Arabidops
735	89.5	3.4	706	6	ABU18600	Abu18600 Protein e	808	88.5	3.4	2141	6	ABR41636	AbR41636 Human DIT
736	89.5	3.4	715	6	ABU36246	Abu36246 Protein e	809	88.5	3.4	2991	7	ADG42624	Adg42624 Human FAT
737	89.5	3.4	815	8	ADL99358	Adl99358 Nanostruc	810	88.5	3.4	4263	5	ABB97541	Abb97541 Novel hum
738	89.5	3.4	982	6	ABU37382	Abu37382 Protein e	811	88.5	3.4	4264	7	ADM47281	Adm47281 Protocadh
739	89.5	3.4	1007	6	ABP80992	Abp80992 N. gonorr	812	88.5	3.4	4349	5	AAU79940	Aau79940 Human pro
740	89.5	3.4	1070	5	ABP73552	Abp73552 Candida a	813	88.5	3.4	4349	5	ABB97540	Abb97540 Novel hum
741	89.5	3.4	1090	5	ABP28458	Abp28458 Streptoco	814	88.5	3.4	4349	6	AAO26792	Aao26792 Human cad
742	89.5	3.4	1179	5	ABB47667	Abb47667 Listeria	815	88.5	3.4	4349	6	ABU62305	Abu62305 Human Cad
743	89.5	3.4	1179	6	ABU32719	Abu32719 Protein e	816	88.5	3.4	4349	7	ADG42571	Adg42571 Novel hum
744	89.5	3.4	1181	3	AAAB01266	Aab01266 SCPA1 pep	817	88.5	3.4	4349	7	ADG42621	Adg42621 Human pro
745	89.5	3.4	1439	6	ABU34837	Abu34837 Protein e	818	88.5	3.4	4349	7	ADG42620	Adg42620 Human FAT
746	89.5	3.4	1724	3	AAU54373	Aay54373 cDNA sequ	819	88.5	3.4	4349	7	ADJ69933	Adj69933 Human hea
747	89.5	3.4	1724	4	AAB51022	Aab51022 Human min	820	88.5	3.4	4349	7	ADM47279	Adm47279 Protocadh
748	89.5	3.4	1724	7	ADB46006	Adb46006 Human min	821	88.5	3.4	4349	8	ADM74201	Adm74201 Human NOV
749	89.5	3.4	1724	8	ADS17664	Ads17664 Human pol	822	88	3.4	75	3	AAG03404	Aag03404 Human sec
750	89.5	3.4	1736	8	ADS17713	Ads17713 Cysteine	823	88	3.4	335	8	ADP07863	Adp07863 Human sec
751	89.5	3.4	1820	8	ADS17717	Ads17717 GAL4 pept	824	88	3.4	357	4	AAB48844	Aab48844 Human RAP
752	89.5	3.4	1854	8	ADS17725	Ads17725 MS2 pepti	825	88	3.4	357	5	AAO18621	Aao18621 Human rec
753	89.5	3.4	1961	8	ADS17721	Ads17721 Green flu	826	88	3.4	357	7	ADD44975	Add44975 Human Pro
754	89.5	3.4	2274	8	ADS17731	Ads17731 Luciferas	827	88	3.4	357	7	ADD44979	Add44979 Human Pro
755	89	3.4	237	5	ABP41753	Abp41753 Human ova	828	88	3.4	357	7	ADD44971	Add44971 Human Pro



829 88 3.4 357 7 ADD44967 Add44967 Human Pro 902 87.5 3.3 1052 8 ADL97782 Adl97782 Human foc  
830 88 3.4 357 7 ADD44963 Add44963 Human Pro 903 87.5 3.3 1052 8 ADS00186 Ads00186 Human foc  
831 88 3.4 357 7 ADD44959 Add44959 Human Pro 904 87.5 3.3 1160 4 AAU33984 Aau33984 Staphyloc  
832 88 3.4 357 7 ADD46492 Add46492 Human Pro 905 87.5 3.3 1168 4 AAU36558 Aau36558 Staphyloc  
833 88 3.4 357 8 ADJ75361 Adj75361 Marker ge 906 87.5 3.3 1168 6 ABU16113 Abul6113 Protein e  
834 88 3.4 357 8 ADQ91471 Adq91471 Amino aci 907 87.5 3.3 1168 6 ABM71924 Abm71924 Staphyloc  
835 88 3.4 357 8 ADP23135 Adp23135 PRO polyp 908 87.5 3.3 1181 5 ABP25823 Abp25823 Streptoco  
836 88 3.4 364 6 ADA35354 Ada35354 Acinetoba 909 87.5 3.3 1181 8 ADR83967 Adr83967 S. pyogen  
837 88 3.4 399 6 AEM69223 Abm69223 Photorhab 910 87.5 3.3 1234 6 ABU36564 Abu36564 Protein e  
838 88 3.4 467 4 ABB60624 ABB60624 Drosophil 911 87.5 3.3 1234 6 ABU34752 Abu34752 Protein e  
839 88 3.4 505 2 AAY19806 Aay19806 B. burgdo 912 87.5 3.3 1265 5 AAO20501 Aao20501 Protein o  
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841 88 3.4 563 8 ADGI2800 Adg12800 Human rho 914 87.5 3.3 1306 2 AAW68155 Aaw68155 Human ang  
842 88 3.4 576 5 ABB55505 ABB55505 Lactococc 915 87.5 3.3 1306 6 ABU07478 Abu07478 Protein d  
843 88 3.4 616 7 ADB64177 Adb64177 Human pro 916 87.5 3.3 1306 6 AAE36412 Aae36412 Human ACE  
844 88 3.4 653 5 ABB47763 Abb47763 Listeria 917 87.5 3.3 1306 7 ADL95400 Adl95400 Human end  
845 88 3.4 682 8 ADQ39604 Adq39604 Human myo 918 87.5 3.3 1858 7 ABO64863 Abo64863 Klebsiell  
846 88 3.4 682 8 ADQ39605 Adq39605 Human myo 919 87.5 3.3 1863 5 AAG79434 Aag79434 Mouse LTR  
847 88 3.4 687 4 ABG25201 Abg25201 Novel hum 920 87.5 3.3 1863 6 ABU62066 Abu62066 Mouse mel  
848 88 3.4 721 5 ABG25155 Abg25155 Novel hum 921 87.5 3.3 3313 4 AAU30134 Aau30134 Novel hum  
849 88 3.4 721 6 ABU32850 Abu32850 Listeria 922 87.5 3.3 4264 8 ADM74227 Adm74227 Human NOV  
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851 88 3.4 779 7 ADE56005 Ade56005 Human Pro 924 87.5 3.3 6815 4 ABB66811 Abb66811 Drosophil  
852 88 3.4 779 7 ADJ68276 Adj68276 Human hea 925 87 3.3 139 6 ADA36040 Ada36040 Acinetoba  
853 88 3.4 780 6 ABU07399 Abu07399 Protein d 926 87 3.3 399 4 AAB96764 Aab96764 Putative  
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855 88 3.4 780 7 ADN95774 Adn95774 Human BEC 928 87 3.3 444 3 AAY49315 Aay49315 Human Z-d  
856 88 3.4 1121 4 ABB63178 Abb63178 Drosophil 929 87 3.3 444 4 AAB74668 Aab74668 Human pro  
857 88 3.4 1241 6 ABU24033 Abu24033 Protein e 930 87 3.3 469 3 AAB10655 Aab10655 BPV1 Ll f  
858 88 3.4 1725 6 ABO14754 Abo14754 Novel hum 931 87 3.3 508 8 ADF77070 Adf77070 Seryl-tRN  
859 88 3.4 4142 4 AAU31616 Aau31616 Novel hum 932 87 3.3 514 6 ABM04796 Abm04796 Human ser  
860 87.5 3.3 160 4 AAB47152 Aab47152 S. aureus 933 87 3.3 514 8 ADF77073 Adf77073 Seryl-tRN  
861 87.5 3.3 160 6 ABM73238 Abm73238 Staphyloc 934 87 3.3 514 8 ABM80117 Abm80117 Tumour-as  
862 87.5 3.3 245 4 AAE09049 Aae09049 Equine in 935 87 3.3 545 4 ABG01445 Abg01445 Novel hum  
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899 87.5 3.3 1052 7 ADF45056 Adf45056 Human kin 971 86.5 3.3 240 8 ADS26565 Ads26565 Bacterial  
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974 86.5 3.3 334 8 ADN17862 Adn17862 Bacterial

1052 8 ADL97782 Adl97782 Human foc  
1052 8 ADS00186 Ads00186 Human foc  
1160 4 AAU33984 Aau33984 Staphyloc  
1168 4 AAU36558 Aau36558 Staphyloc  
1168 6 ABU16113 Abul6113 Protein e  
1168 6 ABM71924 Abm71924 Staphyloc  
1181 5 ABP25823 Abp25823 Streptoco  
1181 8 ADR83967 Adr83967 S. pyogen  
1234 6 ABU36564 Abu36564 Protein e  
1234 6 ABU34752 Abu34752 Protein e  
1265 5 AAO20501 Aao20501 Protein o  
1306 2 AAR04111 Aar04111 Human ang  
1306 2 AAW68155 Aaw68155 Human ang  
1306 6 ABU07478 Abu07478 Protein d  
1306 6 AAE36412 Aae36412 Human ACE  
1306 7 ADL95400 Adl95400 Human end  
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1863 5 AAG79434 Aag79434 Mouse LTR  
1863 6 ABU62066 Abu62066 Mouse mel  
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6685 4 ABG23030 Abg23030 Novel hum  
6815 4 ABB66811 Abb66811 Drosophil  
139 6 ADA36040 Ada36040 Acinetoba  
399 4 AAB96764 Aab96764 Putative  
399 8 ADS43117 Ads43117 Bacterial  
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444 4 AAB74668 Aab74668 Human pro  
469 3 AAB10655 Aab10655 BPV1 Ll f  
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514 6 ABM04796 Abm04796 Human ser  
514 8 ADF77073 Adf77073 Seryl-tRN  
514 8 ABM80117 Abm80117 Tumour-as  
545 4 ABG01445 Abg01445 Novel hum  
571 3 AAG16038 Aag16038 Arabidops  
571 3 AAG48655 Aag48655 Arabidops  
646 5 ABB92838 Abb92838 Herbicida  
663 7 ADF04165 Adf04165 Bacterial  
704 3 AAG48654 Aag48654 Arabidops  
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726 3 AAG16036 Aag16036 Arabidops  
726 3 AAG48653 Aag48653 Arabidops  
738 8 ADS27920 Ads27920 Bacterial  
856 3 AAG49655 Aag49655 Arabidops  
876 4 AAU37030 Aau37030 Staphyloc  
893 2 AAW84011 Aaw84011 Tne DNA p  
893 2 AAW83995 Aaw83995 Tne DNA p  
985 4 AAG90623 Aag90623 C glutami  
989 6 ABU14646 Abul14646 Protein e  
1069 6 ABU43694 Abu43694 Protein e  
1107 3 AAB29693 Aab29693 Mouse apo  
1114 7 ADB70296 Adb70296 C. neofo  
1163 3 AAY71384 Aay71384 Alternati  
1224 6 ABR52763 Abr52763 Protein s  
1224 7 ADK62094 Adk62094 Disease t  
1224 8 ADS43949 Ads43949 Bacterial  
1443 4 AAU33508 Aau33508 Enterococ  
1451 4 AAU35141 Aau35141 Enterococ  
1451 6 ABU14560 Abu14560 Protein e  
1456 7 ADH88542 Adh88542 Enterococ  
1507 6 ABU23883 Abu23883 Protein e  
1507 7 ADC47034 Adc47034 Mouse LTR  
1962 3 AAB29694 Aab29694 Mouse FLA  
2438 4 ABB59970 Abb59970 Drosophil  
2438 8 ADQ89742 Adq89742 Antagonis  
4623 4 ABB71106 Abb71106 Drosophil  
240 8 ADS26942 Ads26942 Bacterial  
240 8 ADS26565 Ads26565 Bacterial  
267 2 AAR63137 Aar63137 Porcine p  
323 6 ABU27643 Abu27643 Protein e  
334 8 ADN17862 Adn17862 Bacterial



975	86.5	3.3	368	6	ABU22554	Abu22554 Protein e	1048	86	3.3	470	8	ADS28317	Ads28317 Bacterial
976	86.5	3.3	403	2	AAR33251	Aar33251 Expressio	1049	86	3.3	520	8	ADN24026	Adn24026 Bacterial
977	86.5	3.3	411	8	ADN73371	Adn73371 Thale cre	1050	86	3.3	520	8	ADN24025	Adn24025 Bacterial
978	86.5	3.3	468	5	ABB93008	Abb93008 Herbicida	1051	86	3.3	573	2	AAR77859	Aar77859 S. clavul
979	86.5	3.3	468	5	ABB93002	Abb93002 Herbicida	1052	86	3.3	573	6	AAE14856	Aae14856 S. clavul
980	86.5	3.3	468	5	ABB93011	Abb93011 Herbicida	1053	86	3.3	574	4	AAE07907	Aae07907 S. clavul
981	86.5	3.3	468	5	ABB93005	Abb93005 Herbicida	1054	86	3.3	574	6	ABU62215	Abu62215 Clavulani
982	86.5	3.3	468	5	ABB93004	Abb93004 Herbicida	1055	86	3.3	574	7	ADD26433	Add26433 Streptomy
983	86.5	3.3	468	5	ABB93006	Abb93006 Herbicida	1056	86	3.3	574	7	ADG47778	Adg47778 Streptomy
984	86.5	3.3	468	5	ABB93010	Abb93010 Herbicida	1057	86	3.3	587	2	AAW10597	Aaw10597 Bst DNA p
985	86.5	3.3	468	5	ABB93003	Abb93003 Herbicida	1058	86	3.3	588	5	ABG92810	Abg92810 Protein e
986	86.5	3.3	468	5	ABB93007	Abb93007 Herbicida	1059	86	3.3	618	5	ABB09169	Abb09169 Methylomo
987	86.5	3.3	468	5	ABB93012	Abb93012 Herbicida	1060	86	3.3	618	5	ABG61554	Abg61554 High grow
988	86.5	3.3	468	5	ABB93009	Abb93009 Herbicida	1061	86	3.3	638	6	ABU41920	Abu41920 Protein e
989	86.5	3.3	468	5	ABB93013	Abb93013 Herbicida	1062	86	3.3	658	6	ABU36293	Abu36293 Protein e
990	86.5	3.3	468	8	ADN20712	Adn20712 Bacterial	1063	86	3.3	682	4	ABB58891	Abb58891 Drosophil
991	86.5	3.3	471	7	ADC95002	Adc95002 E. faeciu	1064	86	3.3	695	4	AAU33237	Aau33237 Novel hum
992	86.5	3.3	516	5	AAU75169	Aau75169 Mouse ROR	1065	86	3.3	702	4	AAG98343	Aag98343 Escherich
993	86.5	3.3	516	8	ADP05679	Adp05679 Mouse nuc	1066	86	3.3	702	6	ABU14832	Abu14832 Protein e
994	86.5	3.3	527	4	ABG15443	Abg15443 Novel hum	1067	86	3.3	760	6	ABU23243	Abu23243 Protein e
995	86.5	3.3	529	2	AAR97547	Aar97547 Arabidops	1068	86	3.3	764	8	ADP84542	Adp84542 Human bre
996	86.5	3.3	594	4	AAB84334	Aab84334 Amino aci	1069	86	3.3	765	6	ADB23036	Adb23036 Corn meth
997	86.5	3.3	594	8	ADK71013	Adk71013 Human met	1070	86	3.3	795	4	AAE12811	Aae12811 Corn isop
998	86.5	3.3	625	4	ABB64289	Abb64289 Drosophil	1071	86	3.3	795	5	ABB78226	Abb78226 Amino aci
999	86.5	3.3	625	6	AAE36100	Aae36100 Drosophil	1072	86	3.3	847	8	ADN18706	Adn18706 Bacterial
1000	86.5	3.3	635	6	ABU47175	Abu47175 Protein e	1073	86	3.3	881	6	ABU49500	Abu49500 Protein e
1001	86.5	3.3	705	6	ABU49632	Abu49632 Protein e	1074	86	3.3	902	6	ABR41754	Abr41754 Human DiT
1002	86.5	3.3	719	6	ABU10383	Abu10383 Mouse pha	1075	86	3.3	911	2	AAR10333	Aar10333 Deduced s
1003	86.5	3.3	732	6	ABU26932	Abu26932 Protein e	1076	86	3.3	1163	5	ABB81074	Abb81074 Rat neuro
1004	86.5	3.3	735	7	ADF18693	Adf18693 Zebrafish	1077	86	3.3	1163	8	ADO26399	Ado26399 Rat trunc
1005	86.5	3.3	826	6	ADA36228	Ada36228 Acinetoba	1078	86	3.3	1163	8	ADP45572	Adp45572 Rat NogoA
1006	86.5	3.3	888	6	ABM68848	Abm68848 Photorhab	1079	86	3.3	1509	5	ABB07586	Abb07586 Human Zne
1007	86.5	3.3	1154	8	ADS10785	Ads10785 Human the	1080	86	3.3	3896	8	ADI39291	Adi39291 S. hygros
1008	86.5	3.3	1169	8	ADS44498	Ads44498 Bacterial	1081	85.5	3.3	131	6	AAE31506	Aae31506 Latex hev
1009	86.5	3.3	1204	8	ADS10784	Ads10784 Human the	1082	85.5	3.3	258	3	AAB11959	Aab11959 Glycated
1010	86.5	3.3	1357	6	ABU39889	Abu39889 Protein e	1083	85.5	3.3	259	8	ADP12473	Adp12473 Protein e
1011	86.5	3.3	1448	6	ABU38544	Abu38544 Protein e	1084	85.5	3.3	259	8	ADO19386	Ado19386 Human PRO
1012	86.5	3.3	1627	7	ABO80117	Abo80117 Pseudomon	1085	85.5	3.3	259	8	ABO84887	Abo84887 Human can
1013	86.5	3.3	1651	5	ABG66725	Abg66725 Human nov	1086	85.5	3.3	259	8	ABO84885	Abo84885 Human can
1014	86.5	3.3	1664	7	ADE47740	Ade47740 Human NOV	1087	85.5	3.3	259	8	ABO84886	Abo84886 Human can
1015	86.5	3.3	1664	8	ADJ79010	Adj79010 Human NOV	1088	85.5	3.3	259	8	ABO84888	Abo84888 Human can
1016	86.5	3.3	1675	3	AAB42658	Aab42658 Human ORF	1089	85.5	3.3	270	5	ABB97202	Abb97202 Novel hum
1017	86.5	3.3	1856	5	ADH48724	Adh48724 NOV4A pro	1090	85.5	3.3	322	7	ADM25679	Adm25679 Hyperther
1018	86.5	3.3	1864	5	AAU79166	Aau79166 Human mel	1091	85.5	3.3	364	6	ABU29969	Abu29969 Protein e
1019	86.5	3.3	1864	5	AAE21179	Aae21179 Human TRI	1092	85.5	3.3	388	7	ABO62697	Abo62697 Klebsiell
1020	86.5	3.3	1864	6	ABU62065	Abu62065 Human mel	1093	85.5	3.3	412	8	ADS12038	Ads12038 Human the
1021	86.5	3.3	1865	3	AAU95435	Aay95435 Human cal	1094	85.5	3.3	412	8	ADS12039	Ads12039 Human the
1022	86.5	3.3	1865	5	AAG79435	Aag79435 Human LTR	1095	85.5	3.3	444	6	ABM70300	Abm70300 Photorhab
1023	86.5	3.3	1865	5	AAG79433	Aag79433 Human LTR	1096	85.5	3.3	594	2	AAU14049	Aay14049 G. oxydan
1024	86.5	3.3	1885	5	AAE18952	Aae18952 Human tra	1097	85.5	3.3	633	4	ABG16690	Abg16690 Novel hum
1025	86.5	3.3	1885	7	ADE31711	Ade31711 Human 186	1098	85.5	3.3	633	3	AAE20543	Aab20543 Bacillus
1026	86.5	3.3	1885	8	ADL14181	Adl14181 Novel hum	1099	85.5	3.3	633	3	AAE20542	Aab20542 Synchocy
1027	86.5	3.3	1885	8	ADQ88182	Adq88182 Human 210	1100	85.5	3.3	633	5	AAO21848	Aao21848 Isoprenoi
1028	86	3.3	222	7	ADH86408	Adh86408 Enterococ	1101	85.5	3.3	633	8	ADS44770	Ads44770 Bacterial
1029	86	3.3	264	6	ABU25473	Abu25473 Protein e	1102	85.5	3.3	655	4	AAE96088	Aab96088 Putative
1030	86	3.3	304	7	ADJ70107	Adj70107 Human hea	1103	85.5	3.3	696	6	ABU24188	Abu24188 Protein e
1031	86	3.3	330	5	ABP27121	Abp27121 Streptoco	1104	85.5	3.3	724	7	ADM25891	Adm25891 Hyperther
1032	86	3.3	330	6	ABU46776	Abu46776 Protein e	1105	85.5	3.3	806	4	AAE94052	Aab94052 Human pro
1033	86	3.3	334	5	ABP60869	Abp60869 Neurospor	1106	85.5	3.3	812	8	ADH22554	Adh22554 Human tra
1034	86	3.3	334	6	AAO20620	Aao20620 Thioeredox	1107	85.5	3.3	843	2	AAR67760	Aar67760 Lys-amino
1035	86	3.3	334	6	AAO20629	Aao20629 Thioeredox	1108	85.5	3.3	849	7	ADF05476	Adf05476 Bacterial
1036	86	3.3	334	7	ADD26555	Add26555 N. crassa	1109	85.5	3.3	867	4	AAE96297	Aab96297 Putative
1037	86	3.3	334	8	ADM30945	Adm30945 N. crassa	1110	85.5	3.3	867	6	ABU27238	Abu27238 Protein e
1038	86	3.3	363	4	AAE52357	Aam52357 NDP-hexos	1111	85.5	3.3	867	8	ADJ49942	Adj49942 Oil-assoc
1039	86	3.3	363	5	ABG91574	Abg91574 Purine/py	1112	85.5	3.3	906	6	ABM67675	Abm67675 Photorhab
1040	86	3.3	381	3	ABG91573	Abg91573 Purine/py	1113	85.5	3.3	1014	4	AAG90902	Aag90902 C glutami
1041	86	3.3	381	3	AAB14144	Aab14144 Bordetell	1114	85.5	3.3	1105	8	ADN20163	Adn20163 Bacterial
1042	86	3.3	393	8	ADS43952	Ads43952 Bacterial	1115	85.5	3.3	1162	6	ABU40048	Abu40048 Protein e
1043	86	3.3	445	2	AAR78275	Aar78275 Chicken T	1116	85.5	3.3	1179	7	ABO69149	Abo69149 Pseudomon
1044	86	3.3	459	5	ABB99393	Abb99393 Amino aci	1117	85.5	3.3	1230	6	ABR52808	Abr52808 Protein s
1045	86	3.3	459	5	ABB80944	Abb80944 M. liquef	1118	85.5	3.3	1230	7	ADK62206	Adk62206 Disease t
1046	86	3.3	467	7	ADG33838	Adg33838 Actinomyc	1119	85.5	3.3	1230	8	ADN19276	Adn19276 Bacterial
1047	86	3.3	468	8	ADS28136	Ads28136 Bacterial	1120	85.5	3.3	1232	7	ADE80764	Ade80764 Microsate

1121 85.5 3.3 1262 5 ABP74021 Candida a  
1122 85.5 3.3 1780 5 ABB92830 Herbicida  
1123 85.5 3.3 2011 6 ABU62068 Mouse kid  
1124 85.5 3.3 2011 6 ABU62067 Human kid  
1125 85 3.2 332 3 AAG55461 Arabidops  
1126 85 3.2 341 3 AAG55460 Arabidops  
1127 85 3.2 384 6 ABU33371 Protein e  
1128 85 3.2 385 6 ABP70996 Epoxide h  
1129 85 3.2 397 8 ADN47224 Thermococ  
1130 85 3.2 405 6 ABU39784 Protein e  
1131 85 3.2 421 8 ADH17654 Human NOV  
1132 85 3.2 426 7 ABO61427 Klebsiell  
1133 85 3.2 451 6 AAE30470 H. influe  
1134 85 3.2 485 6 ABU15862 Protein e  
1135 85 3.2 495 4 AAU34722 E. coli c  
1136 85 3.2 495 4 AAU33544 Klebsiell  
1137 85 3.2 495 4 AAU36123 Klebsiell  
1138 85 3.2 495 6 ABU15338 Protein e  
1139 85 3.2 495 6 ABU31460 Protein e  
1140 85 3.2 495 7 ADD67266 Nusa prot  
1141 85 3.2 495 8 ADR49668 E coli Nu  
1142 85 3.2 498 7 ABO67190 Klebsiell  
1143 85 3.2 500 5 AAU77470 Euphorbia  
1144 85 3.2 535 6 ABM69226 Photorhab  
1145 85 3.2 547 2 AAY06394 Bacillus  
1146 85 3.2 555 8 ADO58596 Nusa prot  
1147 85 3.2 574 8 ADS25316 Bacterial  
1148 85 3.2 592 8 ADN17371 Bacterial  
1149 85 3.2 626 6 ABM64825 Propionib  
1150 85 3.2 631 4 ABB61376 Drosophil  
1151 85 3.2 645 8 ADR08909 Human pro  
1152 85 3.2 672 2 AAW99657 Staphyloc  
1153 85 3.2 713 2 AAR99797 Lysine de  
1154 85 3.2 713 8 ADN18055 Bacterial  
1155 85 3.2 729 8 ADO58584 Human nov  
1156 85 3.2 775 7 ADC31774 Human nov  
1157 85 3.2 780 7 ADC33323 Human nov  
1158 85 3.2 799 4 AAU62421 Propionib  
1159 85 3.2 799 6 ABM58940 Propionib  
1160 85 3.2 809 6 ABU28365 Protein e  
1161 85 3.2 810 4 AAU34090 Staphyloc  
1162 85 3.2 818 4 AAU37196 Staphyloc  
1163 85 3.2 818 4 AAU36831 Staphyloc  
1164 85 3.2 818 6 ABU16354 Protein e  
1165 85 3.2 818 6 ABM72479 Staphyloc  
1166 85 3.2 866 2 AAW99656 Staphyloc  
1167 85 3.2 932 6 ABJ72225 Protein o  
1168 85 3.2 932 6 ABP71831 Orthogona  
1169 85 3.2 932 7 ADE03192 Orthogona  
1170 85 3.2 974 3 AAY71560 Rat Nogo  
1171 85 3.2 1006 3 AAY44455 Modified  
1172 85 3.2 1021 3 AAY77728 Human G p  
1173 85 3.2 1021 7 ADE55164 Human Pro  
1174 85 3.2 1021 7 ADE55168 Human Pro  
1175 85 3.2 1021 7 ADE55172 Human Pro  
1176 85 3.2 1021 7 ADE55176 Human Pro  
1177 85 3.2 1038 6 ABU31186 Protein e  
1178 85 3.2 1126 8 ADS22844 Bacterial  
1179 85 3.2 1144 6 ADB08196 Bacterial  
1180 85 3.2 1162 3 AAY71557 Rat Nogo  
1181 85 3.2 1163 3 AAY71310 Rat neuro  
1182 85 3.2 1274 7 ADJ80176 Novel hum  
1183 85 3.2 1275 8 ADR14634 Human NF-  
1184 85 3.2 1291 8 ADN24296 Bacterial  
1185 85 3.2 1331 8 ADR88900 Anopheles  
1186 85 3.2 1366 8 ADR09464 Human pro  
1187 85 3.2 1390 8 ADS21405 Bacteri  
1188 85 3.2 1433 8 ADR10227 Human pro  
1189 85 3.2 1452 6 ABU29796 Protein e  
1190 85 3.2 1464 5 AAU99676 Potato st  
1191 85 3.2 1464 6 AAE33546 Potato R1  
1192 85 3.2 1464 7 ABR82880 S. tubero  
1193 85 3.2 1498 5 ABB48222 Listeria

1194 85 3.2 1567 6 ABU22447  
1195 85 3.2 1723 4 AAM79157  
1196 85 3.2 1755 8 ADJ95444 Human Ubi  
1197 85 3.2 1755 8 ADS86866 Human E3a  
1198 85 3.2 2102 8 ABO84498 Human can  
1199 85 3.2 3263 4 ABB67210 Drosophil  
1200 84.5 3.2 131 6 AAE31509 Latex Hev  
1201 84.5 3.2 226 7 ADC00872 Enterohae  
1202 84.5 3.2 233 8 ABM80797 Tumour-as  
1203 84.5 3.2 293 4 AAU25470 Human mdd  
1204 84.5 3.2 322 6 ADB06118 Alloiococ  
1205 84.5 3.2 332 6 ABU00632 S. pneumo  
1206 84.5 3.2 332 6 ABP81542 Streptoco  
1207 84.5 3.2 332 6 ABU45844 Protein e  
1208 84.5 3.2 332 8 ADK47548 Streptoco  
1209 84.5 3.2 334 4 AAB96266 Putative  
1210 84.5 3.2 335 8 ADQ20634 Human sof  
1211 84.5 3.2 336 3 AAG39351 Arabidops  
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1214 84.5 3.2 396 8 ADN47805 Thermococ  
1215 84.5 3.2 398 6 ADB06120 Alloiococ  
1216 84.5 3.2 401 8 ADS27905 Bacterial  
1217 84.5 3.2 434 4 AAB80030 Corynebac  
1218 84.5 3.2 437 4 AAG90238 C glutami  
1219 84.5 3.2 442 6 ADB09765 Alloiococ  
1220 84.5 3.2 453 2 AAW13081 Pseudomon  
1221 84.5 3.2 453 6 AAE35702 Pseudomon  
1222 84.5 3.2 455 4 AAB96595 Putative  
1223 84.5 3.2 469 7 ADG33816 Actinomyc  
1224 84.5 3.2 489 4 AAB96357 Putative  
1225 84.5 3.2 517 4 ABB57957 Drosophil  
1226 84.5 3.2 531 6 ABO14652 Novel hum  
1227 84.5 3.2 545 8 ADR15603 Streptoco  
1228 84.5 3.2 571 6 ABU40634 Protein e  
1229 84.5 3.2 575 6 ABU41576 Protein e  
1230 84.5 3.2 575 7 ADF06299 Bacterial  
1231 84.5 3.2 586 2 AAW27300 Bacillus  
1232 84.5 3.2 611 4 AAU33236 Novel hum  
1233 84.5 3.2 643 6 ABU61798 Amino aci  
1234 84.5 3.2 739 6 ABU25261 Protein e  
1235 84.5 3.2 773 5 ABP28543 Streptoco  
1236 84.5 3.2 833 6 ABU27253 Protein e  
1237 84.5 3.2 912 4 AAB96623 Putative  
1238 84.5 3.2 1014 8 ADN20063 Bacterial  
1239 84.5 3.2 1198 8 ABM83554 Human dia  
1240 84.5 3.2 1207 8 ABM83553 Human dia  
1241 84.5 3.2 1225 8 ABM83552 Human dia  
1242 84.5 3.2 1234 8 ABM83551 Human dia  
1243 84.5 3.2 1259 7 ADJ70768 Human hea  
1244 84.5 3.2 1259 7 ABO62323 Klebsiell  
1245 84.5 3.2 1444 5 ABB48622 Listeria  
1246 84.5 3.2 1444 6 ABU33053 Protein e  
1247 84.5 3.2 1544 4 ABB69002 Drosophil  
1248 84.5 3.2 1812 5 AAE18271 Protein e  
1249 84.5 3.2 1812 8 ADN96825 Bugula ne  
1250 84.5 3.2 2021 7 ADJ70511 Human hea  
1251 84.5 3.2 4861 5 AAU84280 Human end  
1252 84.5 3.2 4861 6 AAE32729 HERC1 pro  
1253 84.5 3.2 4861 7 ADC35083 Human bre  
1254 84.5 3.2 4861 7 ADP65241 Human gua  
1255 84.5 3.2 4899 4 ABB65885 Drosophil  
1256 84 3.2 231 4 AAE09048 Equine in  
1257 84 3.2 232 2 AAU77257 Human ade  
1258 84 3.2 232 7 ADJ69026 Human hea  
1259 84 3.2 232 8 ADP56377 Human PRO  
1260 84 3.2 239 7 ADJ68567 Human hea  
1261 84 3.2 319 6 ABU19682 Protein e  
1262 84 3.2 339 6 ABU20860 Protein e  
1263 84 3.2 363 5 ABG91583 Purine/py  
1264 84 3.2 397 2 AAW04270 B.t. alka  
1265 84 3.2 402 6 ABU31826 Protein e  
1266 84 3.2 420 8 ADN27166 Bacterial

Abu22447 Protein e  
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Adj95444 Human Ubi  
Ads86866 Human E3a  
Abo84498 Human can  
Abb67210 Drosophil  
Aae31509 Latex Hev  
Adc00872 Enterohae  
Abm80797 Tumour-as  
Aau25470 Human mdd  
Adb06118 Alloiococ  
Abu00632 S. pneumo  
Abp81542 Streptoco  
Abu45844 Protein e  
Adk47548 Streptoco  
Aab96266 Putative  
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Aag39351 Arabidops  
Aag39350 Arabidops  
Aag39349 Arabidops  
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Adb06120 Alloiococ  
Ads27905 Bacterial  
Aab80030 Corynebac  
Aag90238 C glutami  
Adb09765 Alloiococ  
Aaw13081 Pseudomon  
Aae35702 Pseudomon  
Aab96595 Putative  
Adg33816 Actinomyc  
Aab96357 Putative  
Abb57957 Drosophil  
Abo14652 Novel hum  
Adri5603 Streptoco  
Abu40634 Protein e  
Abu41576 Protein e  
Adf06299 Bacterial  
Aaw27300 Bacillus  
Aau33236 Novel hum  
Abu61798 Amino aci  
Abu25261 Protein e  
Abp28543 Streptoco  
Abu27253 Protein e  
Aab96623 Putative  
Adn20063 Bacterial  
Abm83554 Human dia  
Abm83553 Human dia  
Abm83552 Human dia  
Abm83551 Human dia  
Adj70768 Human hea  
Abo62323 Klebsiell  
Abb48622 Listeria  
Abu33053 Protein e  
Abb69002 Drosophil  
Aae18271 Protein e  
Adn96825 Bugula ne  
Adj70511 Human hea  
Aau84280 Human end  
Aae32729 HERC1 pro  
Adc35083 Human bre  
Adp65241 Human gua  
Abb65885 Drosophil  
Aae09048 Equine in  
Aau77257 Human ade  
Adj69026 Human hea  
Adp56377 Human PRO  
Adj68567 Human hea  
Abu19682 Protein e  
Abu20860 Protein e  
Abg91583 Purine/py  
Aaw04270 B.t. alka  
Abu31826 Protein e  
Adn27166 Bacterial



1267	84	3.2	424	3	AAB41647	Aab41647 Human ORF	1340	83.5	3.2	285	8	ADS29358	Ads29358 Bacterial
1268	84	3.2	436	8	ADQ26344	Adq26344 Chromobac	1341	83.5	3.2	336	3	AAG23022	Aag23022 Arabidops
1269	84	3.2	472	4	AAU35231	Aau35231 Enterococ	1342	83.5	3.2	342	3	AAG23021	Aag23021 Arabidops
1270	84	3.2	482	3	AAy51648	Aay51648 Methanoba	1343	83.5	3.2	343	3	AAG23020	Aag23020 Arabidops
1271	84	3.2	482	3	AAy52019	Aay52019 M. thermo	1344	83.5	3.2	344	6	ADA36700	Ada36700 Acinetoba
1272	84	3.2	501	6	ABU34074	Abu34074 Protein e	1345	83.5	3.2	367	3	AAy66633	Aay66633 Membrane-
1273	84	3.2	504	2	AAR72509	Aar72509 Hamster c	1346	83.5	3.2	367	4	AAB65156	Aab65156 Human PRO
1274	84	3.2	536	6	ABM69225	Abm69225 Photorhab	1347	83.5	3.2	367	5	ABG34032	Abg34032 Human PRO
1275	84	3.2	559	6	ABU25431	Abu25431 Protein e	1348	83.5	3.2	367	6	ABU57971	Abu57971 Human PRO
1276	84	3.2	565	8	ADS41771	Ads41771 Bacterial	1349	83.5	3.2	367	6	ABU59049	Abu59049 Novel hum
1277	84	3.2	582	6	ABU40392	Abu40392 Protein e	1350	83.5	3.2	367	6	ABU82561	Abu82561 Human sec
1278	84	3.2	586	8	ADJ49863	Adj49863 Oil-assoc	1351	83.5	3.2	367	6	ABU60480	Abu60480 Human sec
1279	84	3.2	594	6	ADA54987	Ada54987 Human pro	1352	83.5	3.2	367	6	ABU13862	Abu13862 Human PRO
1280	84	3.2	605	5	ABB91100	Abb91100 Herbicida	1353	83.5	3.2	367	6	ABU72447	Abu72447 Novel hum
1281	84	3.2	633	7	ABM85248	Abm85248 Mouse pro	1354	83.5	3.2	367	6	ABU59196	Abu59196 Human sec
1282	84	3.2	650	8	ADO57712	Ado57712 Actinobac	1355	83.5	3.2	367	6	ABO25893	Abo25893 Human PRO
1283	84	3.2	666	8	ADS42420	Ads42420 Bacterial	1356	83.5	3.2	367	6	ABU58902	Abu58902 Human sec
1284	84	3.2	668	7	ADM26244	Adm26244 Hyperther	1357	83.5	3.2	367	6	ABU92280	Abu92280 Novel hum
1285	84	3.2	724	7	ADF04460	Adf04460 Bacterial	1358	83.5	3.2	367	6	ABU59345	Abu59345 Novel hum
1286	84	3.2	735	2	AAW69761	Aaw69761 Acetobact	1359	83.5	3.2	367	6	ABU92111	Abu92111 Novel hum
1287	84	3.2	754	7	ADF05131	Adf05131 Bacterial	1360	83.5	3.2	367	6	ABU10817	Abu10817 Human PRO
1288	84	3.2	793	8	ADN20400	Adn20400 Bacterial	1361	83.5	3.2	367	6	ABU81569	Abu81569 Novel hum
1289	84	3.2	808	6	ABU36359	Abu36359 Protein e	1362	83.5	3.2	367	6	ABU88508	Abu88508 Human sec
1290	84	3.2	811	4	AAB93464	Aab93464 Human pro	1363	83.5	3.2	367	6	ABO34022	Abo34022 Human PRO
1291	84	3.2	811	8	ADS42600	Ads42600 Bacterial	1364	83.5	3.2	367	6	ADA01274	Ada01274 Human PRO
1292	84	3.2	823	7	ADC96716	Adc96716 E. faeciu	1365	83.5	3.2	367	6	ADA37519	Ada37519 Human sec
1293	84	3.2	832	6	ADA54351	Ada54351 Human pro	1366	83.5	3.2	367	6	ADA21205	Ada21205 Human sec
1294	84	3.2	842	4	ABB65111	Abb65111 Drosophil	1367	83.5	3.2	367	6	ADA09992	Ada09992 Human sec
1295	84	3.2	879	8	ADI57186	Adi57186 Human FAK	1368	83.5	3.2	367	6	ADA17536	Ada17536 Human PRO
1296	84	3.2	893	2	AAW83996	Aaw83996 Tne DNA p	1369	83.5	3.2	367	6	ADA27644	Ada27644 Human sec
1297	84	3.2	917	4	AAU34107	Aau34107 Staphyloc	1370	83.5	3.2	367	6	ADA43703	Ada43703 Human sec
1298	84	3.2	920	4	AAU36588	Aau36588 Staphyloc	1371	83.5	3.2	367	6	ADA43471	Ada43471 Human sec
1299	84	3.2	941	8	ADN21308	Adn21308 Bacterial	1372	83.5	3.2	367	6	ADA01146	Ada01146 Human PRO
1300	84	3.2	953	2	AAR76707	Aar76707 Recombina	1373	83.5	3.2	367	6	ADA94224	Ada94224 Human sec
1301	84	3.2	953	2	AAR90923	Aar90923 F. bident	1374	83.5	3.2	367	6	ADA38449	Ada38449 Human sec
1302	84	3.2	974	4	ABG06406	Abg06406 Novel hum	1375	83.5	3.2	367	6	ADA92570	Ada92570 Human sec
1303	84	3.2	1111	4	AAM80109	Aam80109 Human pro	1376	83.5	3.2	367	7	ADA01030	Ada01030 Human sec
1304	84	3.2	1111	4	AAM80108	Aam80108 Human pro	1377	83.5	3.2	367	7	ADA43587	Ada43587 Human sec
1305	84	3.2	1111	4	ABG09489	Abg09489 Novel hum	1378	83.5	3.2	367	7	ABO53108	Abo53108 Human sec
1306	84	3.2	1111	8	ADJ66557	Adj66557 KIAA0667	1379	83.5	3.2	367	7	ADA22131	Ada22131 Human sec
1307	84	3.2	1119	4	AAM79124	Aam79124 Human pro	1380	83.5	3.2	367	7	ABO22478	Abo22478 Human sec
1308	84	3.2	1119	7	ADC10026	Adc10026 Human NOV	1381	83.5	3.2	367	7	ADA06297	Ada06297 Human sec
1309	84	3.2	1125	8	ADN49840	Adn49840 Turkey as	1382	83.5	3.2	367	7	ADA38990	Ada38990 Human sec
1310	84	3.2	1143	4	AAM79125	Aam79125 Human pro	1383	83.5	3.2	367	7	ADA06849	Ada06849 Human PRO
1311	84	3.2	1230	4	AAU70675	Aau70675 Human oto	1384	83.5	3.2	367	7	ADA08337	Ada08337 Novel hum
1312	84	3.2	1236	7	ADJ80171	Adj80171 Novel hum	1385	83.5	3.2	367	7	ADB99630	Adb99630 Human PRO
1313	84	3.2	1307	4	AAU70672	Aau70672 Human oto	1386	83.5	3.2	367	7	ADB86913	Adb86913 Human PRO
1314	84	3.2	1356	8	ADS27771	Ads27771 Bacterial	1387	83.5	3.2	367	7	ADB96016	Adb96016 Human PRO
1315	84	3.2	1396	6	ABU27289	Abu27289 Protein e	1388	83.5	3.2	367	7	ADB66068	Adb66068 Human sec
1316	84	3.2	1501	7	ABO71520	Abo71520 Pseudomon	1389	83.5	3.2	367	7	ADB99746	Adb99746 Human PRO
1317	84	3.2	1526	4	AAM79777	Aam79777 Human pro	1390	83.5	3.2	367	7	ADB99401	Adb99401 Novel hum
1318	84	3.2	1734	8	ADJ95459	Adj95459 Human Ubi	1391	83.5	3.2	367	7	ADB65952	Adb65952 Human sec
1319	84	3.2	1734	8	ADS86881	Ads86881 Variant h	1392	83.5	3.2	367	7	ADC57488	Adc57488 Human PRO
1320	84	3.2	1738	6	ABP58330	Abp58330 Human cel	1393	83.5	3.2	367	7	ADC54852	Adc54852 Human PRO
1321	84	3.2	1749	8	ADJ95442	Adj95442 Human Ubi	1394	83.5	3.2	367	7	ADC11719	Adc11719 Human sec
1322	84	3.2	1749	8	ADS86864	Ads86864 Human E3a	1395	83.5	3.2	367	7	ADC56141	Adc56141 Human PRO
1323	84	3.2	1849	7	ADM26543	Adm26543 Hyperther	1396	83.5	3.2	367	7	ADC07196	Adc07196 Human sec
1324	84	3.2	1881	2	AAy24025	Aay24025 Amino aci	1397	83.5	3.2	367	7	ADC11186	Adc11186 Human sec
1325	84	3.2	1883	4	ABG19121	Abg19121 Novel hum	1398	83.5	3.2	367	7	ADC23350	Adc23350 Human tra
1326	84	3.2	1997	4	AAU70673	Aau70673 Human oto	1399	83.5	3.2	367	7	ADC26043	Adc26043 Human PRO
1327	84	3.2	2002	4	ABG12556	Abg12556 Novel hum	1400	83.5	3.2	367	7	ADC14308	Adc14308 Novel hum
1328	84	3.2	2165	5	ABG67242	Abg67242 Respirato	1401	83.5	3.2	367	7	ADD07840	Add07840 Novel hum
1329	84	3.2	2383	4	ABG00402	Abg00402 Novel hum	1402	83.5	3.2	367	7	ADC81665	Adc81665 Human PRO
1330	84	3.2	2385	6	ABU18663	Abu18663 Protein e	1403	83.5	3.2	367	7	ADD07307	Add07307 Novel hum
1331	84	3.2	2429	4	ABB62451	Abb62451 Drosophil	1404	83.5	3.2	367	7	ADC82198	Adc82198 Human PRO
1332	84	3.2	3343	8	ADN23132	Adn23132 Bacterial	1405	83.5	3.2	367	7	ADD08378	Add08378 Novel hum
1333	84	3.2	4299	6	ABU52622	Abu52622 Human NOV	1406	83.5	3.2	367	7	ADD06627	Add06627 Novel hum
1334	83.5	3.2	131	6	AAE31508	Aae31508 Latex Hev	1407	83.5	3.2	367	7	ADC82874	Adc82874 Human PRO
1335	83.5	3.2	137	6	ABU34953	Abu34953 Protein e	1408	83.5	3.2	367	7	ADD54981	Add54981 Human PRO
1336	83.5	3.2	212	6	ABU49446	Abu49446 Protein e	1409	83.5	3.2	367	7	ADD55939	Add55939 Human PRO
1337	83.5	3.2	235	4	AAU59870	Aau59870 Propionib	1410	83.5	3.2	367	7	ADD54377	Add54377 Human PRO
1338	83.5	3.2	235	6	ABM56389	Abm56389 Propionib	1411	83.5	3.2	367	7	ADE04870	Ade04870 Human PRO
1339	83.5	3.2	285	5	ABB54173	Abb54173 Lactococc	1412	83.5	3.2	367	7	ADE11176	Ade11176 Human PRO



1413	83.5	3.2	367	7	ADE26531	Adh26531	Novel hum
1414	83.5	3.2	367	7	ADD88107	Add88107	Human PRO
1415	83.5	3.2	367	7	ADD95402	Add95402	Human PRO
1416	83.5	3.2	367	7	ADE06332	Ade06332	Human PRO
1417	83.5	3.2	367	7	ADE38107	Ade38107	Human PRO
1418	83.5	3.2	367	7	ADD88223	Add88223	Human PRO
1419	83.5	3.2	367	7	ADD25998	Add25998	Novel hum
1420	83.5	3.2	367	7	ADD90804	Add90804	Human PRO
1421	83.5	3.2	367	7	ADF66935	Adf66935	Human PRO
1422	83.5	3.2	367	7	ADF99359	Adf99359	Human PRO
1423	83.5	3.2	367	7	ADG06452	Adg06452	Human PRO
1424	83.5	3.2	367	7	ADG05403	Adg05403	Human PRO
1425	83.5	3.2	367	7	ADG82404	Adg82404	Human PRO
1426	83.5	3.2	367	7	ADI35189	Adi35189	Human PRO
1427	83.5	3.2	367	7	ADH99681	Adh99681	Novel hum
1428	83.5	3.2	367	8	ADE51657	Ade51657	Human PRO
1429	83.5	3.2	367	8	ADE51773	Ade51773	Human PRO
1430	83.5	3.2	367	8	ADE37631	Ade37631	Human PRO
1431	83.5	3.2	367	8	ADE37515	Ade37515	Human PRO
1432	83.5	3.2	367	8	ADD95286	Add95286	Human PRO
1433	83.5	3.2	367	8	ADE37986	Ade37986	Human PRO
1434	83.5	3.2	367	8	ADE76075	Ade76075	Human PRO
1435	83.5	3.2	367	8	ADE39398	Ade39398	Human PRO
1436	83.5	3.2	367	8	ADE04202	Ade04202	Human PRO
1437	83.5	3.2	367	8	ADE39799	Ade39799	Human PRO
1438	83.5	3.2	367	8	ADE19664	Ade19664	Human PRO
1439	83.5	3.2	367	8	ADE77242	Ade77242	Human PRO
1440	83.5	3.2	367	8	ADE65350	Ade65350	Human PRO
1441	83.5	3.2	367	8	ADE75959	Ade75959	Human PRO
1442	83.5	3.2	367	8	ADE37870	Ade37870	Human PRO
1443	83.5	3.2	367	8	ADE64480	Ade64480	Human PRO
1444	83.5	3.2	367	8	ADE38815	Ade38815	Human PRO
1445	83.5	3.2	367	8	ADE51889	Ade51889	Human PRO
1446	83.5	3.2	367	8	ADD90920	Add90920	Human PRO
1447	83.5	3.2	367	8	ADE38699	Ade38699	Human PRO
1448	83.5	3.2	367	8	ADE37399	Ade37399	Human PRO
1449	83.5	3.2	367	8	ADE06216	Ade06216	Human PRO
1450	83.5	3.2	367	8	ADD90075	Add90075	Human PRO
1451	83.5	3.2	367	8	ADE38583	Ade38583	Human PRO
1452	83.5	3.2	367	8	ADE39514	Ade39514	Human PRO
1453	83.5	3.2	367	8	ADD89119	Add89119	Human PRO
1454	83.5	3.2	367	8	ADD88886	Add88886	Human PRO
1455	83.5	3.2	367	8	ADE19780	Ade19780	Human PRO
1456	83.5	3.2	367	8	ADE77358	Ade77358	Human PRO
1457	83.5	3.2	367	8	ADE65234	Ade65234	Human PRO
1458	83.5	3.2	367	8	ADE39282	Ade39282	Human PRO
1459	83.5	3.2	367	8	ADE38467	Ade38467	Human PRO
1460	83.5	3.2	367	8	ADF35134	Adf35134	Human PRO
1461	83.5	3.2	367	8	ADG11384	Adg11384	Human PRO
1462	83.5	3.2	367	8	ADG11020	Adg11020	Human PRO
1463	83.5	3.2	367	8	ADG10904	Adg10904	Human PRO
1464	83.5	3.2	367	8	ADH31432	Adh31432	Human PRO
1465	83.5	3.2	367	8	ADH38680	Adh38680	Human PRO
1466	83.5	3.2	367	8	ADH29315	Adh29315	Human PRO
1467	83.5	3.2	367	8	ADH23618	Adh23618	Human PRO
1468	83.5	3.2	367	8	ADH26948	Adh26948	Human PRO
1469	83.5	3.2	367	8	ADH19254	Adh19254	Human PRO
1470	83.5	3.2	367	8	ADH38216	Adh38216	Novel hum
1471	83.5	3.2	367	8	ADH26832	Adh26832	Human PRO
1472	83.5	3.2	367	8	ADH38100	Adh38100	Novel hum
1473	83.5	3.2	367	8	ADH38796	Adh38796	Human PRO
1474	83.5	3.2	367	8	ADH20747	Adh20747	Human PRO
1475	83.5	3.2	367	8	ADH23734	Adh23734	Human PRO
1476	83.5	3.2	367	8	ADH40110	Adh40110	Human PRO
1477	83.5	3.2	367	8	ADH39994	Adh39994	Human PRO
1478	83.5	3.2	367	8	ADH19787	Adh19787	Human PRO
1479	83.5	3.2	367	8	ADH31316	Adh31316	Human PRO
1480	83.5	3.2	367	8	ADH29194	Adh29194	Human PRO
1481	83.5	3.2	367	8	ADH49409	Adh49409	Novel hum
1482	83.5	3.2	367	8	ADH51873	Adh51873	Novel hum
1483	83.5	3.2	367	8	ADH49728	Adh49728	Novel hum
1484	83.5	3.2	367	8	ADH52329	Adh52329	Novel hum
1485	83.5	3.2	367	8	ADH52445	Adh52445	Novel hum

1486	83.5	3.2	367	8	ADH58442	Adh58442	Novel hum
1487	83.5	3.2	367	8	ADH51757	Adh51757	Novel hum
1488	83.5	3.2	367	8	ADH58318	Adh58318	Novel hum
1489	83.5	3.2	367	8	ADI13515	Adi13515	Novel hum
1490	83.5	3.2	367	8	ADK00771	Adk00771	Human PRO
1491	83.5	3.2	367	8	ADL08512	Adl08512	Human PRO
1492	83.5	3.2	408	6	ABU24455	Abu24455	Protein e
1493	83.5	3.2	428	8	ADN20153	Adn20153	Bacterial
1494	83.5	3.2	433	6	ABU44767	Abu44767	Protein e
1495	83.5	3.2	435	6	ABJ18976	Abj18976	Pathogen
1496	83.5	3.2	435	6	ABM72187	Abm72187	Staphyloc
1497	83.5	3.2	444	5	ABP66024	Abp66024	Bifidobac
1498	83.5	3.2	445	8	ADS29606	Ads29606	Bacterial
1499	83.5	3.2	453	2	AAW45452	Aaw45452	Arabidops
1500	83.5	3.2	464	7	ABO61640	Abo61640	Klebsiell

ALIGNMENTS

RESULT 1

AAU72908

ID AAU72908 standard; protein; 507 AA.

XX

AC AAU72908;

XX

DT 26-FEB-2002 (first entry)

XX

DE Human metalloprotease partial protein sequence #20.

XX

KW Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;  
KW vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;  
KW hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;  
KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;  
KW metalloprotease; serine protease; cancer; haematopoietic; breast; colon;  
KW lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain;  
KW immune-related disease; cardiovascular disease; neuronal disease;  
KW migraine; sexual dysfunction; mood disorder; attention disorder;  
KW cognition disorder; hypotension; hypertension; psychotic disorder;  
KW dyskinesia; metabolic disorder; inflammatory disorder.

XX

OS Homo sapiens.

XX

PN WO200183782-A2.

XX

PD 08-NOV-2001.

XX

PF 04-MAY-2001; 2001WO-US014431.

XX

PR 04-MAY-2000; 2000US-0201879P.

XX

PA (SUGE-) SUGEN INC.

XX

PI Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;

PI Payne V;

XX

DR WPI; 2002-041502/05.

DR

N-PSDB; AAS97191.

XX

PS Claim 28; Fig 2I; 232pp; English.

XX

CC The invention relates to an isolated, enriched, or purified protease  
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to  
CC screen for substances (S) that may modulate its activity. Administering S  
CC (which modulates protease activity in vitro) may be used to treat a  
CC disease or disorder selected from cancers (e.g., of tissues, of blood or  
CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,  
CC brain, ovarian, bladder or kidney), immune-related diseases and  
CC disorders, cardiovascular disease, brain or neuronal-associated diseases

CC (e.g., central or peripheral nervous system diseases, migraine, pain,  
CC sexual dysfunction, mood disorders, attention disorders, cognition  
CC disorders, hypotension, hypertension, psychotic disorders, neurological  
CC disorders and dyskinesias), metabolic disorders and inflammatory  
CC disorders. (I) may also be useful as a diagnostic tool for a disease or  
CC disorder such as those above. AAU72876-AAU72910 represent human protease  
CC amino acid sequences of the invention  
XX  
SQ Sequence 507 AA;

Query Match 100.0%; Score 2623; DB 5; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
Db 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
QY 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
QY 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQ 480  
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQ 480  
QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

RESULT 2  
ABB07950  
ID ABB07950 standard; protein; 507 AA.  
XX  
AC ABB07950;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Human metalloprotease, 55054.  
XX  
KW 55054; human; metalloprotease; neural cell; cerebral injury; vulnerary;  
KW enzyme.  
XX  
OS Homo sapiens.  
XX  
PN WO200226948-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 25-SEP-2001; 2001WO-US030016.  
XX  
PR 25-SEP-2000; 2000US-0235055P.

XX (MILL-) MILLENNIUM PHARM INC.  
PA Kapeller-Libermann R;  
XX  
XX WPI; 2002-405051/43.  
DR N-PSDB; ABL58476, ABL58477.  
XX  
XX Identifying modulator of neural cell growth or transition metal  
PT neurotoxicity, involves contacting test compound with novel human  
PT metalloprotease polypeptide and determining if the polypeptide binds the  
PT test compound.  
XX  
PS Claim 21; Fig 1A-D; 105pp; English.  
XX  
CC The invention provides a method for identifying a modulator of neural  
CC cell growth, cerebral injury or wound healing, transition metal  
CC neurotoxicity, histamine production, neural/hepatic cell proliferation or  
CC degradation of extracellular matrix, neurotransmitter or soluble  
CC intracellular/extracellular dipeptide. The method involves contacting a  
CC test compound and metalloprotease polypeptide, selected from a human  
CC metalloprotease polypeptide, termed 55054, and determining if 55054 binds  
CC the test compound. The metalloprotease, 55054 is useful for making a  
CC pharmaceutical composition for inhibiting the ability of a cell selected  
CC from a neural cell such as glial cell or neuron (a sensory neuron or  
CC olfactory sensory neuron), astrocyte, oligodendrocyte and ensheathing  
CC cell, to cleave a polypeptide. The present sequence represents the human  
CC metalloprotease, 55054  
XX  
SQ Sequence 507 AA;

Query Match 100.0%; Score 2623; DB 5; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
Db 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
QY 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
QY 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQ 480  
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQ 480  
QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

ABU69115  
ID ABU69115 standard; protein; 507 AA.  
XX  
AC ABU69115;  
XX  
DT 02-JUN-2003 (first entry)  
XX  
DE Human PRO polypeptide #13.  
XX  
KW Human; secreted and transmembrane protein; bone disorder; obesity;  
KW cartilage disorder; sports injury; arthritis; diabetes mellitus;  
KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;  
KW haemoglobin-associated disorder; kidney disorder; Berger disease;  
KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;  
KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;  
KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
PN US2003032061-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 26-DEC-2001; 2001US-00036214.  
XX  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-DEC-1998; 98US-0112514P.  
PR 22-DEC-1998; 98US-0113300P.  
PR 23-DEC-1998; 98US-0113430P.  
PR 23-DEC-1998; 98US-0113605P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 23-DEC-1998; 98US-0114140P.  
PR 12-JAN-1999; 99US-0115552P.  
PR 22-JAN-1999; 99US-0116843P.  
PR 23-MAR-1999; 99US-0125774P.  
PR 23-MAR-1999; 99US-0125778P.  
PR 24-MAR-1999; 99US-0125826P.  
PR 31-MAR-1999; 99US-0127035P.  
PR 05-APR-1999; 99US-0127706P.  
PR 13-APR-1999; 99US-0129122P.  
PR 21-APR-1999; 99US-0130359P.  
PR 27-APR-1999; 99US-0131270P.  
PR 27-APR-1999; 99US-0131272P.  
PR 27-APR-1999; 99US-0131291P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 04-MAY-1999; 99US-0132379P.  
PR 04-MAY-1999; 99US-0132383P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-MAY-1999; 99US-0135750P.  
PR 08-JUN-1999; 99US-0138166P.  
PR 20-JUL-1999; 99US-0144791P.  
PR 03-AUG-1999; 99US-0146970P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 02-DEC-1999; 99WO-US028551.  
PR 22-DEC-1999; 99WO-US030720.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 16-AUG-2001; 2001US-00931836.  
XX  
(GETH ) GENENTECH INC.  
PA  
XX  
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;

PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2003-341962/32.  
DR N-PSDB; ACA06168.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,  
PT PRO1887, PRO1785, PRO4353, useful for treating sports injuries,  
PT arthritis, diabetes, obesity, hyper- or hypo-insulinemia.  
XX  
PS Claim 12; Fig 26; 194pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful in diagnosing or treating  
CC various bone and/or cartilage disorders (e.g. sports injuries,  
CC arthritis), various insulin deficient states (e.g. diabetes mellitus,  
CC hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated  
CC disorders (e.g. thalassaemias), kidney disorders associated with  
CC decreased mesangial cell function (e.g. Berger disease), or other  
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,  
CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide  
CC sequences may be used as hybridisation probes in chromosome and gene  
CC mapping, or in generating antisense RNA and DNA. They are also useful in  
CC preparing PRO polypeptides, in assays to identify other proteins or  
CC molecules involved in binding reaction, to generate transgenic animals or  
CC knockout animals, which in turn are useful in the development and  
CC screening of therapeutically useful reagents, for chromosome  
CC identification, and tissue typing. The PRO polypeptides and nucleic acid  
CC molecules are also useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be  
CC used in diagnostic assays for PRO polypeptides, or for the affinity  
CC purification of the polypeptides from recombinant cell culture or natural  
CC sources. ABU69103-ABU69125 represent the human PRO polypeptides of the  
CC invention  
XX  
SQ Sequence 507 AA;

Query Match 100.0%; Score 2623; DB 6; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 SDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
QY 121 DPTKGTVCYFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 DPTKGTVCYFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
QY 181 RALEQDLFPVNIKFIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 RALEQDLFPVNIKFIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWIA 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWIA 420  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480









RESULT 6  
ABU81556  
ID ABU81556 standard; protein; 507 AA.  
XX  
AC ABU81556;  
XX  
DT 24-JUN-2003 (first entry)  
XX  
DE Human secreted polypeptide PRO4380.  
XX  
KW Human; inflammatory disease; organ failure; atherosclerosis; cancer;  
KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
KW differentiation disorder; cell adhesion disorder; skin disorder;  
KW neural receptor disorder; diabetic complication; tissue typing.  
XX  
OS Homo sapiens.  
XX  
PN US2002192751-A1.  
XX  
PD 19-DEC-2002.  
XX  
PF 26-DEC-2001; 2001US-00036041.  
XX  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-DEC-1998; 98US-0112514P.  
PR 22-DEC-1998; 98US-0113300P.  
PR 23-DEC-1998; 98US-0113430P.  
PR 23-DEC-1998; 98US-0113605P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 23-DEC-1998; 98US-0114140P.  
PR 12-JAN-1999; 99US-0115552P.  
PR 22-JAN-1999; 99US-0116843P.  
PR 23-MAR-1999; 99US-0125774P.  
PR 23-MAR-1999; 99US-0125778P.  
PR 24-MAR-1999; 99US-0125826P.  
PR 31-MAR-1999; 99US-0127035P.  
PR 05-APR-1999; 99US-0127706P.  
PR 13-APR-1999; 99US-0129122P.  
PR 21-APR-1999; 99US-0130359P.  
PR 27-APR-1999; 99US-0131270P.  
PR 27-APR-1999; 99US-0131272P.  
PR 27-APR-1999; 99US-0131291P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 04-MAY-1999; 99US-0132379P.  
PR 04-MAY-1999; 99US-0132383P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-MAY-1999; 99US-0135750P.  
PR 08-JUN-1999; 99US-0138166P.  
PR 20-JUL-1999; 99US-0144791P.  
PR 03-AUG-1999; 99US-0146970P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 02-DEC-1999; 99WO-US028551.  
PR 22-DEC-1999; 99WO-US030720.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 16-AUG-2001; 2001US-00931836.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-341079/32.  
DR N-PSDB; ACA67734.  
XX  
PT New secreted and transmembrane nucleic acids and polypeptides, designated  
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or  
PT cancer.  
XX  
PS Claim 12; Fig 26; 195pp; English.  
XX  
CC The invention relates to an isolated nucleic acid that encodes a PRO  
CC polypeptide. The nucleic acids and polypeptides are useful for treating  
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,  
CC infertility, birth defects, premature aging, acquired immunodeficiency  
CC syndrome (AIDS), cancer, differentiation disorders, cell adhesion  
CC disorders, neural receptor disorders, skin disorders or diabetic  
CC complications. The nucleic acids are useful as hybridisation probes, in  
CC chromosome and gene mapping and in generating antisense RNA or DNA. The  
CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or  
CC bioreactors. Both are useful in tissue typing. The present sequence  
CC represents the amino acid sequence of a PRO polypeptide of the invention  
XX  
SQ Sequence 507 AA;  
  
Query Match 100.0%; Score 2623; DB 6; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MDPKLGKGRMAASLLAVLLLLLGRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db |||||  
1 MDPKLGKGRMAASLLAVLLLLLGRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Qy 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
Db |||||  
61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
Qy 121 DPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db |||||  
121 DPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Qy 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db |||||  
181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Qy 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db |||||  
241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Qy 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db |||||  
301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Qy 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Db |||||  
361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Qy 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGHSQ 480  
Db |||||  
421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGHSQ 480  
Qy 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db |||||  
481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
  
RESULT 7  
ADA76582  
ID ADA76582 standard; protein; 507 AA.  
XX  
AC ADA76582;  
XX  
DT 20-NOV-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO4380.  
XX KW human; secreted and transmembrane protein; PRO; tumour; gene therapy;  
KW tissue typing; chromosome identification; cytostatic.  
XX OS Homo sapiens.  
XX PN US2003036114-A1.  
XX PD 20-FEB-2003.  
XX XX 26-DEC-2001; 2001US-00035719.  
XX PR 15-MAY-1998; 98US-0085579P.  
PR 15-DEC-1998; 98US-0112514P.  
PR 22-DEC-1998; 98US-0113300P.  
PR 23-DEC-1998; 98US-0113430P.  
PR 23-DEC-1998; 98US-0113605P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 23-DEC-1998; 98US-0114140P.  
PR 12-JAN-1999; 99US-0115552P.  
PR 22-JAN-1999; 99US-0116843P.  
PR 23-MAR-1999; 99US-0125774P.  
PR 24-MAR-1999; 99US-0125778P.  
PR 31-MAR-1999; 99US-0125826P.  
PR 05-APR-1999; 99US-0127035P.  
PR 13-APR-1999; 99US-0127706P.  
PR 21-APR-1999; 99US-0129122P.  
PR 27-APR-1999; 99US-0130359P.  
PR 27-APR-1999; 99US-0131270P.  
PR 27-APR-1999; 99US-0131272P.  
PR 04-MAY-1999; 99US-0131291P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 04-MAY-1999; 99US-0132379P.  
PR 14-MAY-1999; 99US-0132383P.  
PR 25-MAY-1999; 99WO-US010733.  
PR 08-JUN-1999; 99US-0135750P.  
PR 20-JUL-1999; 99US-0138166P.  
PR 03-AUG-1999; 99US-0144791P.  
PR 29-OCT-1999; 99US-0146970P.  
PR 02-DEC-1999; 99US-0162506P.  
PR 22-DEC-1999; 99WO-US028551.  
PR 01-MAR-2000; 99WO-US030720.  
PR 02-MAR-2000; 2000WO-US005601.  
PR 22-MAY-2000; 2000WO-US005841.  
PR 02-JUN-2000; 2000WO-US014042.  
PR 23-AUG-2000; 2000WO-US015264.  
PR 24-AUG-2000; 2000WO-US023522.  
PR 01-DEC-2000; 2000WO-US023328.  
PR 20-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2000WO-US034956.  
PR 01-JUN-2001; 2001WO-US006520.  
PR 20-JUN-2001; 2001WO-US017800.  
PR 29-JUN-2001; 2001WO-US019692.  
PR 09-JUL-2001; 2001WO-US021066.  
PR 16-AUG-2001; 2001WO-US021735.  
XX (GETH ) GENENTECH INC.  
PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
PI WPI; 2003-615764/58.  
XX N-PSDB; ADA76581.  
PT Novel isolated secreted and transmembrane polypeptides, designated as PRO  
PT polypeptides e.g. PRO1484, PRO4334 and PRO1122, useful for inhibiting  
PT tumor cell growth, and for preparing medicaments for therapeutic use.  
XX Claim 12; Fig 26; 201pp; English.

CC The invention describes an isolated secreted and transmembrane PRO  
CC polypeptide (I), having at least 80% identity to or scoring at least 80%  
CC positives when compared to, a sequence (S1) comprising 246, 440, 197, 97,  
CC 273, 571, 209, 888, 502, 310, 251, 800, 507, 248, 223, 134, 136, 468,  
CC 328, 221, 194, 899, or 339 amino acids fully defined in the  
CC specification. An anti-(I)-antibody is useful for determining the  
CC presence of (I) in a cell. (I) is useful for identifying a compound  
CC capable of inhibiting the expression and/or activity of (I). (I) and the  
CC antibody are useful for inhibiting the growth of tumour cells, and for  
CC the preparation of a medicament useful in the treatment of a condition  
CC which is responsive to (I) or the antibody. A polynucleotide (II)  
CC encoding (I) is also useful for isolating full-length PRO cDNA for  
CC generating transgenic animals or knock-out animals, which are, in turn,  
CC are useful in the development in the screening of therapeutically useful  
CC reagents, and in gene therapy. PRO is useful in assays to identify other  
CC proteins or molecules involved in binding interactions, for screening  
CC inhibitors or agonists of binding interactions and for screening chemical  
CC libraries. (I) is useful as molecular weight marker for protein  
CC electrophoresis, and as therapeutic agents. (I) or (II) is useful for  
CC tissue typing and for chromosome identification. Ab is useful in  
CC diagnostic assays for PRO, in affinity purification of PRO, and for  
CC detection of PRO in biological samples. This is the amino acid sequence  
CC of a novel human secreted and transmembrane PRO polypeptide.  
XX  
SQ Sequence 507 AA;  
  
Query Match 100.0%; Score 2623; DB 6; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPALKEVQYIDLHQDEFVQTLKEWVAIE 60  
Db |||||  
QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPALKEVQYIDLHQDEFVQTLKEWVAIE 60  
Db |||||  
QY 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
Db |||||  
QY 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
Db |||||  
QY 121 DPTKGTVCYGHLDVQPADRGDGLTDPYVLTEVDCKLYGRGATDNKGPVLAWINAVSAF 180  
Db |||||  
QY 121 DPTKGTVCYGHLDVQPADRGDGLTDPYVLTEVDCKLYGRGATDNKGPVLAWINAVSAF 180  
Db |||||  
QY 181 RALEQDLPVNKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db |||||  
QY 181 RALEQDLPVNKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db |||||  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db |||||  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db |||||  
QY 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLDFTKERILMHLWRYPSLSIHGIEGAFDEPG 360  
Db |||||  
QY 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLDFTKERILMHLWRYPSLSIHGIEGAFDEPG 360  
Db |||||  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIA 420  
Db |||||  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIA 420  
Db |||||  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVKHSVLIPLGAVDDGEHSQ 480  
Db |||||  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVKHSVLIPLGAVDDGEHSQ 480  
Db |||||  
QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db |||||  
QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db |||||  
  
RESULT 8  
ABO25139  
ID ABO25139 standard; protein; 507 AA.  
XX  
AC ABO25139;  
XX



DT 05-SEP-2003 (first entry)  
XX Human secreted/transmembrane protein PRO4380.  
DE  
XX  
KW Human; PRO; secreted protein; transmembrane protein; septic shock;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX US2003044842-A1.  
PN  
XX  
PD 06-MAR-2003.  
XX  
PF 26-DEC-2001; 2001US-00036160.  
XX  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-DEC-1998; 98US-0112514P.  
PR 22-DEC-1998; 98US-0113300P.  
PR 23-DEC-1998; 98US-0113430P.  
PR 23-DEC-1998; 98US-0113605P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 23-DEC-1998; 98US-0114140P.  
PR 12-JAN-1999; 99US-0115552P.  
PR 22-JAN-1999; 99US-0116843P.  
PR 23-MAR-1999; 99US-0125774P.  
PR 23-MAR-1999; 99US-0125778P.  
PR 24-MAR-1999; 99US-0125826P.  
PR 31-MAR-1999; 99US-0127035P.  
PR 05-APR-1999; 99US-0127706P.  
PR 13-APR-1999; 99US-0129122P.  
PR 21-APR-1999; 99US-0130359P.  
PR 27-APR-1999; 99US-0131270P.  
PR 27-APR-1999; 99US-0131272P.  
PR 27-APR-1999; 99US-0131291P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 04-MAY-1999; 99US-0132379P.  
PR 04-MAY-1999; 99US-0132383P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-MAY-1999; 99US-0135750P.  
PR 08-JUN-1999; 99US-0138166P.  
PR 20-JUL-1999; 99US-0144791P.  
PR 03-AUG-1999; 99US-0146970P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 02-DEC-1999; 99WO-US028551.  
PR 22-DEC-1999; 99WO-US030720.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 16-AUG-2001; 2001US-00931836.  
XX  
(GETH ) GENENTECH INC.  
PA  
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
PI  
XX WPI; 2003-492260/46.  
DR N-PSDB; ACD42296.  
XX  
PT Novel secreted and transmembrane polypeptide for identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers.  
XX  
XX Claim 12; Fig 26; 195pp; English.  
XX

CC The invention relates to an isolated, secreted and transmembrane  
CC polypeptide, termed PRO polypeptide, PRO having at least 80 % sequence  
CC identity to any one of the 23 100-900 residue amino acid sequences, given  
CC in the specification or to a sequence encoded by a nucleic acid molecule  
CC deposited under any one of the ATCC accession numbers given in the  
CC specification. Also included are an isolated nucleic acid molecule having  
CC at least 80 % sequence identity to any one of 23 400-3500 nucleotide  
CC sequences given in the specification, (or a nucleotide sequence encoding  
CC PRO, a full- length PRO coding sequence, a full-length coding sequence of  
CC DNA deposited under any ATCC accession number given in the specification)  
CC or at least 80 % identity to a nucleotide sequence encoding PRO, lacking  
CC its associated signal peptide, a sequence encoding extracellular domain  
CC of PRO with or without its associated signal peptide, a vector comprising  
CC the PRO nucleic acid, a host cell comprising the vector, preparation of  
CC PRO, a chimeric molecule comprising PRO fused to a heterologous amino  
CC acid sequence and an anti-PRO antibody. PRO is useful for identifying  
CC ant/agonists or antagonists of PRO, preparing a variant of PRO, as  
CC molecular weight markers and PRO nucleic acid is useful for recombinantly  
CC expressing those markers. PRO is also useful as therapeutic agent. PRO is  
CC useful in assays to identify molecules or proteins which bind to PRO and  
CC for identifying inhibitors of PRO. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in generation of  
CC antisense RNA and DNA, for generating transgenic animals or knockout  
CC animals which in turn are useful in the development and screening of  
CC therapeutically useful reagents. PRO nucleic acid is also useful in  
CC mapping the gene which encodes the PRO and for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome  
CC identification, as chromosome marker, and for generating probes for PCR,  
CC Northern analysis, Southern analysis and Western analysis. The antibody  
CC useful in diagnostic assays for PRO, for affinity purification of PRO,  
CC and for treating septic shock. PRO or the antibody is useful for the  
CC preparation of medicament for treating conditions which is responsive to  
CC the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are  
CC useful for tissue typing. The present sequence represents a PRO protein  
XX  
SQ Sequence 507 AA;

Query Match 100.0%; Score 2623; DB 7; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGKMAASLLAVLLLLLLERGMFFSSPPPPALLEKVKFOYIDLHQDEFVQTLKEWVAIE 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MDPKLGKMAASLLAVLLLLLLERGMFFSSPPPPALLEKVKFOYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 SDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
QY 121 DPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 DPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
QY 181 RALEQDLFPVNIKFIIEGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAIT 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 RALEQDLFPVNIKFIIEGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAIT 240  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMA DLVALLGSLVDSSGHILVPGIYDEVV 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMA DLVALLGSLVDSSGHILVPGIYDEVV 300  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 PLTEEEINTYKAIHLDLEEYRNSSRVVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA 420  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFOEIVHKSVVLIPLGAVDDGHSQ 480  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFOEIVHKSVVLIPLGAVDDGHSQ 480

QY 481 NEKINRWNYIEGTKLFAAFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFLEMAQLH 507

RESULT 9  
AAE39109  
ID AAE39109 standard; protein; 507 AA.  
XX AAE39109;  
AC AAE39109;  
XX 18-DEC-2003 (first entry)  
XX Human PRO4380 protein.  
DE Human; PRO protein; inflammation; nephropathy; bone disorder; arthritis;  
XX cartilage disorder; diabetes; gene therapy; antisense therapy.  
KW Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1. .26  
FT /label= Signal\_peptide  
FT Protein 27. .507  
FT /note= "Mature human PRO protein"  
FT Modified-site 89. .95  
FT /note= "N-myristoylation site"  
FT Modified-site 119. .125  
FT /note= "N-myristoylation site"  
FT Binding-site 140. .143  
FT /note= "Cell attachment site"  
FT Region 156. .167  
FT /note= "ArgE/dapE/ACY1/CPG"  
FT Modified-site 162. .168  
FT /note= "N-myristoylation site"  
FT Modified-site 197. .203  
FT /note= "N-myristoylation site"  
FT Modified-site 242. .248  
FT /note= "N-myristoylation site"  
FT Modified-site 263. .269  
FT /note= "N-myristoylation site"  
FT Domain 273. .292  
FT /note= "Transmembrane domain"  
FT Modified-site 322. .326  
FT /note= "N-glycosylation site"  
FT Modified-site 351. .357  
FT /note= "N-myristoylation site"  
FT Modified-site 382. .386  
FT /note= "N-glycosylation site"  
FT Modified-site 400. .404  
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
FT Modified-site 402. .406  
FT /note= "N-glycosylation site"  
XX  
PN US2003049733-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 26-DEC-2001; 2001US-00035958.  
XX  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-DEC-1998; 98US-0112514P.  
PR 22-DEC-1998; 98US-0113300P.  
PR 23-DEC-1998; 98US-0113430P.  
PR 23-DEC-1998; 98US-0113605P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 23-DEC-1998; 98US-0114140P.  
PR 12-JAN-1999; 99US-0115552P.  
PR 22-JAN-1999; 99US-0116843P.  
PR 23-MAR-1999; 99US-0125774P.  
PR 23-MAR-1999; 99US-0125778P.  
PR 24-MAR-1999; 99US-0125826P.

PR 31-MAR-1999; 99US-0127035P.  
PR 05-APR-1999; 99US-0127706P.  
PR 13-APR-1999; 99US-0129122P.  
PR 21-APR-1999; 99US-0130359P.  
PR 27-APR-1999; 99US-0131270P.  
PR 27-APR-1999; 99US-0131272P.  
PR 27-APR-1999; 99US-0131291P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 04-MAY-1999; 99US-0132379P.  
PR 04-MAY-1999; 99US-0132383P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-MAY-1999; 99US-0135750P.  
PR 08-JUN-1999; 99US-0138166P.  
PR 20-JUL-1999; 99US-0144791P.  
PR 03-AUG-1999; 99US-0146970P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 02-DEC-1999; 99WO-US028551.  
PR 22-DEC-1999; 99WO-US030720.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 16-AUG-2001; 2001US-00931836.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2003-585109/55.  
N-PSDB; AAD59362.  
XX  
PT New isolated, secreted and transmembrane PRO polypeptides and nucleic  
PT acids, useful for diagnosing, preventing and/or treating inflammation,  
PT nephropathies, bone and cartilage disorders, and diabetes.  
XX  
PS Claim 12; Fig 26; 203pp; English.  
XX  
CC The invention relates to an isolated nucleic acid that encodes a PRO  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for the diagnosis, prevention and/or treatment of inflammation,  
CC nephropathies, bone and cartilage disorders, such as arthritis and  
CC disorders that affect glucose or free fatty acid (FFA) uptake, such as  
CC diabetes, hypoinsulinaemia or hyperinsulinaemia. The PRO polypeptides are  
CC also useful as molecular weight markers or for chromosome identification.  
CC The PRO genes are useful as hybridisation probes or for screening  
CC libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be  
CC used in gene therapy and antisense therapy. The present sequence is human  
CC PRO protein  
XX  
SQ Sequence 507 AA;

Query Match 100.0%; Score 2623; DB 7; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPKLGRRMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MDPKLGRRMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS 120  
Db 61 SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS 120





CC encoding them. The methods and compositions of the present invention are  
CC useful for the diagnosis, prevention and/or treatment of inflammation,  
CC nephropathies, bone and cartilage disorders such as arthritis and  
CC disorders that affect glucose or free fatty acid (FFA) uptake such as  
CC diabetes, hypoinsulinaemia and hyperinsulinaemia. The PRO peptides are  
CC useful as molecular weight markers and for chromosome identification. The  
CC PRO genes may also be used in gene therapy and antisense therapy. The  
CC present sequence is human PRO protein  
XX  
SQ Sequence 507 AA;

Query Match 100.0%; Score 2623; DB 7; Length 507;  
Best Local Similarity 100.0%; Pred. No. 3.7e-234;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLS 120  
Db 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLS 120  
QY 121 DPTKGTVCYFYGHLVDQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 121 DPTKGTVCYFYGHLVDQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
QY 181 RALEQDLPVNIKFIIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db 181 RALEQDLPVNIKFIIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEW 300  
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEW 300  
QY 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIVLPLGAVDDGEHSQ 480  
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIVLPLGAVDDGEHSQ 480  
QY 481 NEKINRWNYIEGTKLFAAFPLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFPLEMAQLH 507

RESULT 11  
ADC29813  
ID ADC29813 standard; protein; 507 AA.

XX AC ADC29813;

XX DT 18-DEC-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO4380.

XX KW human; secreted and transmembrane protein; PRO; vulnery; antiarthritic;  
KW antidiabetic; anorectic; antianaemic; dermatological; antiinflammatory;  
KW antiallergic; immunosuppressive; gastrointestinal;  
KW chondrocyte cell differentiation; glucose uptake stimulator;  
KW pancreatic beta cell differentiation; mesangial cell proliferation;  
KW tissue typing; chromosome identification; gene therapy;  
KW chromosome mapping; gene mapping; sports injury; arthritis; diabetes;  
KW obesity; hyper-insulinaemia; hypo-insulinaemia; thalassaemia;  
KW Berger disease; Schonlein-Henoch purpura; celiac disease;  
KW dermatitis herpetiformis; Crohn's disease.

OS Homo sapiens.  
XX US2003092063-A1.  
XX 15-MAY-2003.  
XX PF 26-DEC-2001; 2001US-00036063.  
XX PR 15-MAY-1998; 98US-0085579P.  
PR 15-DEC-1998; 98US-0112514P.  
PR 22-DEC-1998; 98US-0113300P.  
PR 23-DEC-1998; 98US-0113430P.  
PR 23-DEC-1998; 98US-0113605P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 23-DEC-1998; 98US-0114140P.  
PR 12-JAN-1999; 99US-0115552P.  
PR 22-JAN-1999; 99US-0116843P.  
PR 23-MAR-1999; 99US-0125774P.  
PR 23-MAR-1999; 99US-0125778P.  
PR 24-MAR-1999; 99US-0125826P.  
PR 31-MAR-1999; 99US-0127035P.  
PR 05-APR-1999; 99US-0127706P.  
PR 13-APR-1999; 99US-0129122P.  
PR 21-APR-1999; 99US-0130359P.  
PR 27-APR-1999; 99US-0131270P.  
PR 27-APR-1999; 99US-0131291P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 04-MAY-1999; 99US-0132379P.  
PR 04-MAY-1999; 99US-0132383P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-MAY-1999; 99US-0135750P.  
PR 08-JUN-1999; 99US-0138166P.  
PR 20-JUL-1999; 99US-0144791P.  
PR 03-AUG-1999; 99US-0146970P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 02-DEC-1999; 99WO-US028551.  
PR 22-DEC-1999; 99WO-US030720.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 16-AUG-2001; 2001US-00931836.

(GETH ) GENENTECH INC.

Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
Stewart TA, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-765478/72.  
N-PSDB; ADC29812.

Novel isolated PRO polypeptide such as PRO1484, PRO4334, PRO1122,  
PRO1889, PRO1890, PRO1887, PRO1785, useful for treating arthritis,  
obesity, diabetes mellitus, thalassemia, Crohn's disease.

Claim 12; SEQ ID NO 57; 200pp; English.

The invention describes an isolated secreted and transmembrane PRO  
polypeptide (I) having at least 80% amino acid sequence identity to fully  
defined sequences of 246, 440, 197, 97, 273, 571, 209, 888, 502, 310,  
251, 800, 507, 248, 223, 134, 136, 468, 322, 221, 194, 125 or 339 amino  
acids as given in the specification. (I) is useful for tissue typing, as  
molecular weight markers or as therapeutic agents. A polynucleotide (II)







CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used  
CC to generate transgenic animals for use in development and screening of  
CC therapeutically useful reagents and also for chromosome identification  
CC and tissue typing

```

Query Match      99.9%;   Score 2621;   DB 3;   Length 507;
Best Local Similarity 99.8%;   Pred. No. 5.7e-234;
Matches 506; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY	1	MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKFQYIDLHQDEFVQTLKEWVAIE	60
Db	1	MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKFQYIDLHQDEFVQTLKEWVAIE	60
QY	61	SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS	120
Db	61	SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS	120
QY	121	DPTKGTVCIFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF	180
Db	121	DPTKGTVCIFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF	180
QY	181	RALAEQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWTSQRKPAIT	240
Db	181	RALAEQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWTSQRKPAIT	240
QY	241	YGTRGNSYFMVEVKCRDQDFHSGTFCGILHEPMAIDLVALLGSLVDSSGHILVPGIYDEVV	300
Db	241	YGTRGNSYFMVEVKCRDQDFHSGTFCGILHEPMAIDLVALLGSLVDSSGHILVPGIYDEVV	300
QY	301	PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360
Db	301	PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360
QY	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIA	420
Db	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIA	420
QY	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQ	480
Db	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQ	480
QY	481	NEKINRWNYIEGTKLFAAFFLEMAQLH	507
Db	481	NEKINRWNYIEGTKLFAAFFLEMAQLH	507

**RESULT 14**

AAB97262  
ID AAB97262 standard; protein: 508 AA.

AC AAB97262;

DT 08-AUG-2001 (first entry)

Human carnosinase.

Human; carnosinase; carnosine; anserine; hydrolysis; brain; epilepsy;  
KW  
KW Alzheimer's disease; cognitive disorder; development abnormality;  
KW foetal deficiency; neurodegenerative disorder; schizophrenia;  
KW amyotrophic lateral sclerosis; Parkinson's disease; ischaemic shock.

OS Homo sapiens.

PN EP1097997-A1.

PD 09-MAY-2001.

PF 03-NOV-1999; 99EP-00402723.

PR 03-NOV-1999; 99EP-00402723.

XX

(SNEI ) SANOEI-SYNTHELABO.

Saudek V. Smirnova-Robert T. Teufel M:

WPI: 2001-319238/34.

N-PSDB; AAF27154.

Novel isolated human carnosinase polypeptide useful for prevention and/or treatment of Alzheimer's disease, amyotrophic lateral sclerosis, Parkinson's disease, schizophrenia, ischemic shock, and epilepsy.

Claim 6: Page 19-20; 27pp; English.

The present sequence represents human carnosinase. Carnosinase is a glycoprotein with an isoelectric point of 4.4. The active enzyme is a dimer, with the two subunits being connected by at least one disulphide bond. The enzyme is especially active in hydrolysing carnosine and anserine. Carnosinase is found in high concentration in the brain. Homocarnosine is hydrolysed in the brain, and carnosine and anserine are split in the blood stream by carnosinase. Carnosine and anserine are thought to act as cytosol buffering agents. Carnosinase its agonists and antagonists and compositions containing them are useful for the prevention and/or treatment of Alzheimer's disease and cognitive disorders, developmental abnormalities and foetal deficiencies, neurodegenerative disorders such as amyotrophic lateral sclerosis, Parkinson's disease, schizophrenia, abnormal mental states, ischaemic shock, and epilepsy.

Sequence 508 AA;

Query Match 99.6%; Score 2612.5; DB 4; Length 508;  
Best Local Similarity 99.8%; Pred. No. 3.5e-233;  
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	MDPKLGRMAASLLAV - LLLLLRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI	59
Db	1	MDPKLGRMAASLLAVLLLLLLRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI	60
QY	60	ESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG	119
Db	61	ESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG	120
QY	120	SDPTKGTVCIFYGHLDVQPADRGDWLTDPPVLTVEVDGKLYGRGATDNKGPVLAWINAVSA	179
Db	121	SDPTKGTVCIFYGHLDVQPADRGDWLTDPPVLTVEVDGKLYGRGATDNKGPVLAWINAVSA	180
QY	180	FRALEQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI	239
Db	181	FRALEQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI	240
QY	240	TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMAIDLVALLSGLVDSSGSHILVPGIYDEV	299
Db	241	TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMAIDLVALLSGLVDSSGSHILVPGIYDEV	300
QY	300	VPLTEEBEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP	359
Db	301	VPLTEEBEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP	360
QY	360	GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVMVSMTLGLHPWI	419
Db	361	GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVMVSMTLGLHPWI	420
QY	420	ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHS	479
Db	421	ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHS	480
QY	480	QNEKINRWNYIEGTKLFAAFFLEMAQLH	507
Db	481	QNEKINRWNYIEGTKLFAAFFLEMAQLH	508

RESULT 15  
AAG89122



ID AAG89122 standard; protein; 508 AA.  
XX AAG89122;  
AC  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE Human secreted protein, SEQ ID NO: 242.  
XX  
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;  
KW GENSET.  
XX  
OS Homo sapiens.  
XX  
XX WO200142451-A2.  
PN  
XX  
PD 14-JUN-2001.  
XX  
XX  
PF 07-DEC-2000; 2000WO-IB001938.  
XX  
PR 08-DEC-1999; 99US-0169629P.  
PR 06-MAR-2000; 2000US-0187470P.  
XX  
XX  
PA (GEST ) GENSET.  
XX  
XX Dumas Milne Edwards J, Bougueleret L, Jobert S;  
PI  
XX  
XX WPI; 2001-367870/38.  
DR N-PSDB; AAH64725.  
DR  
XX  
PT Full length GENSET human nucleic acids encoding potentially secreted  
PT proteins, useful in gene therapy and vaccination against a variety of  
PT diseases, and for diagnosis of those diseases.  
XX  
XX  
PS Claim 21; Page 791-792; 921pp; English.  
XX  
CC The invention relates to full length GENSET human nucleic acids encoding  
CC potentially secreted proteins. The nucleic acids and the polypeptides  
CC they encode may be used in the prevention, treatment and diagnosis of  
CC diseases associated with inappropriate GENSET gene expression. For  
CC example, they be used to treat disorders associated with decreased GENSET  
CC gene expression by rectifying mutations or deletions in a patient's  
CC genome that affect the activity of GENSET or by supplementing the  
CC patient's own production of GENSET polypeptides. Conversely, antisense  
CC nucleic acid molecules may be administered to down regulate GENSET  
CC expression by binding with the cells' own genes and preventing their  
CC expression. The sense and antisense nucleic acids may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar nucleic acid sequences in samples, and hence to determine which  
CC patients may be in need of restorative therapy. The GENSET polypeptides  
CC may be used as antigens in the production of antibodies and in assays to  
CC identify modulators (agonists and antagonists) of GENSET polypeptide  
CC expression and activity. The present sequence is a GENSET polypeptide of  
CC the invention  
XX  
SQ Sequence 508 AA;

Query Match 99.6%; Score 2612.5; DB 4; Length 508;  
Best Local Similarity 99.8%; Pred. No. 3.5e-233;  
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDPKLGMAASLLAV-LLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 59  
DB 1 MDPKLGMAASLLAVLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60  
QY 60 ESDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIG 119  
DB 61 ESDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIG 120  
QY 120 SDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
DB 121 SDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180  
QY 180 FRALEQDLPVNIKFTIEGMEEAGSVALEELVEKDRFFSGVDYIVISDNLWISQRKPAI 239

Db 181 FRALEQDLPVNIKFTIEGMEEAGSVALEELVEKDRFFSGVDYIVISDNLWISQRKPAI 240  
QY 240 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299  
Db 241 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300  
QY 300 VPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEILMHLWRYPSLSIHGIEGAFDEP 359  
Db 301 VPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEILMHLWRYPSLSIHGIEGAFDEP 360  
QY 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTPHLEDVFSKRNSSNKMVVSMTLGLHPWI 419  
Db 361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTPHLEDVFSKRNSSNKMVVSMTLGLHPWI 420  
QY 420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTTPIAKMFQEIIVHKSVVLIPLGAVDDGEHS 479  
Db 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTTPIAKMFQEIIVHKSVVLIPLGAVDDGEHS 480  
QY 480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508

RESULT 16  
ABR47759  
ID ABR47759 standard; protein; 508 AA.  
XX  
AC ABR47759;  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Human secreted protein, SEQ ID 650.  
XX  
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
KW vulnery; antiinflammatory; nootropic; neuroprotective;  
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.  
OS Homo sapiens.  
XX WO200295010-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 19-MAR-2002; 2002WO-US009785.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-129429/12.  
XX  
PT Novel human secreted proteins, useful for detecting, preventing,  
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular  
PT disorders such as arrhythmia.  
XX  
PS Claim 13; SEQ ID NO 650; 1881pp; English.  
XX  
CC The present invention relates to novel human secreted proteins (ABR47633-  
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins  
CC and their coding sequences are useful for the preparation of a diagnostic  
CC or pharmaceutical composition for diagnosing or treating a cardiovascular  
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary  
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune  
CC system disorders, muscular disorders, reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, renal disorders,  
CC proliferative disorders and/or cancerous diseases and conditions, for  
CC wound healing and epithelial cell proliferation, to treat inflammation or  
CC infection, for treating thrombosis and arteriosclerosis, for treating or

CC preventing neural damage which occurs in neuronal disorders or  
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
CC disease, to enhance bone and periodontal regeneration and aid in tissue  
CC transplants or bone grafts, to prevent skin aging or hair loss, to  
CC stimulate growth and differentiation of haematopoietic cells and bone  
CC marrow cells when used in combination with other cytokines, to maintain  
CC organs before transplantation or for supporting cell culture of primary  
CC tissues, to increase or decrease differentiation or proliferation of  
CC embryonic stem cells, or to modulate mammalian characteristics or  
CC metabolism. Note: The sequence data for this patent was published in  
CC electronic format and is available from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 508 AA;

Query Match 99.6%; Score 2612.5; DB 6; Length 508;  
Best Local Similarity 99.8%; Pred. No. 3.5e-233;  
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MDPKLG<sup>1</sup>RMASLLAV-LLLLL<sup>1</sup>ERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 59  
Db 1 MDPKLG<sup>1</sup>RMASLLAVLLLLL<sup>1</sup>ERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy 60 ESDSVQ<sup>60</sup>VPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE<sup>60</sup>LG 119  
Db 61 ESDSVQ<sup>61</sup>VPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE<sup>61</sup>LG 120

Qy 120 SDPTKG<sup>120</sup>TVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 121 SDPTKG<sup>121</sup>TVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy 180 FRALEQ<sup>180</sup>DLPVNIKFIIEGME<sup>180</sup>EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ<sup>180</sup>KPAI 239  
Db 181 FRALEQ<sup>181</sup>DLPVNIKFIIEGME<sup>181</sup>EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ<sup>181</sup>KPAI 240

Qy 240 TYGTRG<sup>240</sup>NSYFMVEVKCRDQDFHSGTGGILHEPMA<sup>240</sup>DLVALLGSLVDSSGHILVPGIYDEV 299  
Db 241 TYGTRG<sup>241</sup>NSYFMVEVKCRDQDFHSGTGGILHEPMA<sup>241</sup>DLVALLGSLVDSSGHILVPGIYDEV 300

Qy 300 VPLTEE<sup>300</sup>EINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 359  
Db 301 VPLTEE<sup>301</sup>EINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy 360 GTKTVI<sup>360</sup>PGRV<sup>360</sup>IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 419  
Db 361 GTKTVI<sup>361</sup>PGRV<sup>361</sup>IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 420

Qy 420 ANIDDTQ<sup>420</sup>YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI<sup>420</sup>VHKSVVLIPLGAVDDGEHS 479  
Db 421 ANIDDTQ<sup>421</sup>YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI<sup>421</sup>VHKSVVLIPLGAVDDGEHS 480

Qy 480 QNEKIN<sup>480</sup>RWN<sup>480</sup>YIEG<sup>480</sup>TKLFAAFFLEMAQLH 507  
Db 481 QNEKIN<sup>481</sup>RWN<sup>481</sup>YIEG<sup>481</sup>TKLFAAFFLEMAQLH 508

RESULT 17  
ABR00082  
ID ABR00082 standard; protein; 508 AA.  
XX  
AC ABR00082;  
XX  
DT 03-APR-2003 (first entry)  
XX  
DE Human gene 72 encoded secreted protein HHPEN62, SEQ ID NO:371.  
XX  
KW Human; secreted protein; digestive disorder; gastrointestinal disorder;  
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;  
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;  
KW immune disorder; inflammation; infection; wound healing; drug screening;  
KW chromosome identification; chromosome mapping; cytostatic;  
KW antiinflammatory; immunosuppressive; vulnery; gene therapy.  
XX

OS Homo sapiens.  
XX  
PN WO200276488-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 19-MAR-2002; 2002WO-US008276.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-029900/02.  
DR N-PSDB; ABZ71261.  
XX  
PT New human secreted proteins and nucleic acids, useful for detecting,  
PT preventing, diagnosing, prognosticating, treating and/or ameliorating  
PT e.g. gastrointestinal diseases and disorders, or cancers.  
XX  
PS Claim 13; Page 984-986; 1216pp; English.  
XX  
CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted  
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.  
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The  
CC invention also encompasses antibodies specific for the secreted proteins,  
CC the use of the secreted proteins in drug screening, and recombinant  
CC vectors and host cells comprising a nucleic acid of the invention. The  
CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
CC fragments specific for the secreted proteins, and modulators of protein  
CC activity are useful for diagnosing, treating, ameliorating or preventing  
CC digestive disorders. Such conditions include disorders of the mouth,  
CC oesophagus, stomach, small intestine, large intestine, liver, biliary  
CC tract and pancreas, and include cancers of these organs and tissues. The  
CC secreted proteins and their nucleic acids may also be used in the  
CC treatment of immune disorders, inflammation, infection,  
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids  
CC of the invention may be used for chromosome identification, chromosome  
CC mapping, in gene therapy, for identifying individuals from minute  
CC biological samples, as hybridisation probes, and as molecular weight  
CC markers. The present sequence represents a human secreted protein of the  
CC invention  
XX  
SQ Sequence 508 AA;

Query Match 99.6%; Score 2612.5; DB 6; Length 508;  
Best Local Similarity 99.8%; Pred. No. 3.5e-233;  
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MDPKLG<sup>1</sup>RMASLLAV-LLLLL<sup>1</sup>ERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 59  
Db 1 MDPKLG<sup>1</sup>RMASLLAVLLLLL<sup>1</sup>ERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy 60 ESDSVQ<sup>60</sup>VPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE<sup>60</sup>LG 119  
Db 61 ESDSVQ<sup>61</sup>VPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE<sup>61</sup>LG 120

Qy 120 SDPTKG<sup>120</sup>TVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 121 SDPTKG<sup>121</sup>TVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy 180 FRALEQ<sup>180</sup>DLPVNIKFIIEGME<sup>180</sup>EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ<sup>180</sup>KPAI 239  
Db 181 FRALEQ<sup>181</sup>DLPVNIKFIIEGME<sup>181</sup>EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ<sup>181</sup>KPAI 240

Qy 240 TYGTRG<sup>240</sup>NSYFMVEVKCRDQDFHSGTGGILHEPMA<sup>240</sup>DLVALLGSLVDSSGHILVPGIYDEV 299  
Db 241 TYGTRG<sup>241</sup>NSYFMVEVKCRDQDFHSGTGGILHEPMA<sup>241</sup>DLVALLGSLVDSSGHILVPGIYDEV 300

Qy 300 VPLTEE<sup>300</sup>EINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 359

Db 301 VPLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEP 360  
Qy 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 419  
Db 361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 420  
Qy 420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEI VHKS VVLIPLGAVDDGEHS 479  
Db 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEI VHKS VVLIPLGAVDDGEHS 480  
Qy 480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508

RESULT 18  
ADB91551  
ID ADB91551 standard; protein; 508 AA.  
XX  
AC ADB91551;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human secreted protein #SEQ ID 497.  
XX  
KW Secreted protein; gene therapy; antidiabetic; diabetes; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003004622-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 19-MAR-2002; 2002WO-US008124.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;  
XX  
XX WPI; 2003-229407/22.  
XX  
PT Nucleic acid encoding a human secreted protein is useful in diagnosing or  
treating diabetes or conditions related to diabetes.  
XX  
PS Claim 3; SEQ ID NO 497; 1537pp; English.

XX  
CC The invention relates to isolated nucleic acid molecules ADB91065-  
CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-  
CC ADB91834. Also disclosed is a recombinant vector comprising a  
CC polynucleotide of the invention, and a recombinant host cell comprising  
CC the recombinant vector. The polypeptide of the invention is useful in  
CC identifying a binding partner by contacting the polypeptide with a  
CC binding partner, and determining whether the binding partner increases or  
CC decreases activity of the polypeptide. The polypeptide, polynucleotide,  
CC antibody or its fragment, agonist or antagonist are useful for preparing  
CC a pharmaceutical composition for diagnosing or treating diabetes or  
CC conditions related to diabetes. The present sequence is that of the human  
CC immunoglobulin Fc portion used to generate fusion proteins, increasing  
CC the stability of the fused protein as compared to the secreted protein  
CC only. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 508 AA;  
Query Match 99.6%; Score 2612.5; DB 7; Length 508;  
Best Local Similarity 99.8%; Pred. No. 3.5e-233;  
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MDPKLGRRMAASLLAV-LLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVOTLKEWVAI 59  
Db 1 MDPKLGRRMAASLLAVLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVOTLKEWVAI 60  
Qy 60 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119  
Db 61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120  
Qy 120 SDPTKGTVCYFGHLDVQPADRGDGLWLTDPYVLTTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 121 SDPTKGTVCYFGHLDVQPADRGDGLWLTDPYVLTTEVDGKLYGRGATDNKGPVLAWINAVSA 180  
Qy 180 FRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEDRFFSGVDYIIVISDNLWISQKKPAI 239  
Db 181 FRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEDRFFSGVDYIIVISDNLWISQKKPAI 240  
Qy 240 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299  
Db 241 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300  
Qy 300 VPLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEP 359  
Db 301 VPLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEP 360  
Qy 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 419  
Db 361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 420  
Qy 420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEI VHKS VVLIPLGAVDDGEHS 479  
Db 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEI VHKS VVLIPLGAVDDGEHS 480  
Qy 480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508

RESULT 19  
ADC74152  
ID ADC74152 standard; protein; 508 AA.  
XX  
AC ADC74152;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human secreted protein - SEQ ID 785.  
XX  
KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
KW antidiabetic; immunosuppressive; dermatological; nephrotropic;  
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;  
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;  
KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
KW rheumatoid arthritis; inflammation; diabetes;  
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003038063-A2.  
XX  
PD 08-MAY-2003.  
XX  
PF 19-MAR-2002; 2002WO-US008277.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX





CC	polypeptide of the invention.				
XX	Sequence 508 AA;				
SQ					
Query Match 99.6%; Score 2612.5; DB 7; Length 508;					
Best Local Similarity 99.8%; Pred. No. 3.5e-233;					
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;					
Qy	1	MDPKLGRMAASLLAV-LLLLLL	ERMFSPPPPALLEKFQYIDLHQDEFVQTLKEWVAI	59	
Db	1	MDPKLGRMAASLLAVLLLLL	ERMFSPPPPALLEKFQYIDLHQDEFVQTLKEWVAI	60	
Qy	60	ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMG	PQQLPDGQSLPIPPPVILAE	119	
Db	61	ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMG	PQQLPDGQSLPIPPPVILAE	120	
Qy	120	SDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA	179		
Db	121	SDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA	180		
Qy	180	FRALQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI	239		
Db	181	FRALQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI	240		
Qy	240	TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA	DLVALLGSLVDSSGHILVPGIYDEV	299	
Db	241	TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA	DLVALLGSLVDSSGHILVPGIYDEV	300	
Qy	300	VPLTEEEINTYKAIHLDLEEYRNSRVEKFLD	TKEEILMHLWRYPSLSIHGIEGAFDEP	359	
Db	301	VPLTEEEINTYKAIHLDLEEYRNSRVEKFLD	TKEEILMHLWRYPSLSIHGIEGAFDEP	360	
Qy	360	GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI	419		
Db	361	GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI	420		
Qy	420	ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI	VHKSVLPLGAVDDGEHS	479	
Db	421	ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI	VHKSVLPLGAVDDGEHS	480	
Qy	480	QNEKINRWNYIEGTLKFAAFFLEMAQLH	507		
Db	481	QNEKINRWNYIEGTLKFAAFFLEMAQLH	508		
RESULT 21					
ID	AAAY76144	standard; protein; 509 AA.			
XX	AAAY76144;				
AC	AAAY76144;				
XX	23-MAR-2000	(first entry)			
DT	Human secreted protein encoded by gene 21.				
DE	Human				
XX	Human; secreted protein; cancer; tumour; developmental abnormality;				
KW	foetal deficiency; blood disorder; immune system disorder; inflammation;				
KW	autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;				
KW	schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;				
KW	atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;				
KW	digestive disorder; endocrine disorder; infection; AIDS; leukaemia;				
XX	therapy; chromosome 18q22-23.				
OS	Homo sapiens.				
XX	WO9958660-A1.				
PN	18-NOV-1999.				
XX	06-MAY-1999;	99WO-US0009847.			
PF	12-MAY-1998;	98US-0085093P.			
XX	12-MAY-1998;	98US-0085094P.			
PR					

PR	12-MAY-1998;	98US-0085105P.			
PR	12-MAY-1998;	98US-0085180P.			
PR	18-MAY-1998;	98US-0085906P.			
PR	18-MAY-1998;	98US-0085920P.			
PR	18-MAY-1998;	98US-0085921P.			
PR	18-MAY-1998;	98US-0085922P.			
PR	18-MAY-1998;	98US-0085923P.			
PR	18-MAY-1998;	98US-0085924P.			
PR	18-MAY-1998;	98US-0085925P.			
PR	18-MAY-1998;	98US-0085927P.			
PR	18-MAY-1998;	98US-0085928P.			
XX	(HUMA-) HUMAN GENOME SCI INC.				
PA	Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;				
XX	Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;				
PI	Endress GA, Ebner R;				
PI	WPI; 2000-062296/05.				
XX	N-PSDB; AAZ65270.				
DR	New isolated human genes and the secreted polypeptides they encode,				
XX	useful for diagnosis and treatment of e.g. cancers, neurological				
PT	disorders, immune diseases, inflammation or blood disorders.				
PT	Claim 11; Page 373-374; 475pp; English.				
XX	AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.				
CC	AAAY76124 to AAAY76223 are the secreted proteins encoded by the 97 human				
CC	genes. The gene encoding this protein was found to be on chromosome 18q22				
CC	-23. The genes and their corresponding secreted polypeptides are useful				
CC	for preventing, treating or ameliorating medical conditions, e.g. by				
CC	protein or gene therapy. Also pathological conditions can be diagnosed by				
CC	determining the amount of the new polypeptides in a sample or by				
CC	determining the presence of mutations in the new genes. Specific uses are				
CC	described for each of the 97 genes, based on which tissues they are most				
CC	highly expressed in, and include developing products for the diagnosis or				
CC	treatment of cancer, tumours, developmental abnormalities and foetal				
CC	deficiencies, blood disorders, diseases of the immune system, autoimmune				
CC	diseases, inflammation, allergies, Alzheimer's and cognitive disorders,				
CC	schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,				
CC	atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,				
CC	digestive/endocrine disorders, infections and AIDS. The polypeptides are				
CC	also useful for identifying their binding partners. The sequences shown				
CC	in AAAY76224 to AAAY76424 represent fragments of the secreted proteins				
XX	Sequence 509 AA;				
SQ					
Query Match 99.6%; Score 2612.5; DB 3; Length 509;					
Best Local Similarity 99.8%; Pred. No. 3.6e-233;					
Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;					
Qy	1	MDPKLGRMAASLLAV-LLLLLL	ERMFSPPPPALLEKFQYIDLHQDEFVQTLKEWVAI	59	
Db	1	MDPKLGRMAASLLAVLLLLL	ERMFSPPPPALLEKFQYIDLHQDEFVQTLKEWVAI	60	
Qy	60	ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMG	PQQLPDGQSLPIPPPVILAE	119	
Db	61	ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMG	PQQLPDGQSLPIPPPVILAE	120	
Qy	120	SDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA	179		
Db	121	SDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA	180		
Qy	180	FRALQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI	239		
Db	181	FRALQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI	240		
Qy	240	TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA	DLVALLGSLVDSSGHILVPGIYDEV	299	
Db	241	TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA	DLVALLGSLVDSSGHILVPGIYDEV	300	
Qy	300	VPLTEEEINTYKAIHLDLEEYRNSRVEKFLD	TKEEILMHLWRYPSLSIHGIEGAFDEP	359	

Db 301 VPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360  
QY 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWI 419  
Db 361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWI 420  
QY 420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHS 479  
Db 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHS 480  
QY 480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508

RESULT 22  
ADC77691  
ID ADC77691 standard; protein; 508 AA.  
XX  
AC ADC77691;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human 55054 protein SEQ ID NO:54.  
XX  
KW pain disorder; pain signalling mechanism; analgesic; antinflammatory; antinflammatory; gene therapy; inflammatory pain; chronic pain;  
KW neuropathic pain; neuralgia; fibromyalgia; cancer pain; migraine;  
KW headache; pain; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003073983-A2.  
XX  
PD 12-SEP-2003.  
XX  
PF 19-FEB-2003; 2003WO-US004816.  
XX  
PR 28-FEB-2002; 2002US-0360495P.  
PR 04-APR-2002; 2002US-0370121P.  
PR 16-APR-2002; 2002US-0373010P.  
PR 19-APR-2002; 2002US-0373908P.  
PR 03-MAY-2002; 2002US-0377717P.  
PR 13-MAY-2002; 2002US-0379949P.  
PR 21-MAY-2002; 2002US-0382409P.  
PR 03-JUN-2002; 2002US-0385280P.  
PR 06-JUN-2002; 2002US-0386879P.  
PR 10-JUN-2002; 2002US-0387536P.  
PR 08-JUL-2002; 2002US-0394376P.  
PR 21-AUG-2002; 2002US-0404996P.  
PR 19-SEP-2002; 2002US-0412006P.  
PR 09-OCT-2002; 2002US-0417327P.  
PR 10-OCT-2002; 2002US-0417499P.  
PR 15-NOV-2002; 2002US-0426964P.  
PR 10-DEC-2002; 2002US-0432320P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Rosenfeld JB, Silos-Santiago I;  
XX  
XX WPI; 2003-712843/67.  
DR N-PSDB; ADC77690.  
DR  
XX  
PT Identifying a compound capable of treating a pain disorder e.g.,  
PT neuropathic pain comprises assaying the ability of the compound to  
PT modulate the nucleic acid expression or polypeptide activity.  
XX  
PS Claim 1; SEQ ID NO 54; 277pp; English.  
XX  
XX The present invention describes a method for identifying a compound (C)  
CC capable of treating a pain disorder comprising assaying the ability of  
CC the compound to modulate 9949, 14230, 760, 62553, 12216, 17719, 41897,

CC 47174, 33408, 10002, 16209, 314, 636, 27410, 33260, 619, or 13424 nucleic  
CC acid expression or 9949, 14230, 760, 62553, 12216, 17719, 41897, 47174,  
CC 33408, 10002, 16209, 314, 636, 27410, 33260, 619, 15985, polypeptide  
CC activity. Also described: (1) identifying a compound (C) capable of  
CC modulating a pain signalling mechanism; and (2) treating a subject having  
CC a pain disorder characterised by aberrant nucleic acid expression or  
CC polypeptide activity. (C) has analgesic, antimigraine and  
CC antiinflammatory activities, and can be used in gene therapy. The method  
CC is useful for identifying a modulator compound capable of treating a pain  
CC disorder, e.g. inflammatory pain, chronic pain, migraine/headache pain,  
CC neuralgia, fibromyalgia, cancer pain, migraine/headache pain or tissue  
CC pain comprising administering the modulator to a subject having a pain  
CC disorder characterised by aberrant nucleic acid expression or polypeptide  
CC activity. The present sequence represents the human 55054 protein from  
CC the present invention.  
XX  
SQ Sequence 508 AA;

Query Match 98.6%; Score 2585.5; DB 7; Length 508;  
Best Local Similarity 99.2%; Pred. No. 1.le-230;  
Matches 504; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MDPKLGMAASLLAV-LLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 59  
Db 1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60  
QY 60 ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGL 119  
Db 61 ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGL 120  
QY 120 SDPTKGTVCYGHLDVQPADRGDGLWTDYVLTVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 121 SDPTKGTVCYGHLDVQPADRGDGLWTDYVLTVEVGKLYGRGATDNKGPVLAWINAVSA 180  
QY 180 FRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 239  
Db 181 FRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKLAI 240  
QY 240 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMAIDLGLSLVDSSGHILVPGIYDEV 299  
Db 241 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHELMADLVALLGSLVDSSGHILVPGIYDEV 300  
QY 300 VPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 359  
Db 301 VPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360  
QY 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWI 419  
Db 361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWI 420  
QY 420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHS 479  
Db 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHS 480  
QY 480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508

RESULT 23  
AAU28396  
ID AAU28396 standard; protein; 501 AA.  
XX  
AC AAU28396;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Amino acid sequence for DPI-45 and DPI-213.  
XX  
KW Human; depression associated protein isoform; tryptic digest peptide;  
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic; DPI-213;  
KW maniac-depressive illness; schizoaffective disorder; DPI-45.



XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1. .20  
FT Protein /label= Signal\_peptide  
FT /label= Mature\_DPI-45\_and\_DPI-213  
FT Peptide 49. .63  
FT /label= Tryptic\_peptide  
FT /note= "Specifically claimed in claim 4"  
FT Misc-difference 70  
FT /label= Unknown  
FT /note= "Encoded by ANA"  
FT Peptide 306. .315  
FT /label= Tryptic\_peptide  
FT /note= "Specifically claimed in claim 4"  
XX WO200162787-A1.  
XX 30-AUG-2001.  
XX 23-FEB-2001; 2001WO-GB000786.  
XX 24-FEB-2000; 2000GB-00004412.  
XX 08-DEC-2000; 2000GB-00030050.  
XX 12-DEC-2000; 2000US-0254830P.  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX Herath HMCAC, Parekh RB, Rohlff C, Terrett JA, Tyson KL;  
XX WPI; 2001-570626/64.  
XX N-PSDB; AAS12574.  
XX Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.  
XX Disclosure; Fig 2B; 153pp; English.  
XX The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), manic-depressive illnesses, attention deficit disorders, schizoaffective disorders, and unipolar affective disorders. The present sequence represents the amino acid sequence for DPI-45 and DPI-213  
XX Sequence 501 AA;  
Query Match 97.8%; Score 2566.5; DB 4; Length 501;  
Best Local Similarity 99.4%; Pred. No. 6.5e-229;  
Matches 498; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
QY 8 MAASLLAV-LLLLLRGMFSSPPPPALLEKVFQYIDLHODEFVQTLKEWVAIESDVQP 66  
Db 1 MAASLLAVLLLLLLRGMFSSPPPPALLEKVFQYIDLHODEFVQTLKEWVAIESDVQP 60  
QY 67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGT 126  
Db 61 VPRFRQELFXMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGT 120  
QY 127 VCFYGHLDVQPADRGDGLWLTDPVYLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 186  
Db 121 VCFYGHLDVQPADRGDGLWLTDPVYLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 180

QY 187 LPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246  
Db |||||||  
QY 247 SYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306  
Db |||||||  
QY 307 INTYKAIHLDLSEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKVIP 366  
Db |||||||  
QY 367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVWMTLGLHPWIANIDDTQ 426  
Db |||||||  
QY 427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGGEHSQNEKINR 486  
Db |||||||  
QY 487 WNYIEGTKLFAAFFLEMAQLH 507  
Db |||||||  
RESULT 24  
AAU25426  
ID AAU25426 standard; protein; 501 AA.  
XX AC AAU25426;  
XX DT 18-DEC-2001 (first entry)  
XX DE Human Schizophrenia-Associated Protein Isoform (SPI) 238/240.  
XX KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.  
XX OS Homo sapiens.  
XX PN WO200162785-A2.  
XX PD 30-AUG-2001.  
XX PF 23-FEB-2001; 2001WO-GB000792.  
XX PR 24-FEB-2000; 2000GB-00004415.  
XX PR 28-DEC-2000; 2000US-00750395.  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX Herath HMCAC, Parekh RB, Rohlff C, Terrett JA, Tyson KL;  
WPI; 2001-570624/64.  
N-PSDB; AAS42478.  
New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.  
PS Disclosure; Fig 4A; 148pp; English.  
XX The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs  
XX Sequence 501 AA;  
SQ

PT	Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.	Claim 8; Fig 4A; 160pp; English.
PS		
XX		
CC	The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIs and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neural defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of neuropsychiatric disorders. AAU15114- AAU15762 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention	
XX		
SQ	Sequence 501. AA;	
	Query Match 97.8%; Score 2566.5; DB 4; Length 501;	
	Best Local Similarity 99.4%; Pred. No. 6.5e-229;	
	Matches 498; Conservative 1; Mismatches 1; Indels 1; Gaps 1;	
QY	8 MAASLLAV-LLLLLERGMFSSPPPPALLEKFVQYIDLHQDEFVQTLKEWVAIESDSVQP 66	
DB	1 MAASLLAVLLLLLLERGMFSSPPPPALLEKFVQYIDLHQDEFVQTLKEWVAIESDSVQP 60	
QY	67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT 126	
DB	61 VPRFRQELFXMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT 120	
QY	127 VCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 186	
DB	121 VCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 180	
QY	187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246	
DB	181 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 240	
QY	247 SYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306	
DB	241 SYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 300	
QY	307 INTYKAIHLDLLEYRNSRVEKFLEFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIP 366	
DB	301 INTYKAIHLDLLEYRNSRVEKFLEFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIP 360	
QY	367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWIANIDDTQ 426	
DB	361 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWIANIDDTQ 420	
QY	427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINR 486	
DB	421 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINR 480	
QY	487 WNYIEGTKLFAAFFLEMAQLH 507	
DB	481 WNYIEGTKLFAAFFLEMAQIH 501	
RESULT 25		
AAU15115		
ID	AAU15115 standard; protein; 501 AA.	
XX		
AC	AAU15115;	
XX		
DT	24-OCT-2001 (first entry)	
XX		
DE	Schizophrenia-associated isoform SPI-238/240.	
XX		
KW	Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;	
KW	neurological disorder; neuropathy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200163293-A2.	
XX		
PD	30-AUG-2001.	
XX		
PF	23-FEB-2001; 2001WO-GB000783.	
XX		
PR	24-FEB-2000; 2000GB-00004415.	
PR	28-DEC-2000; 2000US-00750395.	
XX		
PPA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.	
XX		
PI	Herath HMAC, Parekh RB, Rohlff C;	
XX		
DR	WPI; 2001-502868/55.	
DR	N-PSDB; AAS23811.	
XX		
PT	Diagnosing and monitoring Schizophrenia by detecting the presence of	

PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
PT Isoforms in samples of cerebrospinal fluid.  
XX  
PS Claim 8; Fig 4A; 160pp; English.  
XX  
CC The invention relates to methods and compositions for screening,  
CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
CC the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH  
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,  
CC studying the effectiveness of treatments and for identifying potential  
CC therapeutic agents. The method is used for (1) screening or diagnosis of  
CC SCH and the relative abundance of at least 1 chosen feature correlates  
CC with the presence or absence of SCH; and (2) monitoring the effect of  
CC therapy administered to a subject with SCH and the relative abundance of  
CC at least 1 chosen feature which correlates with the severity of SCH. The  
CC expression and activity of the SFs, SPIs and related molecules (e.g.  
CC secondary messengers) are studied to diagnose SCH, monitor the progress  
CC of the disorder and the effectiveness of treatment and as targets to  
CC identify and produce potential therapeutic agents for the treatment of  
CC SCH. The paucity of detectable neuralgic defects distinguishes  
CC neuropsychiatric disorders such as SCH from neurological disorders, where  
CC manifestations of anatomical and biochemical changes have been identified  
CC in many cases. Consequently the identification and characterisation of  
CC cellular and/or molecular causative defects and neuropathies are  
CC necessary for improved treatment of neuropsychiatric disorders. AAU15114-  
CC AAU15762 represent the amino acid sequences of schizophrenia-associated  
CC isoforms used in the method of the invention  
XX  
SQ Sequence 501. AA;

Query Match 97.8%; Score 2566.5; DB 4; Length 501;  
Best Local Similarity 99.4%; Pred. No. 6.5e-229;  
Matches 498; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 8 MAASLLAV-LLLLLERGMFSSPPPPALLEKFVQYIDLHQDEFVQTLKEWVAIESVQP 66  
Db 1 MAASLLAVLLLLLLERGMFSSPPPPALLEKFVQYIDLHQDEFVQTLKEWVAIESVQP 60  
Qy 67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT 126  
Db 61 VPRFRQELFXMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT 120  
Qy 127 VCFYGHLDVQPADRGDGLWLTDPYVLTVEVGKLYGRGATDNKGPVLAWINAVSAFRALEQD 186  
Db 121 VCFYGHLDVQPADRGDGLWLTDPYVLTVEVGKLYGRGATDNKGPVLAWINAVSAFRALEQD 180  
Qy 187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246  
Db 181 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 240  
Qy 247 SYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306  
Db 241 SYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 300  
Qy 307 INTYKAIHLDLLEYRNSRVEKFLEFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIP 366  
Db 301 INTYKAIHLDLLEYRNSRVEKFLEFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIP 360  
Qy 367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWIANIDDTQ 426  
Db 361 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWIANIDDTQ 420  
Qy 427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINR 486  
Db 421 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINR 480  
Qy 487 WNYIEGTKLFAAFFLEMAQLH 507  
Db 481 WNYIEGTKLFAAFFLEMAQIH 501





PS	Disclosure; Fig 2B; 163pp; English.	
XX		
CC	The invention relates to a preparation comprising an isolated Bipolar	
CC	Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are	
CC	used to screen, diagnose or prognose of BAD or unipolar depression,	
CC	determine the stage or severity of BAD or unipolar depression, identify a	
CC	subject at risk of developing BAD or unipolar depression, or monitor the	
CC	effect of therapy in a subject. They are also used to screen for or	
CC	identify agents that interact with a DPI. These agents, antibodies	
CC	against the DPIs, and nucleic acids encoding the DPIs are used to treat	
CC	or prevent BAD or unipolar depression. Diseases that can be treated are	
CC	attention deficient disorder, a schizoaffective disorder, a bipolar or a	
CC	unipolar affective disorder. The DPIs are used in proteomics. The	
CC	proteomic approach of using DPIs for screening, diagnosis or prognosis of	
CC	BAD or unipolar depression overcomes the problems of using gene	
CC	expression analysis, such as not being able to obtain central nervous	
CC	system (CNS) tissue from a living patient under normal circumstances. The	
CC	present sequence is a protein containing a DIP, expressed from a PCR	
CC	fragment generated from two EST (expressed sequence tags) sequences	
CC	AAS326679 and AI589129	
XX		
SQ	Sequence 498 AA;	
Query Match		
Best Local Similarity 94.7%; Score 2483; DB 4; Length 498;		
Matches 489; Conservative 1; Mismatches 7; Indels 4; Gaps 4;		
QY	8 MAASLLAV-LLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVOTLKEWVAIESDSVQP 66	
Db	1 MAASLLAVLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVOTLKEWVAIESDSVQP 60	
QY	67 VPRFRQELFRMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT 126	
Db	61 VPRFRQELFXMVAARDTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT 120	
QY	127 VCFYGHLDVQPADRGDWLTDPYVLTVEVCKLYGRGATDNKGPVLAWINAVSAFRALEQD 186	
Db	121 VCFYGHLDVQPADRGDWLTDPYVLTVEVCKLYGRGATDNKGPVLAWINAVSAFRALEQD 180	
QY	187 LPVNIKFIIIEGMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRPKPAITYGTRGN 246	
Db	181 LPVNIKFIIIEGMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRPKPAITYGTRGN 240	
QY	247 SYFMVEVKCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306	
Db	241 SYFMVEVKCRDQDFESGTGGILHEPMDLVALLGSSVDSGGHILVPGIYDE-WPLTEEE 299	
QY	307 INTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSPSLSIHGEGAFDEPGTKTVIP 366	
Db	300 INTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSPSLSIHGEGAFDEPGTKTVIP 359	
QY	367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQ 426	
Db	360 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKM-WSMTLGLHPWIANIDDTQ 418	
QY	427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIVLPLGAVDDGEHSQNEKINR 486	
Db	419 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKS-WLIPLGAVDDGEHSQNEKINR 477	
QY	487 WNYIEGTKLFAAFLEMAQLH 507	
Db	478 WNYIEGTKLFAAFLEMAQIH 498	
RESULT 28		
AAM41935		
ID	AAM41935 standard; protein; 358 AA.	
XX		
AC	AAM41935;	
XX		
DT	22-OCT-2001 (first entry)	
XX		
DE	Human polypeptide SEQ ID NO 6866.	
XX		
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;	
KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200153312-A1.	
XX		
PD	26-JUL-2001.	
XX		
PF	26-DEC-2000; 2000WO-US034263.	
XX		
PR	23-DEC-1999; 99US-00471275.	
PR	21-JAN-2000; 2000US-00488725.	
PR	25-APR-2000; 2000US-00552317.	
PR	20-JUN-2000; 2000US-00598042.	
PR	19-JUL-2000; 2000US-00620312.	
PR	03-AUG-2000; 2000US-00653450.	
PR	14-SEP-2000; 2000US-00662191.	
PR	19-OCT-2000; 2000US-00693036.	
PR	29-NOV-2000; 2000US-00727344.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;	
PI	Zhou P, Goodrich R, Drmanac RT;	
XX		
DR	WPI; 2001-442253/47.	
DR	N-PSDB; AAI61091.	
XX		
PT	Novel nucleic acids and polypeptides, useful for treating disorders such	
PT	as central nervous system injuries.	
XX		
PS	Example 2; SEQ ID NO 6866; 10078pp; English.	
XX		
CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the	
CC	encoded polypeptides (AAM38642-AAM42213) with nootropic,	
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	localised neuropathies and central nervous system diseases, such as	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilisation of the activities such as: Immune system suppression,	
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	
CC	assays for receptor activity, arthritis and inflammation, leukaemias and	
CC	C.N.S disorders. Note: The sequence data for this patent did not form	
CC	part of the printed specification	
XX		
SQ	Sequence 358 AA;	
Query Match		
Best Local Similarity 66.5%; Score 1743; DB 4; Length 358;		
Matches 340; Conservative 2; Mismatches 8; Indels 0; Gaps 0;		
QY	158 LYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEAGSVALEELVEKEKDRF 217	
Db	9 LYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKFIIIEGMEAGSVALEELVEKEKDRF 68	
QY	218 FSGVDYIVISDNLWISQRPKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLV 277	
Db	69 FSGVDYIVISDNLWISQRPKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLV 128	
QY	278 ALLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSRVEKFLFDTKEEI 337	
Db	129 ALLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSRVEKFLFDTKEEI 188	







Db 360 YLTKKFAELRSPNEFKVYMGHGKPPWVSDFSHPHYLGRAMKTVFGVEPDLTREGGSIP 419

QY 453 IAKMFQEIYVHKSVVLIPLGAVDDGEHSONEKNINRWNYIEGTKLFAAFFLEMAQL 506

Db 420 VTLTFFQATGKNVMLLPVGSADDGAHSONEKNINRWNYIEGTKMLAAYLYEVSQ 473

RESULT 32

AAG67236

ID AAG67236 standard; protein; 475 AA.

XX

AC AAG67236;

XX

DT 13-NOV-2001 (first entry)

XX

DE Amino acid sequence of a human carnosinase 2 (HC2) polypeptide.

XX

DE Human; carnosinase 2; HC2; cognitive disorder; foetal deficiency; trauma; developmental abnormality; neurodegenerative disorder; schizophrenia; amytrophic lateral sclerosis; Parkinson's disease; ischaemic shock; epilepsy; polyarthritits; hypertension; ischaemic heart damage; ulcer; adrenal cortical function; wound healing; inflammatory disease.

XX

OS Homo sapiens.

XX

PN EP1122307-A1.

XX

PD 08-AUG-2001.

XX

PF 04-FEB-2000; 2000EP-00400313.

XX

PR 04-FEB-2000; 2000EP-00400313.

XX

PA (SNFI ) SANOFI-SYNTHELABO.

XX

PI Ledig J, Saudek V;

XX

DR WPI; 2001-543058/61.

DR N-PSDB; AAH75199.

XX

PT Human carnosinase polypeptides and polynucleotides, useful for treating or preventing cognitive disorders, developmental abnormalities and fetal deficiencies, neurodegenerative disorders, or inflammatory disorders.

PS Claim 6; Page 19-21; 30pp; English.

XX

CC The present sequence represents a human carnosinase 2 (HC2) polypeptide. The carnosinase polypeptides and polynucleotides are useful for treating or preventing cognitive disorders, developmental abnormalities and fetal deficiencies, neurodegenerative disorders, such as amytrophic lateral sclerosis, Parkinson's disease, schizophrenia, abnormal mental states, ischaemic shock, epilepsy, polyarthritits, hypertension, ischaemic heart damage, ulcers, adrenal cortical function, wound healing, trauma, and inflammatory diseases. The HC2 polynucleotides may also be used as diagnostic probes or primers, hybridization probes for cDNA and genomic DNA, to isolate full length cDNAs and genomic clones encoding HC2 and other genes having high similarity to the HC2 gene, as research reagents and materials for discovery of treatments and diagnostics for animal and human diseases, and for chromosome identification. The HC2 polypeptides may be used as immunogens to produce antibodies immunospecific for the HC2 polypeptides, to induce immunological response in a mammal against the above mentioned disorders, in screening for candidate compounds which stimulate or inhibit the activity of HC2, and to assess the binding of small molecule substrates and ligands in cells, cell-free preparations, chemical libraries or natural product mixtures

XX

SQ Sequence 475 AA;

Query Match 52.0%; Score 1363; DB 4; Length 475;

Best Local Similarity 53.2%; Pred. No. 3.4e-117;

Matches 252; Conservative 85; Mismatches 135; Indels 2; Gaps 1;

QY 33 ALLEKVQYIDLHQDEFVQTLKEWVAIESDSQVPRFRQELFRMMAVAADTLQRLGARV 92

Db 2 AALTTLFKYIDENQDRYIKKLAKWVAIQ--SVSAWPEKRGEIRRMMEVAAADVQLGGSV 59

QY 93 ASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFYGLDVPADRGDWLTDPPYVLT 152

Db 60 ELVDIGKQKLPDGEIPLPPILLGRLGSDPOKTKVCIYGHLDVQPAALDEGDWSEPFTLV 119

QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEK 212

Db 120 ERDGKLYGRGSTDDKGPVAGWINALEAYQTQGEIPVNVVRFLEGMEESSGGLDELIFA 179

QY 213 EKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP 272

Db 180 RKDTFFKDVYVCISDNYWLGKKKPCITYGLRGICYFFIEVECSNKDLHSGVYGGSVHEA 239

QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAIHLDLLEEYRNSRVEKFLFD 332

Db 240 MTDLILLMGS�VDKRGNILIPGINEAAVTEEEHKLYDDIDFDIEEFAKDVGAQILLHS 299

QY 333 TKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392

Db 300 HKKDILMHRWRYPSSLHGHIEGAFSGGAKTVIPRKVVGKFSIRLVPNMTPEVVGEQVTS 359

QY 393 HLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDIRDGSTIP 452

Db 360 YLTKKFAELRSPNEFKVYMGHGKPPWVSDFSHPHYLGRAMKTVFGVEPDLTREGGSIP 419

QY 453 IAKMFQEIYVHKSVVLIPLGAVDDGEHSONEKNINRWNYIEGTKLFAAFFLEMAQL 506

Db 420 VTLTFFQATGKNVMLLPVGSADDGAHSONEKNINRWNYIEGTKMLAAYLYEVSQ 473

RESULT 33

AAU72910

ID AAU72910 standard; protein; 475 AA.

XX

AC AAU72910;

XX

DT 26-FEB-2002 (first entry)

XX

DE Human metalloprotease partial protein sequence #22.

XX

KW Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder.

XX

OS Homo sapiens.

XX

PN WO200183782-A2.

XX

PD 08-NOV-2001.

XX

PF 04-MAY-2001; 2001WO-US014431.

XX

PR 04-MAY-2000; 2000US-0201879P.

XX

PA (SUGE-) SUGEN INC.

XX

PI Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;

PI Payne V;

XX

DR WPI; 2002-041502/05.

DR N-PSDB; AAS97193.

XX

PT Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular

PT disease, migraine, pain, psychotic and inflammatory disorders.  
XX  
XX Claim 28; Fig 2I; 232pp; English.  
PS  
XX The invention relates to an isolated, enriched, or purified protease  
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to  
CC screen for substances (S) that may modulate its activity. Administering S  
CC (which modulates protease activity in vitro) may be used to treat a  
CC disease or disorder selected from cancers (e.g., of tissues, of blood or  
CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,  
CC brain, ovarian, bladder or kidney), immune-related diseases and  
CC disorders, cardiovascular disease, brain or neuronal-associated diseases  
CC (e.g., central or peripheral nervous system diseases, migraine, pain,  
CC sexual dysfunction, mood disorders, attention disorders, cognition  
CC disorders, hypotension, hypertension, psychotic disorders, neurological  
CC disorders and dyskinesias), metabolic disorders and inflammatory  
CC disorders. (I) may also be useful as a diagnostic tool for a disease or  
CC disorder such as those above. AAU72876-AAU72910 represent human protease  
CC amino acid sequences of the invention  
XX  
SQ Sequence 475 AA;

XX WO2003025138-A2.  
PN  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-US029560.  
XX  
PR 17-SEP-2001; 2001US-0323469P.  
PR 20-SEP-2001; 2001US-0323887P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 08-FEB-2002; 2002US-0355145P.  
PR 08-FEB-2002; 2002US-0355257P.  
PR 12-APR-2002; 2002US-0372246P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;  
PI Zlotnik A;  
XX  
DR WPI; 2003-354600/33.  
DR N-PSDB; ACC72761.  
XX  
PT New genes that are up-regulated or down-regulated in cancers, useful as  
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
PT therapeutic targets for screening drugs for treating these diseases.  
XX  
PS Claim 12; Page 747; 767pp; English.  
XX  
CC The present invention describes an isolated nucleic acid molecule, which  
CC comprises the sequence of any of the genes that are up-regulated or down-  
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
CC related gene nucleotide sequences which encode the proteins given in  
CC ABR58521 to ABR58709. Also described: (1) determining the presence or  
CC absence of a pathological cell in a patient; (2) an expression vector  
CC comprising a nucleic acid molecule described above; (3) a host cell  
CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
CC of (4); (6) specifically targeting a compound to a pathological cell in a  
CC patient by administering to the patient the antibody above; and (7) a  
CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
CC therapeutic targets. In particular, the nucleic acid is useful for  
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
CC drug screening, particularly for identifying agents for treating these  
CC pathologies  
XX  
SO Sequence 475 AA;



Db	240	MTDLILLMGLSLVDKRCGNILIPGINEAAVAVTEEEHKLVDIDFDIEEFAKDVGQAILLHS	299
Qy	333	TKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR	392
Db	300	HKXDILMHRWRYPSSLHIGIEGAFSGSGAKTVIPRKVVGKFSIRLVPMNTPPEVVEQVTS	359
Qy	393	HLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQVLAAKRAIRTVEGTEPDMIRDGSTIP	452
Db	360	YLTKKFAELRSPNEFKVMYMGHGKPKVWSDFSHPHYLAGRRAMKTVFGVEPDLTREGGSIP	419
Qy	453	IAKMFQEIIVHKSIVLPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQL	506
Db	420	VTLTFQEATGKNVMLLPVGSADDDGAHSQNEKLNRYNYIEGTKMLAAYLYEVSOL	473
RESULT 35			
AAG67143			
ID	AAG67143 standard; protein; 475 AA.		
XX			
AC	AAG67143;		
DT	13-NOV-2001 (first entry)		
XX			
DE	Amino acid sequence of a human enzyme.		
XX			
KW	Human; enzyme; cancer; neurological disorder; epilepsy; stroke;		
KW	Alzheimer's disease; Pick's disease; Huntington's disease; dementia;		
KW	multiple sclerosis; Parkinson's disease; amyotrophic lateral sclerosis;		
KW	meningitis; schizophrenic disorder; neuroskeletal disorder; allergy;		
KW	addison's disease; autoimmune disease; anemia; asthma; Crohn's disease;		
KW	adult respiratory distress syndrome; atopic dermatitis; psoriasis;		
KW	diabetes mellitus; osteoporosis; pancreatitis; rheumatoid arthritis;		
KW	infection; genetic disorder; muscular dystrophy; Gaucher's disease;		
KW	Huntington's chorea; sickle cell anemia; thalassemia; atherosclerosis;		
KW	Von Willebrand's disease; Wilms' tumour; cell proliferative disorder;		
KW	leukemia; hepatitis; cirrhosis; arteriosclerosis; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
FH	Location/Qualifiers		
FT	Key	117	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	130	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	150	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	168	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	183	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	223	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	235	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	249	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	270	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	299	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	341	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	362	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	370	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	377	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	423	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	428	
FT	Modified-site	/note= "potential phosphorylation site"	
FT	Modified-site	439	

FT	Modified-site	/note= "potential phosphorylation site"	
FT	446		
FT	/note= "potential phosphorylation site"		
XX			
PN	WO200164896-A2.		
XX			
PD	07-SEP-2001.		
XX			
PF	01-MAR-2001; 2001WO-US006806.		
XX			
PR	01-MAR-2000; 2000US-0186307P.		
PR	28-MAR-2000; 2000US-0192532P.		
PR	30-MAR-2000; 2000US-0193578P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Tang YT, Lu DAM, Bandman O, Yue H, Azimzai Y, Lal P, Burford N;		
PI	Baughn MR;		
XX			
DR	WPI; 2001-550184/61.		
DR	N-PSDB; AAH75171.		
XX			
PT	Novel human enzyme molecule useful for treating and preventing, e.g.,		
PT	cancer, genetic disorders, neurological disorders, autoimmune and		
PT	inflammatory disorders.		
XX			
PS	Claim 1; Page 131-132; 154pp; English.		
XX			
CC	The present sequence represents a human enzyme. The enzyme polynucleotide		
CC	and polypeptide are useful for diagnosis, treatment and prevention of		
CC	cancers, neurological disorders (e.g. epilepsy, stroke, Alzheimer's		
CC	disease, Pick's disease, Huntington's disease, dementia, multiple		
CC	sclerosis, Parkinson's disease, amyotrophic lateral sclerosis, bacterial		
CC	and viral meningitis, schizophrenic disorders and neuroskeletal		
CC	disorders), autoimmune/inflammatory disorders (e.g. allergies, addison's		
CC	disease, autoimmune diseases, adult respiratory distress syndrome,		
CC	anemia, asthma, Crohn's disease, atopic dermatitis, diabetes mellitus,		
CC	osteoporosis, pancreatitis, psoriasis, rheumatoid arthritis, and viral,		
CC	bacterial, fungal, parasitic, protozoal and helminthic infections),		
CC	genetic disorder (e.g. Duchenne and Becker muscular dystrophy, Gaucher's		
CC	disease, Huntington's chorea, sickle cell anemia, thalassemia, Von		
CC	Willebrand's disease and Wilms' tumour), and cell proliferative disorder		
CC	(e.g. atherosclerosis, leukemia, hepatitis, cirrhosis, and		
CC	arteriosclerosis). The polynucleotide is also useful in somatic or		
CC	germline gene therapy		
XX			
SQ	Sequence 475 AA;		
	Query Match 51.8%; Score 1358; DB 4; Length 475;		
	Best Local Similarity 53.0%; Pred. No. 9.8e-117;		
	Matches 251; Conservative 86; Mismatches 135; Indels 2; Gaps 1;		
QY	33 ALLEKVFOYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFQELFRMMAVAADTLQRLGARV	92	
Db	2 AALTTLFKYIDENQDRYIKKLAKWVAIQ--SVSAWPEKRGGEIRRMMEVAADVKQLGGSV	59	
QY	93 ASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLT	152	
Db	60 ELVDIGKQKLPDGSEIPLPILLGRLGSDPQKKTVCIIYGHLDVQPAALDGDWSEPFITLV	119	
QY	153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEK	212	
Db	120 ERDGKLHGRGSTDDKGPVAGWINALEAYQKTQGEIPVNVVRCLEGMEESSGGLDELIFA	179	
QY	213 EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP	272	
Db	180 RKDTFFKDVYVCISDNYWLGKKKPCITYGLRGICYFFIEVECSNKDLHSGVYGGSVHEA	239	
QY	273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLLEEYRNSRVEKFLFD	332	
Db	240 MTDLILLMGLSLVDKRCGNILIPGINEAAVAATEEHKLYDDIDFDIEEFAKDVGQAQILLHS	299	
QY	333 TKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR	392	



Db 300 HKKDILMHRWRYPSLSLHGIEGAFSGGAKTVIPRKWGFKSIRLVNMTPEVVGQVTS 359  
QY 393 HLEDVFSKRNSSNMVSMVTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 452  
Db 360 YLTKKFAELRSPNEFKVMYMGHGKPVWSDFSHPHYLAGRRAMKTVFGVEPDLTREGGSIP 419  
QY 453 IAKMFOEIVHKSIVLPLGAVDDGEHSQNEKINRWNYIEGTLFAAFFLEMAQL 506  
Db 420 VTLTFQEATGKNVMLLPVGSADDDGAHSQNEKLNRYNIEGTMKMLAAYLYEVSQ 473

RESULT 36  
AAM41668  
ID AAM41668 standard; protein; 476 AA.  
XX  
AC AAM41668;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 6599.  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI60824.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
as central nervous system injuries.  
XX  
PS Example 2; SEQ ID NO 6599; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 476 AA;  
Query Match 51.8%; Score 1358; DB 4; Length 476;  
Best Local Similarity 53.0%; Pred. No. 9.8e-117;  
Matches 251; Conservative 86; Mismatches 135; Indels 2; Gaps 1;  
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV 92  
Db 3 AALTTLFKYIDENQDRIYIKKLAKWVAIQ--SVSAWPEKKRGEIRRMMEVAADVKQLGGSV 60  
QY 93 ASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCVFGHLDVQPADRGDWLTDPVYVLT 152  
Db 61 ELVDIGKQKLPDGSEIPLPILLGRLGSDPQKKTVCYIGHLDVQPAALEDGWDSEPF TLV 120  
QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEK 212  
Db 121 ERDGLHGRGSTDDKGPVAGWINALAYQKTQGEIPVNVRFCLGMEESGSEGLDELIFA 180  
QY 213 EKDRFFSGVDYIVISDNLWISQRKPAITYTRGNSYFMVEVKCRDQDFHSGTFFGILHEP 272  
Db 181 RKDTFFKDVYVCISDNYWLKKKPCITYGLRGICVYFFIEVECSNKDLHSGVYGGSVHEA 240  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 241 MTDLILLMSLVDKRGNILIPGINEAFAVTEEEHKLVDIDFIEEFKDVGAQILLHS 300  
QY 333 TKBEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 301 HKXDILMHRWRYPSLSLHGIEGAFSGGAKTVIPRKVVGKFSIRLVNMTPEVVGQVTS 360  
QY 393 HLEDVFSKRNSSNMVSMVTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 452  
Db 361 YLTKKFAELRSPNEFKVMYMGHGKPVWSDFSHPHYLAGRRAMKTVFGVEPDLTREGGSIP 420  
QY 453 IAKMFOEIVHKSIVLPLGAVDDGEHSQNEKINRWNYIEGTLFAAFFLEMAQL 506  
Db 421 VTLTFQEATGKNVMLLPVGSADDDGAHSQNEKLNRYNIEGTMKMLAAYLYEVSQ 474

RESULT 37  
AAB93225  
ID AAB93225 standard; protein; 475 AA.  
XX  
AC AAB93225;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:12214.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-00116126.  
XX  
PR 29-JUL-1999; 99JP-00248036.  
PR 27-AUG-1999; 99JP-00300253.  
PR 11-JAN-2000; 2000JP-00118776.  
PR 02-MAY-2000; 2000JP-00183767.  
PR 09-JUN-2000; 2000JP-00241899.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PT

XX

PS Claim 8; SEQ ID NO 12214; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX

SQ Sequence 475 AA;

Query Match 51.7%; Score 1356; DB 4; Length 475;  
Best Local Similarity 53.0%; Pred. No. 1.5e-116;  
Matches 251; Conservative 85; Mismatches 136; Indels 2; Gaps 1;

QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMMAVAADTLQRLGARV 92  
Db 2 AALTTLFKYIDENQDRIYIKKLAKWVAIQ--SVSAWPEKRGGEIRRMMEVAADVKQLGGSV 59

QY 93 ASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFVGHLDVQPADRGDGLWLTDPYVLT 152  
Db 60 ELVDIGKQKLPDGSEIPLPPIILGRLGSDPQKKTVCYIGHLDVQPAALDGDWDSFPFTLV 119

QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEK 212  
Db 120 ERDGKLYGGSTDDKGPVAGWINALEAYQKTGQETPVNVRFCLEGMEESGSEGLDELIFA 179

QY 213 EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP 272  
Db 180 RKDTFFKDVYVCISDNYWLGKKKPCITYGLRGICYFFIEVECSNKLHSGVYGGSVHEA 239

QY 273 MADLVALLGSLVDSGGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSSRVEKFLFD 332  
Db 240 MTDLILLMGS�VDKRGNLIIPGINEAAVATEEHEHKLYDDIDFIEEFAKDVGQAQILLHS 299

QY 333 TKEEILMHLWRYPSSLIHGIEGAFDEPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 300 HKDILMHRWRYPSSLIHGIEGAFSGGAKTVIPRKVVGKFSIRLVPNMTPEVVGEQVTS 359

QY 393 HLEDVFSKRNSSNMVMSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 452  
Db 360 YLTKKFAELRSPNEFKVYMGHGKPKWVSDFSHPHYLAGRRAMKTVFGVEPDLTREGGSIP 419

QY 453 IAKMFQEIYVHKSVVLIPLGAVDDGESHSONEKNRWNYIEGTLKFAAFLEMAQL 506  
Db 420 VTLTFFQATGKNVMLLPVGSADDDGAHSQNEKLNRYNIEGTMKLAAYLYEVSQ 473

AAE20961

ID AAE20961 standard; protein; 475 AA.

XX

AC AAE20961;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human carboxypeptidase-like enzyme.

XX

KW Human; carboxypeptidase-like enzyme; therapy; cancer; asthma; allergy; chronic obstructive pulmonary disease; cytostatic; antiasthmatic; antiallergic; enzyme.

XX

OS Homo sapiens.

XX

PN WO200220805-A2.

XX

PD 14-MAR-2002.

XX

PF 05-SEP-2001; 2001WO-EP010203.

XX

PR 11-SEP-2000; 2000US-0231546P.

XX

PA (FARB ) BAYER AG.

XX

PI Liou J;

XX

DR WPI; 2002-315660/35.

DR N-PSDB; AAD33906.

XX

PT New purified human carboxypeptidase-like enzyme, useful for identifying modulators of enzyme activity for treating cancer, asthma, allergy or chronic obstructive pulmonary disease.

XX

PS Claim 25; Fig 24; 127pp; English.

XX

CC The invention relates to a purified human carboxypeptidase-like enzyme. The enzyme is useful for screening for agents which decrease the activity of an carboxypeptidase-like enzyme. The invention is also useful for treating a carboxypeptidase-like enzyme dysfunction related diseases condition such as chronic obstructive pulmonary disease, cancer, asthma or allergy. The invention is also useful for modulating carboxypeptidase-like enzyme activity in a disease condition. The invention is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to presence of mutations in the nucleic acid sequences which encode the enzyme. The present sequence is human carboxypeptidase-like enzyme

XX

SQ Sequence 475 AA;

Query Match 51.7%; Score 1356; DB 5; Length 475;  
Best Local Similarity 53.0%; Pred. No. 1.5e-116;  
Matches 251; Conservative 85; Mismatches 136; Indels 2; Gaps 1;

QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMMAVAADTLQRLGARV 92  
Db 2 AALTTLFKYIDENQDRIYIKKLAKWVAIQ--SVSAWPEKRGGEIRRMMEVAADVKQLGGSV 59

QY 93 ASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFVGHLDVQPADRGDGLWLTDPYVLT 152  
Db 60 ELVDIGKQKLPDGSEIPLPPIILGRLGSDPQKKTVCYIGHLDVQPAALDGDWDSFPFTLV 119

QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEK 212  
Db 120 ERDGKLYGGSTDDKGPVAGWINALEAYQKTGQETPVNVRFCLEGMEESGSEGLDELIFA 179

QY 213 EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP 272  
Db 180 RKDTFFKDVYVCISDNYWLGKKKPCITYGLRGICYFFIEVECSNKLHSGVYGGSVHEA 239

QY 273 MADLVALLGSLVDSGGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSSRVEKFLFD 332  
Db 240 MTDLILLMGS�VDKRGNLIIPGINEAAVATEEHEHKLYDDIDFIEEFAKDVGQAQILLHS 299





PR 24-FEB-2000; 2000US-01846664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465573/50.

N-PSDB; AAI99591.

Isolated digestive system associated polypeptide for treating, preventing  
and/ or prognosing disorders related to the digestive system including  
digestive system cancers and also for testing and detection e.g.  
diagnosis.

XX PS Claim 11; SEQ ID NO 103; 509pp + Sequence Listing; English.

XX CC The invention relates to novel genes (AAI99548-AAI99604) and proteins (AAM99936-AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 476 AA;

Query Match 51.7%; Score 1355; DB 4; Length 476;  
Best Local Similarity 53.0%; Pred. No. 1.9e-116;  
Matches 251; Conservative 85; Mismatches 136; Indels 2; Gaps 1;

Qy 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPRFRQELFRMVAVAADTLQRLGARV 92  
Db 3 AALTTLFKYIDENQDRYIKKLAKWVAIQ--SVSAWPEKRGERTRMMEVAADVKQLGGSV 60

Qy 93 ASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFYLHLDVPADRGDGLWLTDPYVLT 152  
Db 61 ELVDIGKQKLPDGSEIPLPILLRLGSDPPQKKTVCYFYLHLDVQPALEDGWDSEFTLV 120

Qy 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEGAGSVALEELVEK 212  
Db 121 ERDGKLYGRGSTDDKGPVAGWINALEAYQKTGOEIPVNVRFCLGMEESGSEGLDELIFA 180

Qy 213 EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP 272  
Db 181 RKDTFFKVDYVVCISDNWLGKKKPCITYGLRGICYFFIEVECSNKDLHSGVYGGSVHEA 240

Qy 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLDEEYRNSRVEKFLFD 332  
Db 241 MTDLILLMGLSLVDKRGNILIPGINEAAVTEEEHKLVDIDFDIEFAKDVGAQILLHS 300

Qy 333 TKEEILMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 301 HKKDILMHRWRYPYSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPEVVGEQVTS 360

Qy 393 HLEDVFSKNSNKMVSMVMTLGLHPNIANIDDTQYLAACKRAIRTVFGTEPDMIRDGSTIP 452  
Db 361 YLTKKFAELRSPNEFKVYMGHGKPPWVSDFSHPHYLGRRAMKTVFGVEPDLTREGGSIP 420

Qy 453 IAKMFOEIVHKSVVLIPLGAVDDGHSQNEKINRWNYIEGTXKLFAPAFFLEMAQL 506  
Db 421 VTLTQFQATGKNVMLLPVGSADGAGHSQNEKLNRYNIEGTXKMLAAYLYEVSQ 474

RESULT 41  
AAU06066  
ID AAU06066 standard; protein; 476 AA.  
XX AC AAU06066;  
XX DT 07-NOV-2001 (first entry)  
XX DE Novel human ADAM or serine protease.  
XX KW Human; ADAM; a disintegrin and metalloprotease domain; adamalysin;  
KW KW serine protease; cancer; immune disease; blood-related disorder; HMMF73;  
KW hyperproliferative disorder; renal disorder; cardiovascular disorder;

KW respiratory disorder; inflammatory disorder; neurological disorder;  
KW endocrine disorder; reproductive system disorder; infectious disease;  
KW gastrointestinal disorder; gene therapy; cytostatic; anti inflammatory;  
KW fertility; thrombolytic; anti coagulant; nootropic; neuroprotective.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT Misc-difference 127 /label= Unknown  
FT /note= "Encoded by YAT"  
XX WO200155309-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001311.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 24-FEB-2000; 2000US-0184664P.  
XX 02-MAR-2000; 2000US-0186350P.  
XX 16-MAR-2000; 2000US-0189874P.  
XX 17-MAR-2000; 2000US-0190076P.  
XX 18-APR-2000; 2000US-0198123P.  
XX 19-MAY-2000; 2000US-0205515P.  
XX 07-JUN-2000; 2000US-0209467P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 30-JUN-2000; 2000US-0215135P.  
XX 07-JUL-2000; 2000US-0216647P.  
XX 07-JUL-2000; 2000US-0216880P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225213P.  
XX 14-AUG-2000; 2000US-0225214P.  
XX 14-AUG-2000; 2000US-0225266P.  
XX 14-AUG-2000; 2000US-0225267P.  
XX 14-AUG-2000; 2000US-0225268P.  
XX 14-AUG-2000; 2000US-0225270P.  
XX 14-AUG-2000; 2000US-0225447P.  
XX 14-AUG-2000; 2000US-0225757P.  
XX 14-AUG-2000; 2000US-0225758P.  
XX 14-AUG-2000; 2000US-0225759P.  
XX 18-AUG-2000; 2000US-0226279P.  
XX 22-AUG-2000; 2000US-0226681P.  
XX 22-AUG-2000; 2000US-0226688P.  
XX 22-AUG-2000; 2000US-0227182P.  
XX 23-AUG-2000; 2000US-0227009P.  
XX 30-AUG-2000; 2000US-0228924P.  
XX 01-SEP-2000; 2000US-0229287P.  
XX 01-SEP-2000; 2000US-0229343P.  
XX 01-SEP-2000; 2000US-0229344P.  
XX 01-SEP-2000; 2000US-0229345P.  
XX 05-SEP-2000; 2000US-0229509P.  
XX 05-SEP-2000; 2000US-0229513P.  
XX 06-SEP-2000; 2000US-0230437P.  
XX 06-SEP-2000; 2000US-0230438P.  
XX 08-SEP-2000; 2000US-0231242P.  
XX 08-SEP-2000; 2000US-0231243P.  
XX 08-SEP-2000; 2000US-0231244P.  
XX 08-SEP-2000; 2000US-0231413P.  
XX 08-SEP-2000; 2000US-0231414P.  
XX 08-SEP-2000; 2000US-0232080P.  
XX 08-SEP-2000; 2000US-0232081P.  
XX 12-SEP-2000; 2000US-0231968P.  
XX 14-SEP-2000; 2000US-0232397P.  
XX 14-SEP-2000; 2000US-0232398P.  
XX 14-SEP-2000; 2000US-0232399P.





Db 361 YLTKKFAELRSPNEFKVYMGHGKXPWVSDFSHPHYLAGRRAMKTVFGVEPDLTREGGSIP 420  
QY 453 IAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFPLEMAQL 506  
Db 421 VTLTFFQATGKNVMLLPVGSADDDGAHSQNEKLNRYNIEGTMLAAYLYEVSQ 474

RESULT 42  
ABB66252  
ID ABB66252 standard; protein; 462 AA.  
XX ABB66252;  
AC  
XX  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 25548.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
XX  
PA (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI WPI; 2001-656860/75.  
XX  
DR N-PSDB; ABL10355.  
DR  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 25548; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 462 AA;

Query Match 45.5%; Score 1194.5; DB 4; Length 462;  
Best Local Similarity 50.3%; Pred. No. 1.4e-101;  
Matches 232; Conservative 83; Mismatches 139; Indels 7; Gaps 3;

QY 35 LEKVFOYIDLHQDEFVQTLKEWVAIESDSVQVPFRFRQELFERMMAVAADTLORLGARVAS 94  
Db 8 LQKFFFAFDGKKEDYIGALKTVVGIQ--SVSAWPEKRGEGRMVETWADRRLRSLGAETEL 65  
QY 95 VDMGPQQLPDGQSLPIPPVILAEIGSDPTKGTVCIFYGHLDVQPADRGDGLWLTDPYVLTIEV 154  
Db 66 ADVGQQLPNGQIILPLPKVLLGLTKGDFSKTTLVYGHLDVQPAKEDGWTNPFELTEV 125  
QY 155 DGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNKIFIEGMEEAGSVALEELVEKEK 214  
Db 126 DGKLFGRGASDDKGPVLCWIHAIEAYQKLNIALPNVKFVFEGMEEESGSEGLDLDLLERK 185

QY 215 DRFFSGVDYIVISDNLWISORKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA 274  
Db 186 DNFLADVDFVCISDNYWLGKKRPCLTYGLRGLAYFOVEVECSSKDLHSGVFGTVHEAMP 245  
QY 275 DLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFD-T 333  
Db 246 DLCHLLSILVDKOTNILVPGVDRDVAPQIKNEQSIYENIDFEVSEYKKDIGVEQLPHNGD 305  
QY 334 KEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRH 393  
Db 306 KTRLLQARWRYPSLSVHGIEGAFYEPGAKTVIPKKVIGKFSIRLVPNQDPKHIECVVKY 365  
QY 394 LEDVFSKRNSSNMVSMVLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDSIPI 453  
Db 366 LNDKWAERGSPNKMKVS-----KPWTEDPNHPHYEAAKRAIKHVFNVPEPDMTREGGSIPV 421  
QY 454 AKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTK 494  
Db 422 TLTQEATGKNVILVPVGACDDGAHSQNEKIDIVNYIEGVR 462

RESULT 43  
ABB66250  
ID ABB66250 standard; protein; 415 AA.  
XX  
AC ABB66250;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 25542.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
DR N-PSDB; ABL10353.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 25542; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 415 AA;

Query Match 43.4%; Score 1139.5; DB 4; Length 415;

Best Local Similarity 52.0%; Pred. No. 1.5e-96;  
Matches 218; Conservative 73; Mismatches 123; Indels 5; Gaps 2;  
QY 77 MNAVAADTLQRLGARVASVDMGPQQLPDQSLPIPPVILAEIGSDPTKGTVCYFGLHDVQ 136  
Db 1 MVEWTADRLRLSGAETELADVGOQTLPLNGQIIPLPKVLGLTKDPSKKTVLVYGHLDVQ 60  
QY 137 PADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIE 196  
Db 61 PALKEDGWNTPFELTEVDGKLFGRGASDDKGPVLCWHAIEAYOKLNIALPVNVKVFEE 120  
QY 197 GMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 256  
Db 121 GMEESGSEGLDLLLLERKDNFLADVDFVCISDNYWLGKRPCLTYGLRGLAYFQVEVECS 180  
QY 257 DQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLD 316  
Db 181 SKDLHSGVFGGTVEAMPDLCHLLSILVDKOTNILVPGVDRDVAPOIKNEQSIYENIDFE 240  
QY 317 LEEYRNSRVEKFLFD-TKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSI 375  
Db 241 VSEYKKGDIGVEQLPHNGDKTRLLQARWRYPSSLVHGIEGAFYEPGAKTVIPKKVIGKFSI 300  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDDTQYLAAKRAIR 435  
Db 301 RLVPNQDPKHIEECVVKYLNDKWAERGS PNMKVSG----KPWTEDPNHPHYEAAKRAIK 356  
QY 436 TVFGTEPDMIRDGSTIPIAKMFQEIIVHKS VVLIPLGAVDDGEHSQNEKINRWNIIEGTK 494  
Db 357 HVFNVEPDMTREGGSIPVTLTQEATGKNVILVPGACDDGAHSQNEKIDINYIEGVR 415

RESULT 44  
ABR52953  
ID ABR52953 standard; protein; 481 AA.  
XX ABR52953;  
AC ABR52953;  
XX 20-JUN-2003 (first entry)  
DT Protein sequence #SEQ ID 771.  
DE Multiprotein complex; eukaryote; drug target; diagnosis.  
XX Saccharomyces cerevisiae.  
XX EP1258494-A1.  
XX 20-NOV-2002.  
XX 20-DEC-2001; 2001EP-00130253.  
XX 15-MAY-2001; 2001EP-00111774.  
XX (CELL-) CELLZOME AG.  
XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;  
PI Marzioch M, Schultz JD, Superti-Furga GD;  
XX WPI; 2003-250078/25.  
DR N-PSDB; ACC60995.  
XX New isolated protein complexes useful for diagnosing a disease or  
PT disorder, or as a target for an active agent of a pharmaceutical,  
PT preferably a drug target in the treatment or prevention of disease or  
PT disorder.  
XX Disclosure; SEQ ID NO 771; 17pp + Sequence Listing; English.  
XX The invention relates to multiprotein complexes from eukaryotes. Proteins  
CC of the invention and DNA sequences encoding them are given in records  
CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are  
CC obtainable by using a protein as a bait and isolating the set of proteins

CC which is attached thereto from cells. Such protein complexes may comprise  
CC up to 30 distinct proteins. Protein complexes of the invention are useful  
CC for diagnosing a disease or disorder, or as a target for an active agent  
CC of a pharmaceutical, preferably a drug target in the treatment or  
CC prevention of a disease or disorder. Note: The sequence data for this  
CC patent is not represented in the printed specification, but is based on  
CC sequence information supplied by the European Patent Office. The complete  
CC document is available on CD-ROM  
XX  
SQ Sequence 481 AA;  
Query Match 39.8%; Score 1044; DB 6; Length 481;  
Best Local Similarity 45.2%; Pred. No. 1.4e-87;  
Matches 212; Conservative 83; Mismatches 168; Indels 6; Gaps 4;  
QY 35 LEKVQYIDLHQDEFVQTLKEWVAIESDSVQVPFRFQELFRMMAVAADTLQRLGAR-VA 93  
Db 5 LTSVFQKIDSLKPQFFSRLTK-AIQIPAVSSDESLSRSKVFDKAKFISEQLSQSGFHDIK 62  
QY 94 SVDMGPQQLP-DGQSLPIPPVILAEIGSDPTKGTVCYFGLHDVQPADRGDGLTDPY-V 150  
Db 63 MVDLGIQPPPISTPNLSLPPVILSRFGSDPSKKTVLVYGHYDVQPAQLEDGWDTEPFKLV 122  
QY 151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEGSVALEELV 210  
Db 123 IDEAKGIMKGRGVTDGTGPLLWINVVDFAKASGGQEFFVNLVTCFEGMEESGSLKLDL 182  
QY 211 EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILH 270  
Db 183 KKEANGYFKGVDAVCISDNYWLGTKPKPVLTYGLRGNYYYQTIIEGPSADLHSGIFGVVA 242  
QY 271 EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSRVEKFL 330  
Db 243 EPMIDLMQVLGSLVDSKGKILIDGIDEMVAPLTEKEKALYKDIEFSVEELNAAATGSKTSL 302  
QY 331 FDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQV 390  
Db 303 YDKXEDILMHRWRYPSSLIHGIEGAFSAQGAQAKTVIPAKVFGKFSIRTVPDMMDSEKLTSLV 362  
QY 391 TRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST 450  
Db 363 QXHCDAKFKSLNSPNKCRTELIHDGAYWVSDPFNAQFTAAKKAATKLVYGVDPDFTRGGS 422  
QY 451 IPIAKMFQEIIVHKS VVLIPLGAVDDGEHSQNEKINRWNIIEGTKLFAAF 499  
Db 423 IPITLTFQDALNTSVLLLPMPGRGDDGAHSINEXKLDISNFFVGMKMTMAAY 471

RESULT 45  
ADK62620  
ID ADK62620 standard; protein; 481 AA.  
XX ADK62620;  
AC ADK62620;  
XX 06-MAY-2004 (first entry)  
XX Disease treating protein complex-derived protein #436.  
DE protein complex; drug target; diagnosis.  
XX Unidentified.  
XX EPI338608-A2.  
XX 27-AUG-2003.  
XX 20-DEC-2002; 2002EP-00102902.  
XX 20-DEC-2001; 2001EP-00130253.  
XX (CELL-) CELLZOME AG.  
PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;

PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
PI Michon A, Leutwein C, Rick J;  
XX  
DR WPI; 2003-638460/61.  
DR N-PSDB; ADK62621.  
XX  
PT New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.  
XX  
PS Disclosure; SEQ ID NO 871; 13pp; English.  
XX  
CC The invention relates to novel protein complexes comprising a first and a  
CC second protein, or its derivative, fragment, homologue or variant. The  
CC proteins are selected from given protein complexes, which are not defined  
CC in the specification. The variants are encoded by nucleic acids that  
CC hybridize to the nucleic acids encoding the proteins under low stringency  
CC conditions. The protein complexes are useful as targets for an active  
CC agent of a pharmaceutical. These protein complexes are particularly  
CC useful as drugs targets for the treatment or preventing of a disease or  
CC disorder. The complexes and methods above are useful in diagnosing or  
CC screening for the presence of a disease or disorder or a predisposition  
CC for developing a disease or disorder in a subject. These are also useful  
CC in screening for a drug for treatment or prevention of a disease or  
CC disorder. The molecule that modulates the amount, activity or protein  
CC components of the complex is useful for the manufacture of a medicament  
CC for the treatment or prevention of a disease or disorder. This sequence  
CC corresponds to a protein of the invention. (Note: the sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained from the EPO in electronic format).  
XX  
SQ Sequence 481 AA;

Query Match 39.8%; Score 1044; DB 7; Length 481;  
Best Local Similarity 45.2%; Pred. No. 1.4e-87;  
Matches 212; Conservative 83; Mismatches 168; Indels 6; Gaps 4;

QY 35 LEKVFOYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGAR-VA 93  
Db 5 LTSVFQKIDSLKPKQFFSRLTK--AIQIPAVSSDESLSRSKVFDKAKFISEQLSQSGFHDIX 62  
QY 94 SVDMGQPQLP-DQOSLPPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLWLTDPY--V 150  
Db 63 MVDLGIQPPPISTPNLSLPPVILSRFGSDPSKKTVLVYGHYDVQPAQLEDGWDTEPFKL 122  
QY 151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFFRALEQDLPVNIKFIIEGMEEGSVALEELV 210  
Db 123 IDEAKGIMKRGVTDGTPLLSWINVDAPKASGOEFPVNLVTCFEGMEESGSLKLDLI 182  
QY 211 EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGILH 270  
Db 183 KKEANGYFKGVDAVCISDNYWLTGTTKPVLTYLGRGCNYYQTIIEGPSADLHSGIFGVVA 242  
QY 271 EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFL 330  
Db 243 EPMIDLMQVLGSLVDSKGKILIDGIDEMVAPLTKYKALYKDIEFSVEELNAATGSKTSL 302  
QY 331 FDTKEEILHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQV 390  
Db 303 YDKKEDILMHRWRYPSSLIHGVEGAFSAQGAKTVPAPKVFKGFSIRTVPDMDSKLTSLV 362  
QY 391 TRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST 450  
Db 363 QKHCDAKFKLSNPKNCRTELIHDGAYWVSDPFPNAQFTAAKKATKLVYGVDPDFTREGGS 422  
QY 451 IPIAKMFOEIVHKSVVLIPLGAVDDGGEHSQNEKINRWNYIEGTKLEAAF 499  
Db 423 IPITLTFQDALNTSVLLPMPGRGDDGAHSINEKLDISNFVGGMKTMMAAY 471

RESULT 46  
ABR58616

ID ABR58616 standard; protein; 391 AA.  
XX  
AC ABR58616;  
XX  
DT 09-JUL-2003 (first entry)  
XX  
DE Human cancer related protein SEQ ID NO:273.  
XX  
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
KW heart disease; atherosclerosis; endometriosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025138-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-US029560.  
XX  
PR 17-SEP-2001; 2001US-0323469P.  
PR 20-SEP-2001; 2001US-0323887P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 08-FEB-2002; 2002US-0355145P.  
PR 08-FEB-2002; 2002US-0355257P.  
PR 12-APR-2002; 2002US-0372246P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;  
PI Zlotnik A;  
XX  
DR WPI; 2003-354600/33.  
DR N-PSDB; ACC72762.  
XX  
PT New genes that are up-regulated or down-regulated in cancers, useful as  
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
PT therapeutic targets for screening drugs for treating these diseases.  
XX  
PS Claim 12; Page 747; 767pp; English.  
XX  
CC The present invention describes an isolated nucleic acid molecule, which  
CC comprises the sequence of any of the genes that are up-regulated or down-  
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
CC related gene nucleotide sequences which encode the proteins given in  
CC ABR58521 to ABR58709. Also described: (1) determining the presence or  
CC absence of a pathological cell in a patient; (2) an expression vector  
CC comprising a nucleic acid molecule described above; (3) a host cell  
CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
CC of (4); (6) specifically targeting a compound to a pathological cell in a  
CC patient by administering to the patient the antibody above; and (7) a  
CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
CC therapeutic targets. In particular, the nucleic acid is useful for  
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
CC drug screening, particularly for identifying agents for treating these  
CC pathologies  
XX  
SQ Sequence 391 AA;

Query Match 38.5%; Score 1010; DB 6; Length 391;  
Best Local Similarity 42.2%; Pred. No. 1.5e-84;  
Matches 200; Conservative 73; Mismatches 115; Indels 86; Gaps 2;  
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV 92  
Db 2 AALTTLFKYIDENQDRIYIKKLAKWVAIQ--SVSAWPEKRGETRRMMEVAADVKQLGGSV 59  
QY 93 ASVDMGPFQQLPDGQSLPIPPVILAEGLSDPTKGTVCFCYGHLDVQPADRGDGLWLTDPYVLT 152  
||:|



Db	60	ELVDIGKQ-----	67
QY	153	EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEK	212
Db	68	-----KEIPVNVRFLECGMEESGSEGLDELIFA	95
QY	213	EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP	272
Db	96	RKDTFFKDVYVCISDNYWLKXKPCITYGLRGICYFFIEVECSNKLHSGVYGGSVHEA	155
QY	273	MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEBEINTYKAIHLDLDEEYRNSSRVEKFLFD	332
Db	156	MTDLILLMGSLVDKRGNILIPGINEAAVATEEEHKLYDDIDFDFIEFAKDVGQAQILLHS	215
QY	333	TKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR	392
Db	216	HKKDILMHRWRYPSSLHIGIEGAFSGGAKTVIPRKVWGKFSIRLVPNMTPEVWGEQVTS	275
QY	393	HLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGIEPDMIRDGSTIP	452
Db	276	YLTCKFAELRSPNEFKVYMGHGKFPWVSDFSHPHYLAGRRAKMTVFGVEPDLTREGG SIP	335
QY	453	IAKMFQEI VHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFLEMAQL	506
Db	336	VTLTTFQEATGKNVMLLPVGSADDCGAHSQNEKLNRYNIEGTMKMLAAVYEVSQL	389

RESULT 47

AAB42872

ID	AAB42872 standard; protein; 385 AA.
1	1
2	2
3	3
4	4
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6	6
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AC AAB42872;

DT 08-FEB-2001 (first entry)

Human ORFX ORF2636 polypeptide sequence SEQ ID NO:5272.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnery; antipsoptic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

31-MAR-2000: 2000WO-US008621.

PR 31-MAR-1999: 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2000-602362/57.

DR N-PSDB; AAC77081.

PT Novel nucleic acids and peptides derived from open reading frame X,

useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 4444-4445; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnery; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease, enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 385 AA;

Query Match	Score	DB 3:	Length
38.4%	1007.5	DB 3:	Length 385:

Best Local Similarity 49.7%; Pred. No. 2.5e-84;

Matches 192; Conservative 57; Mismatches 96; Indels 41; Gaps 2;

Qy 33 ALLEKVFQYIDLHQDEFV-----QTL 53

Qy 54 KEWVAIESDSYQVPRFRQELFRMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPV 113

QY 114 ILAELGSDPTKGTVCYFYGHLDDVQPADRGDGLTDPVVLTEVDGKLYRGATDNKGPVLAW 173

QY 174 INAVSAFRALEQDLPVNIKFIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWIS 233

234 QRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFCGILHEPNADLVALLGSLVDSSGHILVP 293

QY 294 GIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIE 353

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RESULT 48

ABG15876

ID ABG15876 standard; protein; 348 AA.

AC ABG15876:

18-FEB-2002 (first entry)

Novel human diagnostic protein #15867

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI; 2001-639362/73.  
XX DR N-PSDB; AAS80063.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity.  
XX PS Claim 20; SEQ ID NO 46235; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activities. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 348 AA;  
Query Match 38.1%; Score 1000; DB 4; Length 348;  
Best Local Similarity 52.9%; Pred. No. 1.1e-83;  
Matches 183; Conservative 63; Mismatches 100; Indels 0; Gaps 0;  
QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMBEAGSVALEELVEKE 213  
Db 2 VDGKLGHRGSTDDIGPVAGWINALEAYQKTQETPVNVRFCLEGMEESEGDLDELIFAR 61  
QY 214 KDRFFSGVDYIVISDNLWISQRKPAITYTRGNSYFVMEVKCRDQDFHSGTGGILHEPM 273  
Db 62 KDTFFKDVDCVICSDNYWLGKKKPCITYGLRGICYFFIEVECSNKLHSGVYGGVHEAM 121  
QY 274 ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDEEYRNSRVEKFLFDT 333  
Db 122 TDLILLMGSLVDKRGNILLIPGINEAVAAVTEEEHKLDDIDFDIKEFAKDVGQAQILLHSH 181  
QY 334 KEEILMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRH 393  
Db 182 KKDILMHRWRYPSLSLHGIEGAFSGGAKTVIPRKVVGKFSIRLVPHNMTPEVVGEQVTSY 241  
QY 394 LEDVFSKRNSNKMVSMTGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 242 LTKKFAELRSPNEBFKVMYMGHGKPPWVSDFSHPHYLAGRRAMKTVFGVEPDLTREGGSI 301

QY 454 AKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRMWNYIEGTKLFAAF 499  
Db 302 TLTFQEQATGKNVMLLPVGSADDDGAHSONEKLNRNYIEGTKMLAAY 347  
RESULT 49  
AAB92781  
ID AAB92781 standard; protein; 311 AA.  
XX AC AAB92781;  
XX DT 26-JUN-2001 (first entry)  
XX DE Human protein sequence SEQ ID NO:11268.  
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX OS Homo sapiens.  
XX PN EP1074617-A2.  
XX PD 07-FEB-2001.  
XX PF 28-JUL-2000; 2000EP-00116126.  
XX PR 29-JUL-1999; 99JP-00248036.  
XX PR 27-AUG-1999; 99JP-00300253.  
XX PR 11-JAN-2000; 2000JP-00118776.  
XX PR 02-MAY-2000; 2000JP-00183767.  
XX PR 09-JUN-2000; 2000JP-00241899.  
XX PA (HELI-) HELIX RES INST.  
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-  
PT length cDNAs defined in the specification, and for the detection and/or  
PT diagnosis of the abnormality of the proteins encoded by the full-length  
PT cDNAs.  
XX PS Claim 8; SEQ ID NO 11268; 2537pp + Sequence Listing; English.  
XX CC The present invention describes primer sets for synthesising 5602 full-  
CC length cDNAs defined in the specification. Where a primer set comprises:  
CC (a) an oligo-dT primer and an oligonucleotide complementary to the  
CC complementary strand of a polynucleotide which comprises one of the 5602  
CC nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in the  
CC specification. The primer sets can be used in antisense therapy and in  
CC gene therapy. The primers are useful for synthesising polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893  
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent  
CC oligonucleotides, all of which are used in the exemplification of the  
XX present invention  
SQ Sequence 311 AA;  
Query Match 33.6%; Score 882; DB 4; Length 311;  
Best Local Similarity 52.8%; Pred. No. 8e-73;





Wed Feb 16 11:50:31 2005

PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465573/50.

N-PSDB; AAI99566.

Isolated digestive system associated polypeptide for treating, preventing and/ or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection e.g. diagnosis.

Claim 11; SEQ ID NO 78; 509pp + Sequence Listing; English.

The invention relates to novel genes (AAI99548-AAI99604) and proteins (AAM99936-AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 286 AA;

XX  
SQ



PS Claim 20; Page 752; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising the

CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins

CC are useful in genetic vaccination, testing and therapy, and can be used

CC as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon

CC and/or nerve tissue growth or regeneration; immune suppression and/or

CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

CC AAU29510-AAU33304 represent the amino acid sequences of novel human

CC secreted proteins of the invention

XX

SQ Sequence 286 AA;

Query Match 22.9%; Score 601.5; DB 4; Length 286;

Best Local Similarity 43.9%; Pred. No. 7.8e-47;

Matches 118; Conservative 37; Mismatches 57; Indels 57; Gaps 3;

Qy 154 VDGKLYGEGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKE 213

Db 2 VDGKLHGRGSTDDKGPVAGWINALEAYQKTGQEIIPVNVRFCLGMEESGSEGLDELIFAR 61

Qy 214 KDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM 273

Db 62 KOTFFKXDYDVYCISDNYWLGKKKPCITYGLRGICYFFIEVECSNKDLHSGVYGGSVHEAM 121

Qy 274 ADLVALLGSLVDSGSHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVE----- 327

Db 122 TDLILM-----EEHKLYDDIDFDIEEFAKDVGQAQILLHSH 157

Qy 328 -----KFLFDT-----KEEILMLWRYPVSLSIHGIEGAFDEPG 360

Db 158 KSHLHLDLLPVVRLLGQALFHTAHFPDNIPISSKDIILMHRWRYPSLSLHGIEGAFSGS 217

Qy 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQ 389

Db 218 AKTVIPRKVVGKFSIRLVPNMTPEVVGEQ 246

RESULT 54

AAM24283

ID AAM24283 standard; protein; 119 AA.

XX

AC AAM24283;

XX

DT 12-OCT-2001 (first entry)

XX

DE Human EST encoded protein SEQ ID NO: 1808.

XX

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

KW gene therapy; nutrition.

XX

OS Homo sapiens.

XX

PN WO200154477-A2.

XX

PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-US002687.

XX

PR 25-JAN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-AUG-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-00663870.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX

DR WPI; 2001-476164/51.

DR N-PSDB; AAH98942.

XX

PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use.

XX

PS Claim 20; Page 1182; 1275pp; English.

XX

CC The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention

XX

SQ Sequence 119 AA;

Query Match 22.1%; Score 580.5; DB 4; Length 119;

Best Local Similarity 99.2%; Pred. No. 1.8e-45;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 8 MAASLLAV-LLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP 66

Db 1 MAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP 60

Qy 67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDQGSLLPIPPVILAEFGSDPTKG 125

Db 61 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDQGSLLPIPPVILAEFGSDPTKG 119

RESULT 55

ABG15877

ID ABG15877 standard; protein; 408 AA.

XX

AC ABG15877;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #15868.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR N-PSDB; AAS80064.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess





RESULT 57  
ABU20374  
ID ABU20374 standard; protein; 440 AA.  
XX  
AC  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #5901.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Bacteroides fragilis.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA24244.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 48298; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 440 AA;  
Query Match 19.3%; Score 506.5; DB 6; Length 440;  
Best Local Similarity 27.9%; Pred. No. 1e-37;  
Matches 134; Conservative 84; Mismatches 204; Indels 59; Gaps 10;  
QY 34 LLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTL 85  
Db 1 MMEDLFSLIRISIPISALPEHHDDMLACAQRWTQL-----L 35  
QY 86 QRLGARVASVDMGPOQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGL 145  
Db 36 LKAGADEAIV-----MPSKGN----PIVFGQKIVDPNAKTVLIYAHYDVMPAEPDLWK 85  
QY 146 TDPYVLTVEVDGKLYGRGATDNKGPVLAWINA---VSAFRALEQDLPVNIKFIIEGMEEAG 202  
Db 86 SQPFEPEIRDGHIWARGADDDKGQAFIQVKAFEYLVKYNLLEN----NVKFIIEGEEIG 141  
QY 203 SVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHS 262  
Db 142 SPSLEAFCEEHKE--LLKADVILVSDTSMLGADLPSLTTLGLRLAYWEIEITGPNRDLHS 199  
QY 263 GTFGGILHEPMADLVALLGSLVDSSGHILVPGIYD--EVVPLTEEEINTYKAHLDLEEY 320  
Db 200 GHFGGAVANPINVLGMLSKVIDTDGRITIPGFYDAVEEVPQAEREMIAH--IPFNEEKY 257  
QY 321 RNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPQTKTVIPGRVIGKFSIRLVPH 380  
Db 258 KEAIGVKELFGEKGYSTLERNSCRPSFDICGIWGGYTGEGSKTVLPSKAYAKVSCRVLPH 317  
QY 381 MNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGT 440  
Db 318 QDHHVISKLFADYIRQI---APATVEVKVTAMHGGQGVCPISLPAYQAAEKGFETAFGK 374  
QY 441 EPDMIRDGSTIPIAKMFQEIYVHKSVDLIPLGAVDGDGSHSQNEKINRWNYIEGTLFAAFF 500  
Db 375 KPLAVRRGGSIPITSTFEQVLGIKTVLMGFGLESDAIHSPNENFSLDIFRKGIEAVVEFH 434  
QY 501 L 501  
Db 435 L 435  
RESULT 58  
ABP28245  
ID ABP28245 standard; protein; 458 AA.  
XX  
AC ABP28245;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 5666.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus agalactiae.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;







Db 17 HVAQHYPEVLRLTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID-- 63

Qy 99 PQLPDGQSLPIPPVILAEGLSDPTKGTVCYFGLHDVQPADRGDGLWLTDPYVLTEVDGKL 158

Db 64 -----ESYTAPFVMAHFKSSRPDAKTLIFYNHYDTPADGDQVWTEDPFTLSVRNGFM 116

Qy 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFF 218

Db 117 YGRGVDDDKGHITARLSALRYMQHDDLPVNISFIMEGAEESASTDLKYLEKHADK-L 175

Qy 219 SGVDYIVISDNLWISQRKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM 273

Db 176 RGADLLV-----WEQGTKNALEQLEISGNGKGIVTFDAKVKSadVDIHS-SYGGVVESAP 229

Qy 274 ADLVALGSLVDSSGHILVPGIYDEVVPLTE-----EEINTYKAIHLDLEE 319

Db 230 WYLLQALQSLRAADGRILVEGLYEEVQEPNEREMALLETYGQRPNEEVSRIVGLEPLLQ 289

Qy 320 YRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP 379

Db 290 EERMAFLKRFFFD-----PALNIEGQSGYQGQGVKTLPAEASAKLEVRLVP 337

Qy 380 HMNVSAVEKQVTRHLEDVFSKRNSNMVVSMTLG-----LHPWIANIDDTQ---YL 428

Db 338 GLEPHDVLEKIRKQLD-----KNGFDKVELYITLGEYSYRSDMSAPAILNVIELAKKFYP 392

Qy 429 AAKRAIRTVFGTEP-DMIRDSGTPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRW 487

Db 393 QGVSVLPTTAGTGPMTVFDALVP-----MVAFGLGNANSRDHGGDENVRIA 440

Qy 488 NY 489

Db 441 DY 442

RESULT 60

ABP81302

ID ABP81302 standard; protein; 457 AA.

XX AC ABP81302;

XX 04-MAR-2003 (first entry)

DT Streptococcus pneumoniae polypeptide SEQ ID NO 219.

DE Streptococcus pneumoniae; infection; otitis media; antibiotic;

XX diagnosis; gene therapy.

OS Streptococcus pneumoniae.

XX WO200283855-A2.

PN 24-OCT-2002.

XX 12-APR-2002; 2002WO-US011524.

PF 16-APR-2001; 2001US-0283948P.

PR 18-APR-2001; 2001US-0284443P.

XX (AMCY ) AMERICAN CYANAMID CO.

PA Zagursky RJ, Masi AW, Green BA, Chakravarti DN, Russell DP;

PI Wooters JL;

XX WPI; 2003-093010/08.

DR N-PSDB; ABZ42150.

XX New Streptococcus pneumoniae polynucleotides, useful for treating or

PT preventing S. pneumoniae infections, or non-systemic diseases, e.g.

PT otitis media, which are induced or exacerbated by S. pneumoniae.

XX Claim 42; Page 351-353; 1091pp; English.

PS

XX The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of

CC a Streptococcus pneumoniae genomic sequence, a fragment or degenerate

CC variant of the polynucleotide or a nucleic acid sequence 95% identical to

CC one of the polynucleotides. The S. pneumoniae polynucleotides and encoded

CC polypeptides (ABP81299-ABP81674) are useful for treating or preventing S.

CC pneumoniae infections or non-systemic diseases, e.g. otitis media, which

CC are induced or exacerbated by S. pneumoniae. These are also useful for

CC detecting S. pneumoniae in a biological sample or diagnosing S.

CC pneumoniae infection in a subject. The polynucleotides have antibacterial

CC activity and are useful in gene therapy

XX Sequence 457 AA;

SQ

Query Match 16.7%; Score 438.5; DB 6; Length 457;

Best Local Similarity 27.6%; Pred. No. 2.2e-31;

Matches 133; Conservative 80; Mismatches 180; Indels 89; Gaps 15;

Qy 41 YIDLHQDEFVQTL--KEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMG 98

Db 17 HVAQHYPEVLRLTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID-- 63

Qy 99 PQLPDGQSLPIPPVILAEGLSDPTKGTVCYFGLHDVQPADRGDGLWLTDPYVLTEVDGKL 158

Db 64 -----ESYTAPFVMAHFKSSRPDAKTLIFYNHYDTPADGDQVWTEDPFTLSVRNGFM 116

Qy 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFF 218

Db 117 YGRGVDDDKGHITARLSALRYMQHDDLPVNISFIMEGAEESASTDLKYLEKHADK-L 175

Qy 219 SGVDYIVISDNLWISQRKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM 273

Db 176 RGADLLV-----WEQGTKNALEQLEISGNGKGIVTFDAKVKSadVDIHS-SYGGVVESAP 229

Qy 274 ADLVALGSLVDSSGHILVPGIYDEVVPLTE-----EEINTYKAIHLDLEE 319

Db 230 WYLLQALQSLRAADGRILVEGLYEEVQEPNEREMALLETYGQRPNEEVSRIVGLEPLLQ 289

Qy 320 YRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP 379

Db 290 EERMAFLKRFFFD-----PALNIEGQSGYQGQGVKTLPAEASAKLEVRLVP 337

Qy 380 HMNVSAVEKQVTRHLEDVFSKRNSNMVVSMTLG-----LHPWIANIDDTQ---YL 428

Db 338 GLEPHDVLEKIRKQLD-----KNGFDKVELYITLGEYSYRSDMSAPAILNVIELAKKFYP 392

Qy 429 AAKRAIRTVFGTEP-DMIRDSGTPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRW 487

Db 393 QGVSVLPTTAGTGPMTVFDALVP-----MVAFGLGNANSRDHGGDENVRIA 440

Qy 488 NY 489

Db 441 DY 442

RESULT 61

ADM92061

ID ADM92061 standard; protein; 457 AA.

XX AC ADM92061;

XX 03-JUN-2004 (first entry)

DT S pneumoniae antigenic protein sequence SeqID258.

DE antibacterial; gene therapy; Streptococcus pneumoniae infection;

XX antigenic.

XX Streptococcus pneumoniae.

OS WO2004020609-A2.

XX 11-MAR-2004.

PD

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XX 02-SEP-2003; 2003WO-US027401.
PF
XX
XX 30-AUG-2002; 2002US-0407082P.
XX
XX (TUFT ) UNIV TUFTS.
XX
XX Camilli A, Hava DL;
XX
XX WPI; 2004-239189/22.
XX
XX N-PSDB; ADM91824.
XX
XX New Streptococcus pneumoniae nucleic acid molecules, useful for
PT diagnosing, treating and preventing active infections of Streptococcus
PT pneumoniae.
PT
XX
XX Claim 8; SEQ ID NO 258; 123pp; English.
XX
XX This invention relates to novel isolated Streptococcus pneumoniae nucleic
CC acid molecules and the antigenic polypeptides encoded by them. The
CC invention may be useful for the production of compounds with an
CC antibacterial activity or for gene therapy. The nucleic acid molecules,
CC compositions and methods disclosed are useful for treating Streptococcus
CC pneumoniae infection. The present sequence is that of an S pneumoniae
CC protein of the invention.
XX
XX Sequence 457 AA;
SQ
Query Match 16.7%; Score 438.5; DB 8; Length 457;
Best Local Similarity 27.6%; Pred. No. 2.2e-31;
Matches 133; Conservative 80; Mismatches 180; Indels 89; Gaps 15;
QY 41 YIDLHQDEFVQTL--KEWVAIESDSVQVPFRFRQELFRMMVAADTLQRLGARVASVDMG 98
Db 17 HVAQHYFEVLRTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID-- 63
QY 99 PQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKL 158
Db 64 -----ESYTAPFVMAHFKSSRPDAKTLIFYNHYDTPADGDQVWTEDPFTLSVRNGFM 116
QY 159 YRGATDNKGPVLAWINAVSAFRALEQDLPVNKFIEGMEEAGSVALEELVEKEKDRFF 218
Db 117 YGRGVDDDKGHITARLSALRKYMQHDDLPVNISFIMEGAEESASTDLDKYLEKHADK-L 175
QY 219 SGVDYIVISDNLWISQRKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM 273
Db 176 RGADLLV-----WEQGTKNALEQLEISGGNKGIVTFDAKVSADVDIHS-SYGGVVESAP 229
QY 274 ADLVALGSLVDSSGHILVPGIYDEVVPLTE-----EEINTYKAHLDLEE 319
Db 230 WYLLOALQSLRAADGRILVEGLYEEVQEPNEREMALLEITYGQRPNEEVSRIYGLELPLQ 289
QY 320 YRNSSRVEKFLFTDKEEILMHLWRYPSLSIHGIEGAFDEPGTKTIVIPGRVIGKFSIRLVP 379
Db 290 EERMAFLKRFFFD-----PALNIEGIQSGYQGQGVKTILPAEASAKLEVRLVP 337
QY 380 HMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLG-----LHPWIANIDDTQ---YL 428
Db 338 GLEPHDVLEKIRKQLD-----KNGFDKVELYYTLGMSYRSDMSAPAILNVIELAKKFYP 392
QY 429 AAKRAIRTVFGTER-DMIRDCSTIPIAKMFQEIHKSVVLIPLGAVDDGGEHSQNEKINRW 487
Db 393 QGVSVLPTTAGTGPMHTVFDALVPE-----MVAFGLGNANSRDRHGGDENVRIA 440
QY 488 NY 489
Db 441 DY 442
RESULT 62
ADK48314
ID ADK48314 standard; protein; 457 AA.
XX
```

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AC ADK48314;
XX
XX 20-MAY-2004 (first entry)
XX
XX Streptococcus pneumoniae protein, Seq ID No 4829.
XX
XX Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
XX
XX Streptococcus pneumoniae.
XX
XX US6699703-B1.
XX
XX 02-MAR-2004.
XX
XX 26-MAY-2000; 2000US-00583110.
XX
XX 02-JUL-1997; 97US-0051553P.
XX
XX 12-MAY-1998; 98US-0085131P.
XX
XX 30-JUN-1998; 98US-00107433.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;
XX
XX WPI; 2004-212399/20.
XX
XX N-PSDB; ADK45653.
XX
XX New nucleic acid molecules and polypeptides useful for diagnosing,
PT preventing and treating pathological conditions resulting from bacterial
PT infection, e.g. Streptococcus pneumoniae infection, and in drug
PT screening.
XX
XX Disclosure; SEQ ID NO 4829; 301pp; English.
XX
XX The invention relates to isolated Streptococcus pneumoniae nucleic acids
CC and polypeptides. The nucleic acids and proteins are useful for
CC diagnosing, preventing and treating pathological conditions resulting
CC from bacterial infection, such as S. pneumoniae infection. These may also
CC be used for drug screening procedures. The present sequence represents a
CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence
CC data for this patent did not appear in the printed specification but was
CC obtained in electronic format directly from USPTO at
CC segdata.uspto.gov/sequence.html.
XX
XX Sequence 457 AA;
SQ
Query Match 16.5%; Score 432.5; DB 8; Length 457;
Best Local Similarity 29.2%; Pred. No. 8e-31;
Matches 138; Conservative 75; Mismatches 181; Indels 79; Gaps 17;
QY 45 HQDEFVQTL--KEWVAIESDSVQVPFRFRQELFRMMVAADTLQRLGARVASVDMGPQQL 102
Db 21 HYFEVLRTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID----- 63
QY 103 PDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRG 162
Db 64 ---ESYTAPFVMAHFKSSRPDAKTLIFYNHYDTPADGDQVWTEDPFTLSVRNGFMYGRG 120
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNKFIEGMEEAGSVALEELVEKEKDRFFSGVD 222
Db 121 VDDDKGHITARLSALRKYMQHDDLPVNISFIMEGAEESASTDLDKYLEKHADK-LHGAD 179
QY 223 YIVISDNLWISQRKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLV 277
Db 180 LLV-----WEQGTKNALEQLEISGGNKGIVTFDAKVSADVDIHS-SYGGVVESAPWYLL 233
QY 278 ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEE--RNSSRVEKF----LF 331
Db 234 QALQSLRAADGRILVEGLYEEVHEPNERNAL-----LETYQQRNPEEVSRIYGLELP 286
QY 332 DTKEEILMHLWRY---PSLSIHGIEGAFDEPGTKTIVIPGRVIGKFSIRLVPHMNVSAVEK 388
Db 287 LLQERMAFLKXRPFFFEFEPALNIEGIQSGYQGQGVKTILPAEASAKLEVRLVPGLEPHDVLE 346
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CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
CC (I) is useful in DNA arrays or chips to carry out analysis of the
CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
CC Bifidobacterium related nucleotide sequences given in the Sequence
CC Listing from the present invention but not mentioned further within the
CC specification. N.B. The sequence data for this patent is not represented
CC in the printed specification but is based on sequence information
CC supplied by the European Patent Office
XX
SQ Sequence 455 AA;

Query Match      15.8%; Score 413.5; DB 5; Length 455;
Best Local Similarity 28.4%; Pred. No. 4.6e-29;
Matches 132; Conservative 73; Mismatches 210; Indels 49; Gaps 14;

QY 36 EKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASV 95
Db 7 DEIRSRVETDWNRIKVLAEKVALQISAKGIT--AEQMKRSAEFVADEL-----RLVGV 59

QY 96 DMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLTDPVYLTEVD 155
Db 60 DTKVQASNADGTPGAWGVIGSHIVSPDAPTVLLYAHHDVQVPDPAPAEWNTDPFVATEID 119

QY 156 GKLYGRGATDNKGPVLAWINAV--SAFRALEQDLPNVNIKFIEGMEEAGSVALBELVEKE 213
Db 120 GRLYGRGSADGGGI-----AIHSGALKALGDDLNVNIKVFIEGEEEMGSPSPFFIEAH 174

QY 214 KDRFFSGVDYIVISDNLWISQKPKAITYGTGRGNSYFMVEVKCRDQDFHSGTFCGILHEPM 273
Db 175 RDEF--AADVLIIVADSGNWSADIPSLTTSLRGNTCVDVTVOGLEHPVHSGQYGGPILDSN 232

QY 274 ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEE---YRNSSRVEKFL 330
Db 233 TLAAMLIASMYDENGDLAVPGV-----AAEPIG---GLQHDLDETTTRKDSGVVAGYE 283

QY 331 FDTKEEILMHLWRVPSLSI-----HGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSA 385
Db 284 FAGTGLASRLWTKPSVTVIGFDAHPVEGSFN-----VIAPETRFRLSLRTAPTQRPEE 337

QY 386 VEKQVTRHLED--VFSKRNSNKMVMSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPD 443
Db 338 AQEALAAFLSHAPFGAKVTVERGENGMGWAMDPTAVATKD-----ALEAMTEAFGVEPI 392

QY 444 MIRDGSTIPIAKMFQEIHKSVVLIPLGAVDD--GEHSQNEKIN 485
Db 393 NKGEGGSIPFIPELQRIFFPNAQVLV-TGPEDPKANAHSPNESIS 435

RESULT 65
AAU46872
ID AAU46872 standard; protein; 460 AA.
XX
AC AAU46872;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #7768.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
```

```
PR 07-JUL-2000; 2000US-0216747P.
XX (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59535.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 8067; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 460 AA;

Query Match      15.2%; Score 399; DB 4; Length 460;
Best Local Similarity 27.5%; Pred. No. 1e-27;
Matches 127; Conservative 69; Mismatches 200; Indels 66; Gaps 13;

QY 42 IDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ 101
Db 27 VDSGFDDAVEQLTRHVAVRSVSSQRPDGVRSAGAEFVAAAKE-----AGAADTVVTVEN 80

QY 102 LPDQGSLLPIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLTDPVYLTEVDGKLYGR 161
Db 81 --DGL-----PAVIAHWPAPEGMPTVLLYSHGDVQPTGNLDEWHTPEFVATAKERLYGR 133

QY 162 GATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIEGMEEAGSVALEELVEKEKDRFFSGV 221
Db 134 GTADDKGGVAAHL--AAIRAFDGKPPVGVTLFVEGEEIIGSASMEVIAEHKDEL--AA 188

QY 222 DYIVISDNLWISQKPKAITYGTGRGNSYFMVEVKCRDQDFHSGTFCGILHEPMADLVALLG 281
Db 189 DVIVVADSVNWEQGVPSVTTTLRGVVDClVEVSTLDHALHSGQFGGIVPDALTLCRLIA 248

QY 282 SLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEI---- 337
Db 249 TLHDTGTGEVTVDLGQGFAGP-----ELDYPEDR--LRAETGILDGVQWVGRGR 294

QY 338 -LMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLED 396
Db 295 AVEKMWTKPSVTVIAID-ATPVKDAINILPASARAKISLRVAPGQDAGEAMEALVKHLES 353

QY 397 VFSSKRNSNKMVMSMTLGLH-----PWIANIDDTQYLAAKRAIRTVFGTEPDMIR 446
Db 354 -----HVEFGAHIKVTRGQLGQPGVWPFTGDKAEVAKEAFRLAWQEPVEMG 400

QY 447 DGSTIPIAKMFQEIHKSVVLIPLGAVDDGE---HSQNEKIN 485
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Db 130 SASTDLDKYLEKHADK-LHGADLLV-----WEQGTKNALEQLEISGNGKGI VTFDAKVKS 183

QY 256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEHINTYKA IHL 315

Db 184 ADVDIHS-SYGGVVESAPWYLLQALQSLRAADGRILVEGLYEEVHEPNEREMAL----- 236

QY 316 DLEEY--RNSSRVEKF----LFDTKEEILMHLWRY---PSLSIHGIEGAFDEPGTKTVIP 366

Db 237 -LETYGQRNPEEVSRIYGLELPLLOERMAFLKRRFFFEFEPALNIEGQSGYQGQGVKTIVP 295

QY 367 GRVIGKFSI 375

Db 296 AEASAKLEV 304

RESULT 69

AAAY48560

ID AAY48560 standard; protein; 141 AA.

XX

AC AAY48560;

XX

DT 08-DEC-1999 (first entry)

DE Human breast tumour-associated protein 21.

XX

KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;

KW treatment; tumour; cytostatic; medicament.

XX

OS Homo sapiens.

XX

PN DE19813839-A1.

XX

PD 23-SEP-1999.

XX

PF 20-MAR-1998; 98DE-01013839.

XX

PR 20-MAR-1998; 98DE-01013839.

XX

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosentahl A;

XX

DR WPI; 1999-528981/45.

DR N-PSDB; AAZ33635.

XX

PT Human nucleic acid sequences and protein products from tumor breast

PT tissue, useful for breast cancer therapy.

XX

PS Claim 22; 152; 188pp; German.

XX

CC This invention describes novel human nucleic acid sequences from tumor

CC breast tissue which have cytostatic activity. The nucleic acid sequences

CC can be used to produce and isolate full-length gene sequences. They can

CC be used to express proteins, which can be used as tools to find an

CC activity against breast cancer. The sequences can be used in sense or

CC antisense form. They are especially useful for medicaments for gene

CC therapy to treat breast cancer. AAY48540-Y48617 represent protein

CC fragments encoded by the expressed sequence tags described in the method

CC of the invention

XX

SQ Sequence 141 AA;

Query Match 12.5%; Score 329; DB 2; Length 141;

Best Local Similarity 49.6%; Pred. No. 5.2e-22;

Matches 61; Conservative 26; Mismatches 36; Indels 0; Gaps 0;

QY 384 SAVEKQVTRHLEDVFSKNSNKNVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPD 443

Db 17 SLVGEQVTSYLTKKFAELRSPNEFKVMGHGKWPVSDFSHPHYLAGRRAMKTVFGVEPD 76

QY 444 MIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDDGCHSQNEKINRWNYIEGTKLFAAFLEM 503

Db 77 LTREGGSIPTLTTFQEATGKQNVMLLPVGSADGHAHQNEKLNRYNIEGTKMLAAYLYEV 136

QY 504 AQL 506

Db 137 SQL 139

RESULT 70

ABG01653

ID ABG01653 standard; protein; 157 AA.

XX

AC ABG01653;

XX

DT 13-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #1644.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR N-PSDB; AAS65840.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX

PS Claim 20; SEQ ID NO 32012; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activities. The

CC polypeptide and polynucleotide sequences have application of mutations

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 157 AA;

Query Match 12.2%; Score 321; DB 4; Length 157;

Best Local Similarity 49.7%; Pred. No. 3.4e-21;

Matches 76; Conservative 6; Mismatches 11; Indels 60; Gaps 4;

QY 5 LGRM-----AASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKE 55

Db 42 LGEMLLMAPPDVQAASLLAVLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQT--- 98  
Qy 56 WVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ-----LPGDQS- 107  
Db 99 -----PNNVMSLNFLEEQHSIFENVIPDHSAA 124  
Qy 108 -----LPPIPPVILAEGLSDPTKGTVCIFYGHLD 134  
Db 125 ARMVRVFQIPPIILAEGLSDPTKGTVCIFYGHLD 157

RESULT 71  
AAG92742  
ID AAG92742 standard; protein; 457 AA.  
XX AAG92742;  
AC  
XX 26-SEP-2001 (first entry)  
DT  
DE C glutamicum protein fragment SEQ ID NO: 6496.  
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
KW organic acid synthesis.  
KW  
XX Corynebacterium glutamicum.  
OS  
XX EP1108790-A2.  
PN  
XX 20-JUN-2001.  
PD  
XX 18-DEC-2000; 2000EP-00127688.  
PF  
XX 16-DEC-1999; 99JP-00377484.  
PR  
PR 07-APR-2000; 2000JP-00159162.  
PR 03-AUG-2000; 2000JP-00280988.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA  
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
PI  
XX WPI; 2001-376931/40.  
DR N-PSDB; AAH67961.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analyzing  
PT expression profile or pattern of a gene and identifying homologous gene.  
XX  
PS Claim 17; SEQ ID NO 6496; 246pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of coryneform bacterium, measuring expression amount and analysing  
CC the expression profile or expression pattern of a gene derived from  
CC Coryneform bacterium, and identifying a homologue of a gene derived from  
CC Coryneform bacterium. Coryneform bacteria are useful for producing amino  
CC acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a protein described in the  
CC exemplification of the invention. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the European Patent Office  
XX  
SQ . Sequence 457 AA;

Query Match 11.5%; Score 302.5; DB 4; Length 457;  
Best Local Similarity 24.6%; Pred. No. 9.4e-19;  
Matches 127; Conservative 72; Mismatches 184; Indels 133; Gaps 21;  
Qy 42 IDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ 101  
Db 14 IENQREQIFTQLKEIVSF--NSVHSDPNLLEDYAGAKWVVKETLTNAGLTVSE----- 64

Qy 102 LPDQSLPIPPVILAEGLSDPTKGT-----VCFYGHLDVQPADRGDGLTDPYVLT 152  
Db 65 -----FAAEDGTNTFIGTRKGSAGPKVLLYSHFDVWPSGLDLWDTNPELT 112  
Qy 153 EVDG----KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEE 208  
Db 113 ERDAGHGRWYGRGAADCKGNLVMHLAALRAVEA-SGDTTLNLTYYVEGSEEMGGGALSA 171  
Qy 209 LVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268  
Db 172 LI-KDKPELFD-ADVILIADSGNASVGTPTLTTLRGGGQVTVTDTLEGAVHSGQYCGA 229  
Qy 269 LHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEBEINT---YKAIHLDLEEVRNSSR 325  
Db 230 APDAVAALVRVLDTLRDEHGRTVIDG-----VNTTANWKGEPYDPETFRSDAG 277  
Qy 326 V---EKFLFDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKT-----VIPGRVIGKFSI 375  
Db 278 ILDGVDIMGDGDNPSAM-LWSRPAISITGF-----TSTPVAEALNAVPATASAKLNL 328  
Qy 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMVMTLGLHPWIA---NIDDTQVLAAG 431  
Db 329 RVPAGLEANDVAEKLKQHL-----INHPTWGAKITVEIDD----- 363  
Qy 432 RAIRTVFGTE-----PDMIRDGS--TIPIAKMFOEIVHKSVVLI-- 468  
Db 364 --INQPFSTDITGPAMSTLASCLSAAYEGKDLVTEGSGGSIPLCTELIEVNPPEALALYG 421  
Qy 469 ---PLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL 501  
Db 422 VEEPLTVI---HSANESVDP-NEIRDIAATAEALFL 452

RESULT 72  
ABG01654  
ID ABG01654 standard; protein; 100 AA.  
XX ABG01654;  
AC  
XX 13-FEB-2002 (first entry)  
DT  
XX Novel human diagnostic protein #1645.  
DE  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
KW  
XX Homo sapiens.  
OS  
XX WO200175067-A2.  
PN  
XX 11-OCT-2001.  
PD  
XX 30-MAR-2001; 2001WO-US008631.  
PF  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
PR  
XX (HYSE-) HYSEQ INC.  
PA  
XX Drmanac RT, Liu C, Tang YT;  
PI  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS65841.  
DR  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 32013; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)





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XX      Sequence 98 AA;
SQ
Query Match      9.5%; Score 248; DB 3; Length 98;
Best Local Similarity 49.5%; Pred. No. 9.9e-15;
Matches 49; Conservative 18; Mismatches 30; Indels 2; Gaps 1;

QY      33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRFQELFRMMAVAADTLQRLGARV 92
Db      2 AALTTLFKYIDENQDRYIKLAKWVAIQ--SVSAWPEKRGETRRMMEVAADVKQLGGSV 59

QY      93 ASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYG 131
Db      60 ELVDIGKQKLPDGSXIPLPILXGRLGSDPQKKTVCIYG 98

RESULT 75
AAB79812
ID      AAB79812 standard; protein; 267 AA.
XX
AC      AAB79812;
XX
DT      30-APR-2001 (first entry)
XX
DE      Corynebacterium glutamicum MP protein sequence SEQ ID NO:358.
XX
KW      Corynebacterium glutamicum; metabolic pathway protein; MP protein;
KW      fine chemical production; microorganism; organic acid; nucleoside;
KW      nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
KW      lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
KW      carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
XX
OS      Corynebacterium glutamicum.
XX
PN      WO200100843-A2.
XX
PD      04-JAN-2001.
XX
PF      23-JUN-2000; 2000WO-IB0000923.
XX
PR      25-JUN-1999; 99US-0141031P.
PR      01-JUL-1999; 99DE-01030476.
PR      02-JUL-1999; 99US-0142101P.
PR      08-JUL-1999; 99DE-01031415.
PR      08-JUL-1999; 99DE-01031418.
PR      08-JUL-1999; 99DE-01031419.
PR      08-JUL-1999; 99DE-01031420.
PR      08-JUL-1999; 99DE-01031424.
PR      08-JUL-1999; 99DE-01031428.
PR      08-JUL-1999; 99DE-01031434.
PR      08-JUL-1999; 99DE-01031435.
PR      08-JUL-1999; 99DE-01031443.
PR      08-JUL-1999; 99DE-01031453.
PR      08-JUL-1999; 99DE-01031457.
PR      08-JUL-1999; 99DE-01031465.
PR      08-JUL-1999; 99DE-01031478.
PR      08-JUL-1999; 99DE-01031510.
PR      08-JUL-1999; 99DE-01031541.
PR      08-JUL-1999; 99DE-01031573.
PR      08-JUL-1999; 99DE-01031592.
PR      08-JUL-1999; 99DE-01031632.
PR      08-JUL-1999; 99DE-01031634.
PR      08-JUL-1999; 99DE-01031636.
PR      09-JUL-1999; 99DE-01032125.
PR      09-JUL-1999; 99DE-01032126.
PR      09-JUL-1999; 99DE-01032130.
PR      09-JUL-1999; 99DE-01032186.
PR      09-JUL-1999; 99DE-01032206.
PR      09-JUL-1999; 99DE-01032227.
PR      09-JUL-1999; 99DE-01032228.
PR      09-JUL-1999; 99DE-01032229.
PR      09-JUL-1999; 99DE-01032230.
PR      14-JUL-1999; 99DE-01032922.

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PR      14-JUL-1999; 99DE-01032926.
PR      14-JUL-1999; 99DE-01032928.
PR      14-JUL-1999; 99DE-01033004.
PR      14-JUL-1999; 99DE-01033005.
PR      14-JUL-1999; 99DE-01033006.
PR      12-AUG-1999; 99US-0148613P.
PR      27-AUG-1999; 99DE-01040764.
PR      27-AUG-1999; 99DE-01040765.
PR      27-AUG-1999; 99DE-01040766.
PR      27-AUG-1999; 99DE-01040832.
PR      31-AUG-1999; 99DE-01041378.
PR      31-AUG-1999; 99DE-01041379.
PR      31-AUG-1999; 99DE-01041380.
PR      31-AUG-1999; 99DE-01041394.
PR      31-AUG-1999; 99DE-01041396.
PR      03-SEP-1999; 99DE-01042076.
PR      03-SEP-1999; 99DE-01042077.
PR      03-SEP-1999; 99DE-01042079.
PR      03-SEP-1999; 99DE-01042086.
PR      03-SEP-1999; 99DE-01042087.
PR      03-SEP-1999; 99DE-01042088.
PR      03-SEP-1999; 99DE-01042095.
PR      03-SEP-1999; 99DE-01042124.
PR      03-SEP-1999; 99DE-01042129.
PR      09-MAR-2000; 2000US-0187970P.
XX
PA      (BADI ) BASF AG.
XX
PI      Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
DR      WPI; 2001-137957/14.
DR      N-PSDB; AAF71931.
XX
PT      Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway
PT      proteins, useful for producing fine chemicals in microorganisms,
PT      including organic acids, nonproteinogenic amino acids, and purine and
PT      pyrimidine bases.
XX
PS      Claim 20; Page 686-687; 1737pp; English.
XX
CC      AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
CC      pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP
CC      nucleic acids are useful for the production of fine chemicals in
CC      microorganisms, including organic acids, nonproteinogenic amino acids,
CC      purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated
CC      and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,
CC      vitamins, cofactors, polyketides and enzymes
XX
SQ      Sequence 267 AA;

Query Match      9.2%; Score 242.5; DB 4; Length 267;
Best Local Similarity 29.7%; Pred. No. 1.5e-13;
Matches 79; Conservative 37; Mismatches 113; Indels 37; Gaps 7;

QY      42 IDLHQDEFVQTLKEWVAIESDSVQVPFRFQELFRMMAVAADTLQRLGARVASVDMGPQQ 101
Db      14 IENQREQIFTQLKEIVSF--NSVHSDPNLLEDYAGAKEWVKETLTNAGLTVSE----- 64

QY      102 LPDQGQSLPIPPVILAEGLSDPTKGT-----VCFYGHLDVQPADRGDWLTDPYVLT 152
Db      65 -----FAAEDGTTNFIGTRKSGEAPKVLVLSHFVDVPSGPLDLWDTNPFELT 112

QY      153 EVDG----KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEE 208
Db      113 ERDAGHGTRWYGRGAADCKGNLVHMLAALRAVEA-SGDTTLNLTYYVEGSEEMGGGALSA 171

QY      209 LVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268
Db      172 LI-KDKPELFD-ADVILIADSGNASVGTPTLTTLTTRGGGQVTVTDTLEGAVHSGQNGGA 229

QY      269 LHEPMADLVALLGSLVDSSGHILVPG 294
Db      230 APDAVAALVRVLDTLRDEHGRTVIDG 255

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Db 213 NAVLKVQ-----GKQGHVAYPHLARPIHEASPALAELCQTWDNG-----NE 255  
QY 299 VVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDE 358  
Db 256 YFPATSFQIS-----NIHAGTGA--- 273  
QY 359 PGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPW 418  
Db 274 ---TNVIPGALEVTENFR---YSTEVTAEQLKQRVHEILDKHGLQYEIVWNLS-GL-PF 324  
QY 419 IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVMVLPLGAVDDGEH 478  
Db 325 LTPVGEL-VNAAQTAILNVTGTETELSTSGGT---SDGRFIAPTGAQVLELGVLNATIH 379  
QY 479 SQNEKIN 485  
Db 380 QINEHVD 386  
RESULT 79  
ABM67132  
ID ABM67132 standard; protein; 376 AA.  
XX AC ABM67132;  
XX DT 20-NOV-2003 (first entry)  
XX DE Photorhabdus luminescens protein sequence #229.  
XX KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX OS Photorhabdus luminescens.  
XX PN WO200294867-A2.  
XX PD 28-NOV-2002.  
XX PF 07-FEB-2002; 2002WO-IB003040.  
XX PR 07-FEB-2001; 2001FR-00001659.  
XX PA (INSP ) INST PASTEUR.  
XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
XX DR WPI; 2003-148459/14.  
XX PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX PS Claim 2; SEQ ID NO 229; 1205pp; French.  
XX CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful

CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
SQ Sequence 376 AA;  
Query Match 8.3%; Score 218; DB 6; Length 376;  
Best Local Similarity 22.4%; Pred. No. 4.9e-11;  
Matches 105; Conservative 71; Mismatches 167; Indels 126; Gaps 19;  
QY 66 PVPRFRQELFRMMAVAADT-----LQRLGARVASVDMGPPQLPDGQSLPIPPVIL 115  
Db 4 PVIELAQQILIRQPSISPDCKGQDIMIAHLQITIGFTI-----ERMPFGDT---NNFW 52  
QY 116 AELGSDPTKGTVCYFCHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWIN 175  
Db 53 AYRGIGP---TLAFAGHTDVVPAGDESQWEYPPFPFTIRNGMLYGRGAADMKGSLAAMIV 109  
QY 176 AVSAFRALEQDLVPNIKFIEGMEEA----GSVALEELVEKEKDRFFSGVDYIVISDNLW 231  
Db 110 AAERFVAAPHNHNGLAFLITSDEEAKATHGTVKVVEALMSRNER----LDYCLIGEPPSS 165  
QY 232 ISQKPAITYGTRGNSYEMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSGHIL 291  
Db 166 QHRLGDMVKNGRRGS-----LTANL-TVHGIQGHVA 195  
QY 292 VPGIYD---EVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSL 347  
Db 196 YPHLADNPPIHRVLPALQTLVNTH-----WDEGNEF-----FPAT 229  
QY 348 SIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNM 407  
Db 230 SMQ-IANIHAGTGSNHNVPNGVQVQFNFRFSTELTDSQIREQV----ETILKNHN----- 279  
QY 408 VVSMTLGLHPWIANIDDTQYLAAK-----RAIRTVFGTEPDMIRDGSTIP---IAKM 456  
Db 280 -LNYTI---EWI--LAGQPFLLTAKGELVNAVISOYCGYQPELSTSGGTS DGRFIAQM 333  
QY 457 FQEIIVHKSVMVLPLGAVDDGEHSQNEKINRWNYIEGTKLPAAFFLEMAQ 505  
Db 334 GAQVVE-----LGPLNSTIHKVNESVSAADLQQLSRIYQVRVMEQLIQ 375  
RESULT 80  
ABB47976  
ID ABB47976 standard; protein; 379 AA.  
XX AC ABB47976;  
XX DT 05-FEB-2002 (first entry)  
XX DE Listeria monocytogenes protein #680.  
XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;  
KW vitamin B12; bacterial infection; disease.  
XX OS Listeria monocytogenes.  
XX PN WO200177335-A2.  
XX PD 18-OCT-2001.  
XX PF 11-APR-2001; 2001WO-FR001118.  
XX PR 11-APR-2000; 2000FR-000004629.  
XX PA (INSP ) INST PASTEUR.  
XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;  
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;

PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;  
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;  
XX  
DR WPI; 2002-010914/01.  
XX  
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related  
PT polypeptides.  
XX  
PS Claim 6; SEQ ID NO 681; 192pp; French.  
XX  
CC The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccines compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 379 AA;

Query Match 8.1%; Score 211.5; DB 5; Length 379;  
Best Local Similarity 23.0%; Pred. No. 2e-10;  
Matches 105; Conservative 75; Mismatches 176; Indels 101; Gaps 19;  
QY 44 LHQDEFVQTLKEWVAIESDS--VQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ 101  
Db 1 MDQQKIQILKDLVNIIDSTNGHEEQVANYLQKLLAEHIESEKVQ-----YDL---- 48  
QY 102 LPDGQSLPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGR 161  
Db 49 --DRASL-----VSEIGSSNEK-VLAFSGHMDVVDAGDVSKWKFPPFEATEHEGKLYGR 99  
QY 162 GATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGV 221  
Db 100 GATDMKSGLAAMVIAMELHEEKQKLGKIRLLATVGGEEIGELGAEQLTKQ--GYADDL 156  
QY 222 DYIVISDNLWISORKPA---ITYGTRGNSYFMVEVKCRDQDFHSG--TFGGILHEPMADL 276  
Db 157 DGLIIGE-----PSGHRIVYAHKGSINY--TVKSTGKNAHSSMPEFG----- 196  
QY 277 VALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFL--FDTK 334  
Db 197 -----VNAIDNLLL--FYNE-----VEKPFVKSIDAT 220  
QY 335 EEILMHLWRYPSSLIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVEKQVTRHL 394  
Db 221 NEILGDF-----IHNVT-VIDGNGQVNSIPEKAQLQGNIRSIPEMDNETV-KQVLVKI 271  
QY 395 EDVFSKRNSNMVSMVMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMRDGSTIPIA 454  
Db 272 INKLNQENVNLELI-FDYDKQPVFSDKNLWHIAKSVASDIVKEEIPLLGISGTTDAA 330  
QY 455 KNFQEIHKSVVLPLGAVDDGGEHSQNEKINRWNYIE 491  
Db 331 EFTK--AKKEFPVITFGPGNETPHQVNVENVSIGNYLE 365

RESULT 81  
ABP39493  
ID ABP39493 standard; protein; 431 AA.  
XX  
AC ABP39493;  
XX  
DT 24-JUL-2002 (first entry)  
XX  
XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4338.  
DE  
XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
KW antibacterial; gene therapy.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN US6380370-B1.  
XX  
PD 30-APR-2002.  
XX  
PF 13-AUG-1998; 98US-00134001.  
XX  
PR 14-AUG-1997; 97US-0055779P.  
PR 08-NOV-1997; 97US-0064964P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2002-381255/41.  
DR N-PSDB; ABN92038.  
XX  
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis  
PT polypeptide, useful for diagnosing and treating bacterial infections.  
XX  
PS Disclosure; SEQ ID NO 4338; 267pp; English.  
XX  
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
CC antibacterial activity and can be used in gene therapy. The sequences can  
CC also be used in the diagnosis and treatment of bacterial infections,  
CC particularly S. epidermidis infections. The sequences can be used to  
CC screen for compounds able to interfere with the S. epidermidis life cycle  
CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from the USPTO web site  
XX  
SQ Sequence 431 AA;

Query Match 8.0%; Score 211; DB 5; Length 431;  
Best Local Similarity 22.2%; Pred. No. 2.7e-10;  
Matches 111; Conservative 89; Mismatches 179; Indels 122; Gaps 25;  
QY 37 KVFOYID-----LHQDEFVQTLKEWVAIE--SDSVQPVPRFRQELFRMMAVAADTLQR 87  
Db 9 KVLQFMKGGIMMSVLSNEERVEILSDIVSIKTVNSNELEVAQYFERLF-----SQ 58  
QY 88 LGARVASVDMGPQQLPDGQSLPIPPVILAEIGSD-PTKGTVCFYGHLDVQPADRGDGLWLT 146  
Db 59 YGIR-SYIDI-----VADGRA-----NLIA TVGSSHPVIG---ISGHMDVVSEGNHDDWTY 105  
QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI---EGMEEAGS 203  
Db 106 DPFTLTEDQGYLYGRGAADMKSGLAALALALIEIKESGKLTQGTIKFMATVGEEME QSGS 165  
QY 204 VALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSG 263  
Db 166 ---QQLFEK---GYADDL DALLIAEPSF-----PSLVYAHKSGMDFRIKSKGR----- 207  
QY 264 TFGGILHEPMADLVALLGSLVDSSGHILVPGI-YDEVVPLTE--EEIN-----TYKA 312  
Db 208 -----ASHSSIPFLGQNAIKPLLEFIQINQIEYKIMQTVKG 244

QY 313 IHLDEEYRNSRVEKFLFDTK-----EILMHLWRYPSLSIHGIEGAFDEPGTK-TVIPGR 368

Db 245 ESLDFSNMINKLENQLPNHITKERAQELIQLGLVMTNSI-----VQG-----GTQVNSVPDF 295

QY 369 VIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYL 428

Db 296 ATAENVRTIPEYNNKVKALFNKYVEQA---NHNGASLTQELYLDLEPVVTTGQNRLVE 352

QY 429 AAKRAIRTVGTEPDMI-----RDGSTIPIAKMFQEIHKSVVLIPLGAVDGGEHSQN 481

Db 353 LGFDIAKSHFSNERDLIITPTVAVTDASNLLKGK-----DENFFFLMFGP-GNGPHQIN 405

QY 482 EKINRWNYIEGTKLFAAFFLE 502

Db 406 ECVEKVNYLE-----FVEYYIE 422

RESULT 82

ADS05394

ID ADS05394 standard; protein; 431 AA.

XX ADS05394;

AC

XX

DT 04-NOV-2004 (first entry)

XX

DE Staphylococcus epidermis polypeptide seqid 4689.

XX

KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;

KW recombinant expression vector; infection; computer readable medium;

KW computer based system.

XX

OS Staphylococcus epidermidis.

XX

XX US2004147734-A1.

PN

XX

PD 29-JUL-2004.

XX

XX

PF 01-DEC-2003; 2003US-00724972.

XX

XX

PR 08-NOV-1997; 97US-0064964P.

PR 13-AUG-1998; 98US-00134001.

PR 29-NOV-1999; 99US-00450969.

XX

XX

PA (DOUC/) DOUCETTE-STAMM L.

PA (BUSH/) BUSH D.

XX

PI Doucette-Stamm L, Bush D;

XX

DR WPI; 2004-580138/56.

DR N-PSDB; ADS01622.

XX

PT New isolated polypeptide and encoding nucleic acid derived from

PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or

PT treating an S. epidermidis bacterial infection.

XX

PS Claim 17; SEQ ID NO 4689; 74lpp; English.

XX

XX

CC The invention describes an isolated nucleic acid comprising a nucleotide

CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:

CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any

CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as

CC given in the specification. Also described are: a recombinant expression

CC vector; a cell comprising a recombinant expression vector of (1);

CC producing an S. epidermidis polypeptide; an isolated nucleic acid

CC comprising a nucleotide sequence of at least 8 nucleotides in length; a

CC vaccine composition for prevention or treatment of an S. epidermidis

CC infection, comprising a nucleic acid cited above and a carrier; treating

CC a subject for S. epidermidis infection; a recombinant or substantially

CC pure preparation of an S. epidermidis polypeptide or its fragment; a

CC vaccine composition for prevention or treatment of an S. epidermidis

CC infection; detecting the presence of a Staphylococcus nucleic acid in a

CC sample; a computer readable medium having recorded in it the nucleotide

CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based

CC system for identifying fragments of the Staphylococcus genome of

CC commercial importance; a computer based system for identifying fragments

CC of the Staphylococcus plasmids of commercial importance; identifying

CC commercially important nucleic acid fragments of the Staphylococcus

CC genome and/or plasmids; and identifying an expression modulating fragment

CC of the Staphylococcus genome and/or plasmids. The methods and

CC compositions of the present invention are useful for the diagnosis,

CC prevention and/or treatment of an Staphylococcal epidermidis bacterial

CC infection. This is the amino acid sequence of a S. epidermis protein of

CC the invention.

XX

SQ Sequence 431 AA;

Query Match 8.0%; Score 211; DB 8; Length 431;

Best Local Similarity 22.2%; Pred. No. 2.7e-10;

Matches 111; Conservative 89; Mismatches 179; Indels 122; Gaps 25;

QY 37 KVFQYID-----LHQDEFYQTLKEWVAIE--SDSVQVPRFRQELFRMMAVAADTLQR 87

Db 9 KVLQPMKGGIMMSVLSNEERVEILSDIVSIKTVNSNELEVAQYFERLF-----SQ 58

QY 88 LGARVASVDMGPQQLPDGQSLPIPPVILAELGSD-PTKGTVCFYGHLDVQPADRGDGLT 146

Db 59 YGIR-SYIDI----VADGRA-----NLIATVGSSHPVIG---ISGHMDVVSSEGNHDDWTY 105

QY 147 DPVVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFI---EGMEEAGS 203

Db 106 DPFTLTEDQGYLYGRGAADMKSGLAALALALIEIKESKLTQGTIKFMATVGEEMEQQSGS 165

QY 204 VALLELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYTRGNSYFMVEVKCRDQDFHSG 263

Db 166 ---QQLFEK---GYADDDLALLIAEPSF-----PSLVYAHKGSMDFRICKGR----- 207

QY 264 TFGGILHEPMAIDLVALGLSLVDSSGHILVPGI-YDEVVPLTE--EIN-----TYKA 312

Db 208 -----ASHSSIPFLGQNAIKPLLEFIQINQOEYKIMQTVKG 244

QY 313 IHLDEEYRNSRVEKFLFDTK-----EILMHLWRYPSLSIHGIEGAFDEPGTK-TVIPGR 368

Db 245 ESLDFSNMINKLENQLPNHITKERAQELIQLGLVMTNSI-----VQG-----GTQVNSVPDF 295

QY 369 VIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYL 428

Db 296 ATAENVRTIPEYNNKVKALFNKYVEQA---NHNGASLTQELYLDLEPVVTTGQNRLVE 352

QY 429 AAKRAIRTVGTEPDMI-----RDGSTIPIAKMFQEIHKSVVLIPLGAVDGGEHSQN 481

Db 353 LGFDIAKSHFSNERDLIITPTVAVTDASNLLKGK-----DENFFFLMFGP-GNGPHQIN 405

QY 482 EKINRWNYIEGTKLFAAFFLE 502

Db 406 ECVEKVNYLE-----FVEYYIE 422

RESULT 83

ABO62608

ID ABO62608 standard; protein; 376 AA.

XX

AC ABO62608;

XX

DT 29-JUL-2004 (first entry)

XX

DE Klebsiella pneumoniae polypeptide seqid 9125.

XX

KW Recombinant expression vector; transcription regulatory element;

KW Klebsiella pneumoniae protein; antibacterial; vaccine.

XX

OS Klebsiella pneumoniae.

XX

XX US6610836-B1.

XX

PD 26-AUG-2003.

XX





ADB07680  
ID ADB07680 standard; protein; 376 AA.  
XX  
AC ADB07680;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Alloiooccus otitis antigenic protein SEQ ID NO:1620.  
XX  
DE Alloiooccus otitis;  
KW Alloiooccus otitis; antigenic protein; immunogenic; immunisation;  
KW gene therapy; Gram-positive bacterium; infection.  
XX  
OS Alloiooccus otitis.  
XX  
PN WO2003048304-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 25-NOV-2002; 2002WO-US036123.  
XX  
PR 29-NOV-2001; 2001US-0333777P.  
PR 18-NOV-2002; 2002US-0426742P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
XX  
PI Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;  
XX  
PI WPI; 2003-505284/47.  
DR N-PSDB; ADB07679.  
XX  
PT New Alloiooccus otitis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.  
XX  
PS Claim 33; SEQ ID NO 1620; 1019pp; English.  
XX  
SS The present invention describes an isolated polynucleotide (I) of  
CC Alloiooccus otitis genomic DNA, which encodes an antigenic protein.  
CC Alloiooccus otitis is a Gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its  
CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloiooccus otitis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloiooccus  
CC otitis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloiooccus  
CC otitis. The present sequence represents an Alloiooccus otitis  
CC antigen protein from the present invention.  
XX  
SQ Sequence 376 AA;  
Query Match 8.0%; Score 209.5; DB 6; Length 376;  
Best Local Similarity 23.9%; Pred.No. 3e-10;  
Matches 109; Conservative 69; Mismatches 142; Indels 137; Gaps 24;  
QY 82 ADTLQRL---GARVASVDMGPPQQLFDGQSLPIPPVILAEELGSDPTKGTVC-FYGHLDVQ 136  
Db 21 ADFLQELLKENGIPSKQVEYSP-----GRN---GLIATFEGEBP--GSVLGFSGHLDV 69

QY 137 PADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 196  
Db 70 PVGEVE-WENDPFAAVEKDGKVGSGCDMKSLISAIVALIRFKQKEKFKGTIKFIIT 128  
QY 197 GMEAGSVALEELVEKEKDRFFSGVDYIVISD-----NLWISQRKPAITYGTR 244  
Db 129 VGEETSSLGATQLV---KAGYADDLDAMIINEPTDLKVGVAHKGALW-----PRIT----- 176  
QY 245 GNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTE 304  
Db 177 -----TYGKTAHGSMP-----HRGVNAI--NNMVKLIN 202  
QY 305 EEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTV 364  
Db 203 ELNNT-----IDFLQY-----NDELLGE-----PTSSINIIRGG---SGT-NV 236  
QY 365 IPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMVMTLGLHPWIANIDD 424  
Db 237 VPDKATIEIDIRTVPQQDHSQIKKIDIEEILENL-SRKDDDFKY-----E 279  
QY 425 TQYLAAKRAIRT-----VFGTEPDMIRDGSTIPIAKMFQE-----IVHKSVVLIPL 470  
Db 280 IEYVNDLLAIKTDTEDPFTHLVSSSVQEVLEDSATVFAPSYITDGSEFVLADKDFPIII 339  
QY 471 G-AVDDGGEHSQNEKIN---RWNYIE-GTKLFAAFFLE 502  
Db 340 GPGEEEMAHQPNEYVDIEKFYDMIEINTKIMKNFFAQ 376  
RESULT 86  
ABU24254  
ID ABU24254 standard; protein; 463 AA.  
XX  
AC ABU24254;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #9781.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
OS Clostridium botulinum.  
XX  
XX WO200277183-A2.  
PD 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002WO-US0009107.  
PF 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA28124.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 52178; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid





```
XX      Sequence 465 AA;
SQ
      Query Match      7.7%; Score 201; DB 6; Length 465;
      Best Local Similarity 20.7%; Pred. No. 2.6e-09;
      Matches 111; Conservative 91; Mismatches 197; Indels 138; Gaps 20;

QY      35 LEKVQYIDLHODEFVQTLKEWVAIESDS--VQPVPFRQELFRMMAVAADTLQRLGARV 92
Db      1 MDKINEKIDLLKDDMWSSIQEILRIKSISGEAENAPFGKDTAKALDYALKLAERLGFKT 60

QY      93 ASVD--MGPOQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYV 150
Db      61 VNLNDYVGYAEVGEDEDY-----VAVLGHLDVVP--EGDGNYPYPA 100

QY      151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGS-VALEEL 209
Db      101 AEIHDGKLYARGSMDDKGTVACLYSLKAIADAGLTMSKKVRIIFGLDEETGSGKDEHY 160

QY      210 VEKEKD---RFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGT-- 264
Db      161 LKNEKPPVLGFTPDAEYPIIN-----GEKGITIFNL-VKDFKNDYEGDTKI 205

QY      265 -----FGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN 308
Db      206 IYVKGGRSNNVPPYAEAGIRADLKGEIIDKCESFAERTGYDIKAEKDDMVIVKSKI- 264

QY      309 TYKAIHLDLEEYRNSRVEKFLFDTKEEI-----LMHLWRYPSLSIHGIEGAFDE 358
Db      265 ---AAHGSMPBLGNAIMQLLAF--LEELNLGKSDFNNDYIAFLNRYVGMETNGESFGIG- 318

QY      359 PGTKTVIPGRVIGKFSIRL-VPHMN-----VSAVEKQVTRHLEDVFSKRNSNKMVMSM 411
Db      319 -----MEDKVSGLSFNLGIIDFNKDQKVNLNRYVPVTCYEDWMDGIN----- 363

QY      412 TLGLHPWIANIDDT----QYLAAKRAIRTVFGTEPDMIRGDSSTIPIAKMFQEIIVHKSUVL 467
Db      364 -----ARIADTGIRVENMTHQKSL--YFPEDHELVK-----LLQKVYKEQTSEEPKL 408

QY      468 IPLG-----AVDDGEHSQNEKINRWNYIEGTYKLFAAFFLEMAQ 505
Db      409 LSIGGGTYAKEMPNIYAFGPIFPGEPPVDHQANEFIKIEHLILNAKIYAHAIYELAR 465

RESULT 88
ABB49465
ID      ABB49465 standard; protein; 470 AA.
XX
AC      ABB49465;
XX
DT      05-FEB-2002 (first entry)
XX
DE      Listeria monocytogenes protein #2169.
XX
KW      Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW      vitamin B12; bacterial infection; disease.
XX
OS      Listeria monocytogenes.
XX
PN      WO200177335-A2.
XX
PD      18-OCT-2001.
XX
PF      11-APR-2001; 2001WO-FR001118.
XX
PR      11-APR-2000; 2000FR-00004629.
XX
PA      (INSP ) INST PASTEUR.
XX
PI      Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI      Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI      Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI      Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
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PI      Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI      Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI      Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI      Rose M, Voss H;
XX
DR      WPI; 2002-010914/01.
XX
PT      Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT      and prevention of Listeria and related bacterial infections, and related
PT      polypeptides.
XX
PS      Claim 6; SEQ ID NO 2170; 192pp; French.
XX
CC      The present invention relates to the genome sequence of Listeria
CC      monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC      it are useful for selecting probes and primers for detecting genes in L.
CC      monocytogenes and related organisms, and for studying genetic
CC      polymorphisms and other genomes. The present sequence is a protein
CC      encoded by the genome sequence of the present invention. Proteins
CC      expressed from the genome sequence are useful for raising specific
CC      antibodies, identification of L. monocytogenes and related organisms, and
CC      for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC      B12. The genome sequence and proteins encoded by it are also useful for
CC      selecting compounds that regulate gene expression and cell replication
CC      and modulate L. monocytogenes-related diseases. In addition, the genome
CC      sequence and proteins encoded by it are useful in pharmaceutical and
CC      vaccines compositions for the treatment or prevention of infections by L.
CC      monocytogenes and related organisms. Note: The sequence data for this
CC      patent did not form part of the printed specification, but was obtained
CC      in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 470 AA;
```

```
Query Match      7.5%; Score 197.5; DB 5; Length 470;
Best Local Similarity 21.0%; Pred. No. 5.5e-09;
Matches 97; Conservative 67; Mismatches 165; Indels 133; Gaps 18;

QY      42 IDLHQDEFVQTLKEWVAI-----ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVD 96
Db      10 VEARKDDFLEDLKGLLRIPSVRDDSCKTEDAP-FGPDVKR----ALDYMMELGKK----- 59

QY      97 MGPOQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDG 156
Db      60 -----DGFTAKEVGNVAGHLEYGQGEELVGLGHVDVVPV--GDGWTNGPFPETLRDG 110

QY      157 KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKBD- 215
Db      111 KLYARGVADDKGPTIAGYALKIIKELGLPLSRVRRIIGSDEESGMSCVRYFETEEOQ 170

QY      216 --RFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPM 273
Db      171 TLGFVPDAEFPPIIHAKEGISE-----LDVSFKDGEAGG----- 203

QY      274 ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEY-RNSSRVEKFLPD 332
Db      204 -EAAFRLLSVESGERYNMVP--DHATAILE-----DVKDFDKVASAFKTFILAN 248

QY      333 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392
Db      249 -----HPVEGTLEENGKSVKI--NIVGKSAHAMEPNNGVNA----- 282

QY      393 HLEDVFSKRNSNKMVMSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRGDSSTIP 452
Db      283 -----GLH-LVAFLGKFKLTGAANDFVT-FGRD-YLFGDSRAVK 318

QY      453 IAKMFQEIIVHKSUVLPLGAVDDGEHSQNEKINRWNYIEGTYKL 494
Db      319 LGISYED-----AESGELTMNVGVIRYDVAEGGK 347
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RESULT 89  
ABU32593



CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html

XX  
SQ Sequence 632 AA;

Query Match 7.5%; Score 195.5; DB 7; Length 632;  
Best Local Similarity 22.9%; Pred. No. 1.3e-08;  
Matches 111; Conservative 60; Mismatches 174; Indels 139; Gaps 23;

QY 54 KEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQL----- 102  
Db 240 RETCALEPD---MPSGRDILADL--VAFDTVSR-ESNLALIDYVRDYLAGFGVDSELPFF 292  
QY 103 -PDGQSLPIPPVILAEIG-SDPKGTVCYFCHLDVQPADRGDWLTDPYVLTEVDGKLYG 160  
Db 293 DADGRKAN---LYATIGPSD--RGGVCLSGHTDVPAD-QQAWSVPFRLSERDGRLYG 345  
QY 161 RGATDNKGPVLAWINAVSAFRALEQDLPVNKIFIIEGMEAGSVALEELVEKEKDRFFSG 220  
Db 346 RGTADMKGYLACVLAAPPAFLAPLRLPVHLAFSYD--EEVCLGVRSLLAALERRPHKP 403  
QY 221 VDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMAD----- 275  
Db 404 LLCIGEP----TELKPVL--GHKGKLAMRCEV-----HGAACHSAYAPQGVNA 446  
QY 276 ---LVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 447 IEYAARLIGRLGEIGARLAAPERHDR-----RFD 475  
QY 333 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 476 PP-----YSTVQTGLIOGG---RALNIVPAECRDFEVRALPADDPRQVAEELRD 522  
QY 393 HLEDVFSKRNSSNMVSM---TLGLHPWIANIDDTQ-----YLAAKRAIRTV-FGTEP 442  
Db 523 YAESELLPRMRAVERSTDIRFTPLSAYPGLLTADDSQAELIGLLSGSTDFSTVAFGTG 582  
QY 443 DMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKINRWNYIEGTLKFAAFLE 502  
Db 583 GLFHQAG-IP-----AVICGPGSMDQG-HKPDE-----FVS 611  
QY 503 MAQL 506  
Db 612 LAQL 615

RESULT 91

ADF07953

ID ADF07953 standard; protein; 386 AA.

AC ADF07953;

XX 12-FEB-2004 (first entry)

DE Bacterial polypeptide #4066.

XX Proteus mirabilis infection; bacterial infection; antibacterial;

KW immunostimulant.

OS Proteus mirabilis.

XX  
PN  
PD  
XX  
PF  
XX  
PR  
XX  
PA  
XX  
PI  
XX  
DR  
DR  
XX  
PT  
PT  
PT  
XX  
PS  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
XX  
SQ

US6605709-B1.  
12-AUG-2003.  
05-APR-2000; 2000US-00543681.  
09-APR-1999; 99US-0128706P.  
(GENO-) GENOME THERAPEUTICS CORP.  
Breton GL;  
WPI; 2003-895291/82.  
N-PSDB; ADF03781.

New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.

Disclosure; SEQ ID NO 8238; 870pp; English.

The invention relates to new Proteus mirabilis polypeptides and polynucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.

Sequence 386 AA;

Query Match 7.2%; Score 188.5; DB 7; Length 386;  
Best Local Similarity 21.3%; Pred. No. 2.8e-08;  
Matches 97; Conservative 66; Mismatches 167; Indels 125; Gaps 17;

QY 67 VBRFRQELFRMMAVAADTLQRLGAR--VASVDMGPQQLPDGQSLPIPPVI--LAELGSDP 122  
Db 1 LPDFYRSLIFMSCPVIELAQQLISRPSVSPDDQGCQL-----IIERLAPLGFTI 50  
QY 123 TK-----GTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATD 165  
Db 51 EKMPFGQTNLWACRGGEGETLAFAGHTDVVPPGANALWNPFPFESIRDMGLYGRGAAD 110  
QY 166 NKGPVLAWINAVSAFRALEQDLPVNKIFIIEGMEEA-----GSVALEELVEKEKDRFFSGV 221  
Db 111 MKGSLAAMVVAERFVHAYPQHRGLAFLITSDEADADHDGTVKVVESLISRGER----L 166  
QY 222 DYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLG 281  
Db 167 DYCLVGEPPSSQHLGDMIKNGRRGS-----ITANV 196  
QY 282 SLVDSSGHILVPGIYDEVV---PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKKEI 337  
Db 197 TIYGTQGHVAYPHLAQNPIHMASPFIHELVT-----VWDNGNEY 236  
QY 338 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV 397  
Db 237 -----FPATTMQ-IANINSGTGSNNVIPGELFIOQFNFR----FSTAITDEEIRQTEAL 285  
QY 398 FSKRNSSNMVSMVMTLGLHPWIAN-----IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP- 452  
Db 286 LQKYQL--RYHISWSLSGQPFITGEGKLLDAVRY-----SVKHYTNIEPTLSTSGGTS DG 338  
QY 453 --IAKWFQEIIVHKSVVLIPLGAVDGGEHSQNEKIN 485  
Db 339 RFTAQMG AQVVE-----LGPINATIHKVNECVS 366





CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 471 AA;

Query Match 7.2%; Score 188; DB 6; Length 471;  
Best Local Similarity 22.8%; Pred. No. 4.2e-08;  
Matches 111; Conservative 73; Mismatches 192; Indels 110; Gaps 24;

QY 42 IDLHQDEFVQTLKEWVAI--ESDSVQVPVRFR-----QELFRMMAVAADTLQRLGARVA 93  
Db 9 VEARKDDLEDLQNLRLINSEDDAQATPEAPFGPGVPAGLKHMLAYG---ERDGFYVK 64  
QY 94 SVDMGPPQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFGLHDVQPADRGDGLTDPYVLTE 153  
Db 65 NVDNYAGHTEYGE-----GDETIG---IFGHMDVVPA--GDGWETDPYEPVI 106  
QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKE 213  
Db 107 KDGKIYARGASDDKGPSMAAYYAMKIIKELGLPVSCKIRFVVSDEESGWGMDYYFQHE 166  
QY 214 K--DRFFS-GVDYIVIS---DNLWISQKKPAITY-GTRGNSYFMVEVKC-RDQDFHSGTF 265  
Db 167 EAPDFGFSPPDAEFPIINGEKGNTI-----RLTFRGGNGADYKLESFKSGLRENMPVGT 221  
QY 266 GGILHEPMADLVALLGSLVDS-----SG-----HILVPGIYDEVVPLTEEE 306  
Db 222 DAVVTAASADEAASLAASFETFIKQEAKISGNAELSDKTVTTFHVVGKAHG---ASPQSG 278  
QY 307 INTYKAHLDLEEYRNSRVEKFLFDTKBEILMLWRYPSLSIHGIEGAFDEPGTKTVIP 366  
Db 279 INAAFTLATFLNDYSFAEGAYSFI-NTIAEFIHEDFYGEKLGV-----AFED----- 324  
QY 367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGL-HPWIANIDDT 425  
Db 325 -EKMGKLT-----MNAGIVN-----FDPENPENSLV---TLNFRYPKGTSAEEL 364  
QY 426 QYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVKSVLLIPLGAVDD--GEHSQNEK 483  
Db 365 QAKVQTTVGTVTATQGRNQEPHYVP-----VDDPLVATLLQVYEDHTGKGEQEI 416  
QY 484 INRWNY 489  
Db 417 IGGGT 422

RESULT 94  
ADS44683  
ID ADS44683 standard; protein; 426 AA.

XX AC ADS44683;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #23113.

XX KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

XX PA (HINK/) HINKLE G J.

XX PA (SLAT/) SLATER S C.

XX PA (CHEN/) CHEN X.

XX PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 23113; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 426 AA;

Query Match		7.1%;	Score 187;	DB 8;	Length 426;
Best Local Similarity		20.1%;	Pred. No. 4.5e-08;		
Matches 106;		Conservative 70;	Mismatches 162;	Indels 190;	Gaps 23;
QY	42	IDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ	101		
Db	12	VEEKEELIQLAKTLISYQT----PAPPAR-NTEGIQSWIAGYLNELGFSIDKWDVYPGD	66		
QY	102	LPGQSLPIPPVILAEGLSDPTKGT-----VCFYGHLDVQPADRGDWLTDPYVLTEV	154		
Db	67	-----PNVVGRL-----KGTDSADYSLIINGHVDVAEVKEDEWKHPFPIEK	111		
QY	155	DGKLYGRGATNKGVLAWINAVSAFRALEQDLPVNIKFIEGM--EEAGSVALEELVEK	212		
Db	112	NGLLTGRGASDMKGMACVLFVAVKLIREASIELPGDL--ILQSVIGEVEAGTLECCKR	169		
QY	213	EKDRFFSGVDYIVISD--NLWISQKPAITYGTRGNSYFWEVVKCRDQDFH-----	261		
Db	170	GYH-----ADFAIVADTSDMHIOGGVIT-----GWIEIK-SSQTFHDGTRRNMIH	215		
QY	262	--SGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEE	319		
Db	216	AGGTFGASAIEKMAKIIAGLGEL-----ERHWSIMKS-----	248		
QY	320	YRNSRVEKFLFDTKEEILMLWRYPSLSIHGIEGAFDEPGTKVIPGRVIG-----	371		
Db	249	-----YPGF-----KPGTNTINPAVIEGGRHAAPFA	274		
QY	372	-KFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAA	430		
Db	275	DECLWITVHFYPNETHDQVAABIEDYVNRLSDS-----IWL-----	312		
QY	431	KRAIRTVF--GTEPDMIRD--GSTIP-----IAKMEQIRIVHKSVVLIPLGAV	473		
Db	313	-RENRPVKWGS--SMIEDRGEIFPALEVDPGHPGVLTALTASHQKVRECPIIDVSQSV	369		
QY	474	DDG-----EHSQNEKINRWNYIEGTKLFAAFL	501		
Db	370	TGGWLYDAGIPCVIYGPDILHNAHSVNEKVSIEQLVEYTKIILDFII	417		
RESULT 95					
ADC94444					
ID	ADC94444	standard; protein; 440 AA.			
XX	AC	ADC94444;			
XX	DT	01-JAN-2004 (first entry)			
XX	DE	E. faecium protein sequence SEQ ID 4071.			
XX	KW	Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;			
XX	KW	abdominal-pelvic infection.			
OS	OS	Enterococcus faecium.			
XX	FN	US6583275-B1.			
XX	PD	24-JUN-2003.			
XX	PF	30-JUN-1998; 98US-00107532.			
XX	PR	02-JUL-1997; 97US-0051571P.			
PR	PR	14-MAY-1998; 98US-0085598P.			
XX	PA	(GENO-) GENOME THERAPEUTICS CORP.			
XX	PI	Doucette-Stamm LA, Bush D;			
XX	DR	WPI; 2003-799836/75.			
DR	DR	N-PSDB; ADC90790.			
XX	PT	New isolated nucleic acid derived from Enterococcus faecium encoding an			

Query Match		7.1%;	Score 187;	DB 7;	Length 440;
Best Local Similarity		27.3%;	Pred. No. 4.7e-08;		
Matches 73;		Conservative 40;	Mismatches 92;	Indels 62;	Gaps 11
QY	68	PRFRQELFRMMAVAADTLQRLGARVASVD--MGPPQLPDGQSLPIPPVILAEGLSDPTKG	125		
Db	11	PGPRDALKHMLAYG----ERDGFVKVNDVNYAGHIDLGE-----DETGL	51		
QY	126	TVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQ	185		
Db	52	---IFGHMDVVPA--GDGWDTPPYEPVKDGKIFARGSSDDKGPSMAAYAMKIIKELD	106		
QY	186	DLPVNIKFIEGMEEA--GSVALEELVEKEKDRFFS-GVDYIVISDNLWISQKPAITYG	242		
Db	107	KLSKKVRFVVGSDDESGWGMAYYFEHEEPPDFGSPDAEFPIN-----G	152		
QY	243	TRGNSYFMEVVKCRDQDFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEV--V	300		
Db	153	EKGN----VSLALRFKGDNAGDY-----VLKSFVSGLRENNMVPGTATAALQV	195		
QY	301	PLTEEEINTYKAHLDLEEYRNSSRVE	327		
Db	196	PSADAAIAAMEEAFYQFIEANPVSQTIE	222		
RESULT 96					
ABU25446					
ID	ABU25446	standard; protein; 453 AA.			
XX	AC	ABU25446;			
XX	DT	19-JUN-2003 (first entry)			
XX	DE	Protein encoded by Prokaryotic essential gene #10973.			
XX	KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.			
XX	OS	Clostridium difficile.			
XX	FN	WO200277183-A2.			
XX	PD	03-OCT-2002.			
XX	PF	21-MAR-2002; 2002WO-US009107.			
XX	PR	21-MAR-2001; 2001US-00815242.			

PT	Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection.				
XX					
PS	Example 1; SEQ ID NO 4071; 243pp; English.				
XX					
CC	The invention relates to an isolated nucleic acid derived from				
CC	Enterococcus faecium encoding an Enterococcus faecium polypeptide having				
CC	one of 10 fully defined sequences given in the (or comprising 40				
CC	sequential nucleotides chosen from any of the nucleic acids, its				
CC	complement or sequences hybridising to it). Also included are a				
CC	recombinant vector comprising the nucleic acid operably linked to				
CC	transcription regulatory element, a cell comprising the vector and a				
CC	single-stranded probe comprising the nucleic acid. The nucleic acids are				
CC	chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.				
CC	The nucleic acids is useful for diagnosing pathological conditions				
CC	resulting from E. faecium bacterial infection (e.g. urinary tract				
CC	infection, bacteraemia, endocarditis, wounds and abdominal-pelvic				
CC	infection) and for screening drugs such as agonists and antagonists. The				
CC	nucleic acid is useful for recombinant production of Candida albicans -				
CC	derived peptides or antisense polypeptides. Pharmaceutical compositions				
CC	and vaccines containing the nucleic acid are useful for preventing or				
CC	treating Enterococcus faecium infections. The present sequence represents				
CC	one if the disclosed E. faecium proteins.				
XX					
SQ	Sequence 440 AA;				
Query Match 7.1%; Score 187; DB 7; Length 440;					
Best Local Similarity 27.3%; Pred. No. 4.7e-08;					
Matches 73; Conservative 40; Mismatches 92; Indels 62; Gaps 11					
QY	68	PRFRQELFRMMAVAADTLQRLGARVASVD--MGPOQLPDGQSLPIPPVILAEGLSDPTKG	125		
Db	11	PGPRDALKHMLAYG-----ERDGFVKVNVNDNYAGHIDLGE-----DETIG	51		
QY	126	TVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQ	185		
Db	52	---IFGHMDVWPA--GDGWDTPYEPVIKDGKIFARGSSDDKGPSMAAYYAMKIKELDL	106		
QY	186	DLPVNIKFIIEGMEEA--GSVALEELVEKEKDRFFS-GVDYIVISDNLWISQRKPAITYG	242		
Db	107	KLKKKRVFVVGSGDESGWDMAYYFEHEEPEDFGFPDAEFPIN-----G	152		
QY	243	TRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV--V	300		
Db	153	EKGN-----VSLALRFKGNAGDY-----VLKSFVSGLRNRMVPGTATAALQV	195		
QY	301	PLTEEEINTYKAHLDLEEYRNSSRVE	327		
Db	196	PSADAAIAAMEEAFYQFIEANPVSQTIE	222		
RESULT 96					
ABU25446					
ID	ABU25446 standard; protein; 453 AA.				
XX					
AC	ABU25446;				
XX					
DT	19-JUN-2003 (first entry)				
XX					
DE	Protein encoded by Prokaryotic essential gene #10973.				
XX					
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.				
XX					
OS	Clostridium difficile.				
XX					
PN	WO200277183-A2.				
XX					
PD	03-OCT-2002.				
XX					
PF	21-MAR-2002; 2002WO-US009107.				
XX					
PR	21-MAR-2001; 2001US-00815242.				













CC animal is advantageous in that the expression can be tissue- or organ-  
CC specific  
XX  
SQ Sequence 318 AA;  
  
Query Match 6.7%; Score 176; DB 2; Length 318;  
Best Local Similarity 22.4%; Pred. No. 3e-07;  
Matches 83; Conservative 55; Mismatches 158; Indels 74; Gaps 12;  
  
QY 127 VCFYGHLDVQPADRGDGLTDPVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 186  
Db 4 LAFSGHMDVVDAGDVSWKWFPPEATEHEGKLYGRGATDMKSGLAAMVIAMIELHEEKQK 63  
  
QY 187 LPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPA---ITYGT 243  
Db 64 LNKIRLLATVGEIEGELGAEQLTQK---GYADDLHGLLIGE-----PSGHRIVYAH 112  
  
QY 244 RGNSEFMVEVKCRDQDFHSGTFCGILLHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLT 303  
Db 113 KGSINY--PVKSTGKNAHSS-----MP 132  
  
QY 304 EEEINTYKAIHLGLEEYRNSRVEKFL--FDTKEEILMHLWRYPSLSIHGIEGAFDEPGT 361  
Db 133 ESGVNAIDNLLFYNE-----VEKFVKSVDATNEILGDF-----IHNVT-VIDGGNQ 178  
  
QY 362 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRSSNKMVVSMTLGLHPWIAN 421  
Db 179 VNSIPEKAQLQGNIRSIPEDMNETV-KQVLVKIINKLNQENVNLELI-FDYDKQPVFSD 236  
  
QY 422 IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDGEHSQN 481  
Db 237 KNSDLVHIAKSVASDIVKEEIPLLGISGTTDAAEFTK--AKKEFPVLIIFGPGNETPHQVN 294  
  
QY 482 EKINRWNYIE 491  
Db 295 ENVSIGNYLE 304  
  
RESULT 101  
ADJ33264  
ID ADJ33264 standard; protein; 432 AA.  
XX  
AC ADJ33264;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Enterococcus faecalis XAA-His dipeptidase protein SEQ ID NO:24.  
XX  
KW Enterococcal; virulence factor; drug discovery; vaccine;  
KW microbial infection; antimicrobial; bacterial pathogenesis;  
KW XAA-His dipeptidase; enzyme.  
XX  
OS Enterococcus faecalis.  
XX  
PN WO2003056295-A2.  
XX  
PD 10-JUL-2003.  
XX  
PF 18-JUL-2002; 2002WO-US022979.  
XX  
PR 18-JUL-2001; 2001US-0306212P.  
XX  
PA (GENO ) GEN HOSPITAL CORP.  
XX  
PI Ausubel FM, Garsin D, Mylonakis EE, Calderwood SB, Sifri CD;  
XX  
DR WPI; 2003-559298/52.  
XX  
DR N-PSDB; ADJ33262, ADJ33263.  
XX  
PT New polypeptide, useful for preparing a composition for treating or  
XX preventing a microbial infection.  
PS Claim 81; SEQ ID NO 24; 140pp; English.

XX  
CC The present invention describes Enterococcal virulence factors (I), which  
CC can act as targets for drug discovery. Also described: (1) an isolated  
CC nucleic acid encoding (I); (2) a vector or host cell comprising the  
CC nucleic acid; (3) a method of screening a compound for effectiveness as  
CC an antagonist of (I); (4) a composition comprising the antagonist  
CC compound; (5) a method of screening a compound for effectiveness in  
CC altering expression of (I); (6) a method of treating an individual; (7) a  
CC vaccine composition comprising the polypeptide and a vehicle; and (8) a  
CC method of treating or preventing a microbial infection. (I) is useful for  
CC preparing a composition having antimicrobial activity for treating or  
CC preventing a bacterial pathogenesis e.g. microbial infection. The present  
CC sequence represents Enterococcal XAA-His dipeptidase, which is used in  
XX the exemplification of the present invention.  
SQ Sequence 432 AA;  
  
Query Match 6.7%; Score 176; DB 7; Length 432;  
Best Local Similarity 22.3%; Pred. No. 4.8e-07;  
Matches 99; Conservative 68; Mismatches 179; Indels 98; Gaps 18;  
  
QY 37 KVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVR--FRQELFRMMAVAADTLQRLGARVAS 94  
Db 2 KIKEEIAAQKDLFYEDLNKIIAIRSVKGPSKKEAPFGGPKRALEETLKLAEYGFQTGI 61  
  
QY 95 VDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPVLTVEV 154  
Db 62 VN-----DAVGYAQWGT--AEEYLGIIHGLDVVP--EGSGWSVPPFQLTKK 103  
  
QY 155 DGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEK 214  
Db 104 NQRLYGRGILDNKGPIILACLYGMKLLKELGYQPKKTIRLMFGTDEESGSDIPLYLEKEN 163  
  
QY 215 DRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFCGILLHEPMA 274  
Db 164 APVFG-----FTPDCKYPVVYGERGIVNY--EITTTIPDDSSSEQIGIIGDQAK 210  
  
QY 275 DLV-----ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLGLEEYR 321  
Db 211 DHVPDQLSVVIAGTKTAITGRAPSN---APELGKNAITLLAQKISEEQLVKGNLLQY- 265  
  
QY 322 NSSRVEKFLFDTKEEILMHLWRYPSL-SIHGIEG-AFDEPGTKTVIPGRVIGKFSIRLVP 379  
Db 266 -----FD-----WLTASFHEKHVGEVALD---FKDQDSGQLI-----LTP 298  
  
QY 380 HMNVSAVEK---QVTRHLEDVFSKRSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 436  
Db 299 Y----ALEKRGQQLVLSLAVRYPVSITENEVTTQLTKALFP-----ESEVTVIRRLPST 348  
  
QY 437 VFGTEPDMIRDGSTIPIAKMFQEI 460  
Db 349 LFPKDERNVQ-----KLTKVYEQI 367  
  
RESULT 102  
ADH87450  
ID ADH87450 standard; protein; 402 AA.  
XX  
AC ADH87450;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Enterococcus faecalis polypeptide #1930.  
XX  
KW Enterococcus faecalis infection; transcription regulatory element;  
KW antibacterial.  
XX  
OS Enterococcus faecalis.  
XX  
PN US6617156-B1.  
XX  
PD 09-SEP-2003.  
XX

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PF 13-AUG-1998; 98US-00134000.
XX
PR 15-AUG-1997; 97US-0055778P.
XX
XX (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
XX
PI Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-895394/82.
DR N-PSDB; ADH84045.
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating E. faecalis infection.
XX
XX Disclosure; SEQ ID NO 5335; 193pp; English.
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polypeptide of the invention.
XX
XX Sequence 402 AA;
SQ
Query Match 6.7%; Score 175; DB 7; Length 402;
Best Local Similarity 28.1%; Pred. No. 5.3e-07;
Matches 54; Conservative 32; Mismatches 62; Indels 44; Gaps 7;
QY 126 TVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQ 185
Db | : : : : | | | | | | | | | | | | | | | | : : :
12 TLGIFGHMDVVPA--GDGWETDPYEPVIKDKIYARGASDDKGPSMAAYYAMKIIKELGL 69
QY 186 DLPVNIKFIIEGMEEAGSVALEELVEKEK--DRFFS-GVDYIVISDNLWISQRKPAITYG 242
Db | : : : | | : : : | : : | | | : : : :
70 PVSKKIRFVVGSDSWGMDYFYFQHEEAPDFGFSPDAEFFPII-----G 115
QY 243 TRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPL 302
Db | : : : | | | | | | | | | | | | | | | | : : :
116 EKGN---VTIRL-----TFRG-----GNGADYKLESFKSLRENMVPG 150
QY 303 TEEEINTYKAIH 314
Db | : : : | : |
151 TADAVVTAASAH 162
RESULT 103
ADR31503
XX ADR31503 standard; protein; 394 AA.
AC ADR31503;
XX
XX 18-NOV-2004 (first entry)
XX Succinyl diaminopimelate desuccinylase.
DE amino acid biosynthesis; succinyl diaminopimelate desuccinylase; enzyme.
XX
XX Methylophilus methylotrophus.
OS
XX US2004170986-A1.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 28-FEB-2003; 2003US-00375039.
XX
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PR 28-FEB-2003; 2003US-00375039.
XX (AJIN ) AJINOMOTO CO INC.
PA
XX Usuda Y, Nishio Y, Yasueda H, Sugimoto S;
XX WPI; 2004-642013/62.
DR N-PSDB; ADR31502.
XX
XX New isolated polynucleotides and polypeptides involved in biosynthesis of
PT amino acids in Methylophilus methylotrophus, useful for production of
PT amino acids involved in the biosynthesis of amino acids.
XX
XX Claim 41; SEQ ID NO 44; 75pp; English.
PS
XX
XX The invention describes an isolated polynucleotide (I) involved in
CC biosynthesis of amino acids in Methylophilus methylotrophus. An isolated
CC polynucleotide (I) involved in biosynthesis of amino acids in
CC Methylophilus methylotrophus comprises: a nucleotide sequence encoding a
CC protein selected from 27 fully defined sequences comprising 180-926 amino
CC acids (SEQ ID NO. 2-54, even numbers only); a nucleotide sequence
CC selected from 27 fully defined sequences comprising 438-2781 bp (SEQ ID
CC NO. 1-53, odd numbers only); a nucleotide sequence which hybridizes to
CC (b); or a nucleotide sequence which is 95% identical to (b). Also
CC described are: a vector comprising (I); a host cell comprising (I); a
CC method for detecting a polynucleotide with at least 70% homology to (I);
CC a method for producing a polynucleotide with at least 70% homology to (I);
CC a method of making a protein; a method of producing at least one amino
CC acid; and an isolated polypeptide comprising: (a) an amino acid sequence
CC selected from SEQ ID NO. 2-54, even numbers only; or (b) an amino acid
CC sequence which is at least 95% identical to SEQ ID NO. 2-54, even numbers
CC only. The polynucleotides and polypeptides are useful for the production
CC of amino acids involved in the biosynthesis of amino acids. The
CC polynucleotides can be used as probes to isolate and/or identify RNA,
CC cDNA, or DNA molecules. They can also be used to design primers for PCR
CC to amplify, identify, and/or isolate full-length DNA, RNA, or other
CC polynucleotides. This is the amino acid sequence of succinyl
CC diaminopimelate desuccinylase, a protein involved in amino acid
CC biosynthesis.
XX
XX Sequence 394 AA;
SQ
Query Match 6.6%; Score 174; DB 8; Length 394;
Best Local Similarity 22.7%; Pred. No. 6.4e-07;
Matches 87; Conservative 48; Mismatches 144; Indels 104; Gaps 14;
QY 124 KGT----VCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179
Db | : : : | | | | | | | | | | | | | | | | : : :
68 RGTGTLIVFAGTDDVPTGTLDPQWHTPPFPTIKDGMLYARGAADMKTSLAAFTSIEE 127
QY 180 FRALEQDLPVNIKFII---EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQR 235
Db | : : : | | : : : | : : | : : | : : :
128 FIAENPHPGSIGLLITSDEEGIAIEGTVKVEALQARGETF----DYCIVGEPTS NKV 183
QY 236 KPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGI 295
Db | : : : | | : : : | | : : : | : : | : : | : : :
184 GDMIXNGRRGSLSGKLTVK-----GIQGHIAYP-----HLVKNPIHLAAPAI 225
QY 296 YDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKEKFLDFTKEEILMHLWRYP--SLSIHGIE 353
Db | : : : | | : : : | : : | : : | : : :
226 KDMVETVWDHG-----NEY-----FPPTSQWQISNMN 251
QY 354 GAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTL 413
Db | : : : | | : : : | : : | : : | : : :
252 GG---TGATNVVPGVEVEILFNFRYCPEVEGGSGSEQ-----SLRSRVHAIL 294
QY 414 GLHPWIANID---DTQYL-----AAKRAIRTVFGTEPDMIRDGSTIP---IAKMFQE 459
Db | : : : | : : : | : : | : : | : : :
295 DSHGFDYTLWEHNSQYITPRGELVAAISQAIEHSYGVSPELSTGGTSDGRFIADICKE 354
QY 460 IVHKSVVLIPLGAVDDGEHSQNE 482
Db | : : : | : : | : : | : : :
355 V-----IEFGPLNATIHKLNE 370
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The present invention relates to the isolation of novel lactic acid bacteria (*Lactobacillus rhamnosus* strain HN001) polynucleotide sequences, and the proteins encoded by them. Also disclosed are oligonucleotide probes and primers, and genetic constructs comprising the polynucleotide sequences of the invention. The polynucleotide sequences are useful for preparing a vaccine against bacterial infections or for improving the properties of microbes used in the manufacture of milk-derived products, food products, food additives, nutritional supplements, bioactive substances or probiotic supplements, and for modifying the flavour, aroma, texture and/or nutritional value of foods. They are also useful for identifying microorganisms having a trait associated with the polynucleotide. The present sequence represents a novel *L. rhamnosus* polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at [seqdata.uspto.gov](http://seqdata.uspto.gov).

Query Match 6.6%; Score 174; DB 8; Length 439;  
 Best Local Similarity 22.6%; Pred. No. 7.5e-07;  
 Matches 112; Conservative 58; Mismatches 182; Indels 144; Gaps 18;

QY	49	FVQTLKEWVAIES--DSVQPVPRFRQELFRMMAVADTLQRLGARVASVDMGPQQLPDGQ	106
DB	17	FIQALRQIMQIKSVRGSQQADAPFGRGPRAALTAAEELGKAYGFKTGIVNSAMAYIQWG-	75
QY	107	SLPIPPVILAEELGSDPTKGTVCYFGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDN	166
DB	76	-----DDQHVIIGVGHLDVVPAGETD-WHFPPYDLSEKAGRLYGRGILDN	120
QY	167	KGPVLAWINAVSAFRALEQDLPNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVI	226
DB	121	KGPSIACLFAMKLLKDAGFQPKRTIRLILGSDSESGADVPLYLAKAPEFG-----	173
QY	227	SDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS	286
DB	174	----FTPDCKFPVVYGERGIVNFN-----LRTPTID-----DS	202
QY	287	SGHILVPGIYDEVVPLTEEEINTYKAHLD-----LEEYRNSRVEKFLFDT-	333
DB	203	-----LDKVATITGQASDHVPDHLQATINDKRYTASGIRAPSNAPELGKNAITTL	253
QY	334	-KEEILMHL-----WRYPSLSIH-----GIEGAFDEPGTKVIP-----GRVI	370
DB	254	AKELLDEHAIHGQFANYCQWLVTLANQHHGEGGLGMDFAAASGRLLIVTPYQLQKIGAVI	313
QY	371	GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMTLGLHPWIANIDDTQYLAA	430
DB	314	---SLRVAVRYPVTYQEHVDVTRALTAAVFPRTQIT-VIRSMEGILH---DKNDPRLAAL	365
QY	431	KRAIRTVFGE-----PDMIRDGSTIPTAKMFEQIVHKS-----	464
DB	366	TQAYEQVTGREGQPVTTTGATYARKMPNIVAFGPSFPGQK---GIAHKADEWMDEHDLKL	422
QY	465	-----VLIPLGAVD	474
DB	423	NMMIDMNMAMIRLGAMD	438

RESULT 106  
 ABP61032  
 ID ABP61032 standard; protein; 331 AA.  
 XX AC ABP61032;  
 XX DT 09-SEP-2002 (first entry)  
 XX DE *Lactobacillus rhamnosus* HN001 polypeptide SEQ ID NO 74.  
 XX KW *Lactobacillus rhamnosus*; strain HN001; vulnery; antilipaemic; milk;  
 XX QW immunostimulant; anti-infection; lactose digestion; immune system;

metabolic activity; nutrition; health; transgenic; lactic acid bacteria; genome mapping; gastrointestinal disorder; dairy processing; vaccine; fermentation; probiotic; cholesterol; wound healing.

Lactobacillus rhamnosus.

WO200244383-A1.

06-JUN-2002.

28-NOV-2001; 2001WO-NZ000286.

28-NOV-2000; 2000US-00724623.

(GENE-) GENESIS RES & DEV CORP LTD.  
(VIAL-) VIALACTIA BIOSCIENCE NZ LTD.

Glenn M, Havukkala IJ, Lubbers MW, Dekker J;  
WPI; 2002-519588/55.  
N-PSDB; ABQ86197.

Novel isolated Lactobacillus rhamnosus polynucleotides encoding polypeptide with anti-infection/lactose digestion modulating activity, useful to improve properties of microbes used in milk-derived products manufacture.

Claim 11; Page 96-97; 128pp; English.

The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence (ABQ86185-ABQ86243) present in Lactobacillus rhamnosus strain HN001 that encodes a polypeptide (ABP61020-ABP61060) with activity such as enzyme activity; anti-infection activity; lactose digestion modulating activity; immune system modulating activity; amino acid, lipid, vitamin or carbohydrate metabolic activity; flavour, texture or aroma modulating activity. (I) is useful for improving the properties of microbes used in the manufacture of milk-derived products and probiotic supplements, which involves modulating the polynucleotide content or composition of the microbes by transforming the microbes with (I). (I) is also useful for identifying an organism (preferably a bacterial or yeast cell) or reproductive material or an extract from the organism, as having a specific origin. Proteins encoded by (I) are useful for modifying the flavour, aroma, texture and/or nutritional and health benefits of milk-derived products, which involves adding one or more polypeptides to the milk being processed. Genetic constructs comprising (I) are useful for modulating the polynucleotide content or composition of a organism. (I) is useful for identifying, isolating or synthesising DNA molecules such as promoter, DNA binding elements, open reading frames or full-length genes, that then can be used as expressible DNA in transgenic organisms. (I) may be used to detect lactic acid bacteria, preferably L. rhamnosus in a sample material. (I) is also useful for genome mapping, physical mapping, and in positional cloning of genes of more or less related microbes, and to design probes and primers. (I) is also useful for transforming microbes for use in a therapeutic composition that is effective for treating or preventing a gastrointestinal condition or disorder caused by the presence of pathogenic microbes in the gastrointestinal tract or by the absence of normal intestinal microbes in the intestinal tract. Proteins are used to raise antibodies, to isolate corresponding interacting proteins, as nutritional additives and as additives in dairy processing and fermentation processing. (I) and encoded proteins are used for the selection and production of more effective probiotic bacteria, as bioactive (health promoting) ingredients and health supplements, for immune function enhancement; for reduction of blood lipids such as cholesterol; for production of bioactive material from genetically modified bacteria as adjuvants; for wound healing; in vaccine development, in selection and production of genetically modified rumen microorganisms for improved animal nutrition and productivity, better flavour and improved milk composition. Note: Proteins SEQ ID NO 62 to 120 are claimed in claim 11. However, only proteins SEQ ID NO 62 to 101 and SEQ ID NO 120 are given in the printed specification

Sequence 331 AA;

Query Match 6.6%; Score 172; DB 5; Length 331;  
Best Local Similarity 34.9%; Pred. No. 7.4e-07;  
Matches 53; Conservative 20; Mismatches 47; Indels 32; Gaps 7;

Qy 66 PVPRFRQELFRMMAVAADTLQRLGARVASVD--MGPOQLPDGQSLPIPPVILAEGLSDPT 123  
Db 43 PGPAKALEAF--LAIA-----QDGFKTLNVHDVAGRIELGDGDEI----- 81

Qy 124 KGTVCFYGHLDVQPADRGDGLTDPYVLTETVDGKLYGRGATDNKGPVLAWINAVSAFRA 183  
Db 82 ---FGLFGHVVDVPA--GPGWQTDPPFDPVIRDGKIYGRGTSDDKGPSIAAYVALKLIRD 136

Qy 184 EQDLPVN--IKFIIEGMEEAGSVALEELVEKE 213  
Db 137 K--LPINKKIHFILGTDEESDWDVGIHRYLETE 166

RESULT 107  
ADE12747  
ID ADE12747 standard; protein; 331 AA.  
XX  
AC ADE12747;  
DT 29-JAN-2004 (first entry)  
XX  
DE L. rhamnosus polypeptide #16.  
XX  
XW cancer; gene therapy.  
XX  
OS Lactobacillus rhamnosus.  
XX  
PN US2003138822-A1.  
PD 24-JUL-2003.  
XX  
PF 05-NOV-2002; 2002US-00288930.  
XX  
PR 28-NOV-2000; 2000US-00724623.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Glenn M, Lubbers MW, Dekker J;  
XX  
DR WPI; 2003-874738/81.  
DR N-PSDB; ADE12809.  
XX  
PT New polynucleotide from Lactobacillus rhamnosus strain HN001, useful for  
PT preparing a composition for treating a disorder in a mammal, e.g.,  
PT cancer.  
XX  
PS Claim 10; SEQ ID NO 78; 20pp; English.  
XX  
CC The invention relates to an isolated polynucleotide. The polynucleotide  
CC is useful for preparing a composition for treating a disorder in a  
CC mammal, e.g., cancer. The present sequence represents the amino acid  
CC sequence of a L. rhamnosus polypeptide.  
XX  
SQ Sequence 331 AA;

Query Match 6.6%; Score 172; DB 7; Length 331;  
Best Local Similarity 34.9%; Pred. No. 7.4e-07;  
Matches 53; Conservative 20; Mismatches 47; Indels 32; Gaps 7;

Qy 66 PVPRFRQELFRMMAVAADTLQRLGARVASVD--MGPOQLPDGQSLPIPPVILAEGLSDPT 123  
Db 43 PGPAKALEAF--LAIA-----QDGFKTLNVHDVAGRIELGDGDEI----- 81

Qy 124 KGTVCFYGHLDVQPADRGDGLTDPYVLTETVDGKLYGRGATDNKGPVLAWINAVSAFRA 183  
Db 82 ---FGLFGHVVDVPA--GPGWQTDPPFDPVIRDGKIYGRGTSDDKGPSIAAYVALKLIRD 136

Qy 184 EQDLPVN--IKFIIEGMEEAGSVALEELVEKE 213

Db 137 K--LPINKKIHFILGTDEESDWDVGIHRYLETE 166

RESULT 108  
ADH85976  
ID ADH85976 standard; protein; 425 AA.  
XX  
AC ADH85976;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Enterococcus faecalis polypeptide #456.  
XX  
XW Enterococcus faecalis infection; transcription regulatory element;  
XW antibacterial.  
XX  
OS Enterococcus faecalis.  
XX  
PN US6617156-B1.  
XX  
PD 09-SEP-2003.  
XX  
PF 13-AUG-1998; 98US-00134000.  
XX  
PR 15-AUG-1997; 97US-0055778P.  
XX  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-895394/82.  
DR N-PSDB; ADH82571.  
XX  
PT New nucleic acid comprising a sequence encoding an Enterococcus faecalis  
PT polypeptide, useful for preparing a composition for diagnosing or  
PT treating E. faecalis infection.  
XX  
PS Disclosure; SEQ ID NO 3861; 193pp; English.  
XX  
CC The invention relates to Enterococcus faecalis polynucleotides and  
CC polypeptides. The invention also relates to a recombinant expression  
CC vector comprising a polynucleotide operably linked to a transcription  
CC regulatory element, a cell comprising a recombinant vector, a method for  
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising  
CC a sequence not given in the specification, a recombinant vector  
CC comprising the nucleic acid and a cell comprising the recombinant vector.  
CC The polynucleotides can be used to detect the presence of E. faecalis in  
CC a sample. The sequences are useful for preparing a composition for  
CC diagnosing or treating Enterococcus faecalis infection. This sequence  
CC represents an E. faecalis polypeptide of the invention.  
XX  
SQ Sequence 425 AA;

Query Match 6.6%; Score 172; DB 7; Length 425;  
Best Local Similarity 22.5%; Pred. No. 1.1e-06;  
Matches 99; Conservative 70; Mismatches 167; Indels 104; Gaps 20;

Qy 44 LHQDEFVQTLKEWVAIESDSVQVPRFRQELF-----RMMVAADTLQRLGARVASVDMG 98  
Db 2 VQKDLFYEDLTKIMAIR--SVKGSPPK-KEALFEGGPKRALEETLKLAEYRGFGTGIVN-- 56

Qy 99 PQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTETVDGKL 158  
Db 57 -----DAVGYAQWGT--AEYLGIIGHLDWVP--EGSGWSVPPFQLTKNQRL 100

Qy 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFF 218  
Db 101 YGRGILDNKGPIILACLYGMKLLKELGYQPKKIRLMFGTDEESGSDIPLYLEKENAPVF 160

Qy 219 SGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLV- 277

Db 161 G-----FTPDCKYPVVYGERGIVNY--EITTTIPDDSSSEQIIGDQAKOHVP 207

QY 278 -----ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSR 325

Db 208 DQLSVVIAGKTAITGRAPSN---APELGKNAITLLAQKISEEQLVKGNLLQY----- 258

QY 326 VEKFLFDTKBEILMHLWRYP SL-SIHGIEG-AFDEPGTKTVIPGRVIGKFSIRLVPHMNV 383

Db 259 -----FD-----WLTA SFHEKH YGEGVALD---FKDQDSGQLI-----LTPY--- 292

QY 384 SAVEK---QVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDTQYLAAKRAIRTVFGT 440

Db 293 -ALEKRGQQLVLSLAVRYPVSITENEVTTQLTKALFP-----ESEVTVIRRLPSTLFPK 345

QY 441 EPDMIRGDGSTPIAKMFQEI 460

Db 346 DERNVQ-----KLTKVYEQI 360

RESULT 109

ADI67225

ID ADI67225 standard; protein; 465 AA.

XX ADI67225;

AC

XX

DT 22-APR-2004 (first entry)

XX

DE Lactobacillus rhamnosus polypeptide sequence #99.

XX

KW Lactic acid bacteria; vaccine; bacterial infection; microbe;

KW milk-derived product; food product; food additive;

KW nutritional supplement; bioactive substance; probiotic supplement;

KW flavour; aroma; texture; nutritional value; food; microorganism;

KW antibacterial.

XX

OS Lactobacillus rhamnosus; strain HN001.

XX

PN US2004009490-A1.

XX

PD 15-JAN-2004.

XX

PF 03-OCT-2002; 2002US-00264213.

XX

PR 09-AUG-1999; 99US-0147852P.

PR 09-AUG-1999; 99US-0147853P.

PR 01-SEP-1999; 99US-0152031P.

PR 01-SEP-1999; 99US-0152032P.

PR 08-AUG-2000; 2000US-00634238.

PR 02-OCT-2001; 2001US-00971536.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Glenn M, Havukkala IJ, Lubbers M, Dekker J;

XX

DR WPI; 2004-090459/09.

DR N-PSDB; ADI67100.

XX

PT New polynucleotide from Lactobacillus rhamnosus HN001 strain, useful for preparing a vaccine against bacterial infections or for modifying the flavor, aroma or nutritional benefits of a bioactive or probiotic supplement product.

PT

XX

PS Claim 21; SEQ ID NO 220; 54pp; English.

XX

CC The present invention relates to the isolation of novel lactic acid bacteria (Lactobacillus rhamnosus strain HN001) polynucleotide sequences, and the proteins encoded by them. Also disclosed are oligonucleotide probes and primers, and genetic constructs comprising the polynucleotide sequences of the invention. The polynucleotide sequences are useful for preparing a vaccine against bacterial infections or for improving the properties of microbes used in the manufacture of milk-derived products, food products, food additives, nutritional supplements, bioactive substances or probiotic supplements, and for modifying the flavour,

CC aroma, texture and/or nutritional value of foods. They are also useful for identifying microorganisms having a trait associated with the polynucleotide. The present sequence represents a novel L. rhamnosus polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov.

XX

SQ Sequence 465 AA;

Query Match 6.6%; Score 172; DB 8; Length 465;

Best Local Similarity 34.9%; Pred. No. 1.3e-06;

Matches 53; Conservative 20; Mismatches 47; Indels 32; Gaps 7;

QY 66 PVPRFRQELFRMMAVAADTLQRLGARVASVD--MGPPQQLPDGQSLPIPPVILAE LGS DPT 123

Db 43 PGPAKALEAF--LAIA-----QRDGFKTLNVDHVAGRIELGDGEI----- 81

QY 124 KGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRAL 183

Db 82 ---FGLFGHVDVWPA--GPGWQTDPPFDPVIRDGKIYGRGTSDDKGPSIAAYYALKLIRD L 136

QY 184 EQDLPVN--IKFIIEGMEEAGSVALEELVEKE 213

Db 137 K--LPINKKIHFILGTDEESDWDVGIHRYLETE 166

RESULT 110

ABP38707

ID ABP38707 standard; protein; 418 AA.

XX

AC ABP38707;

XX

DT 24-JUL-2002 (first entry)

XX

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3552.

XX

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.

KW

XX

OS Staphylococcus epidermidis.

XX

PN US6380370-B1.

XX

PD 30-APR-2002.

XX

PF 13-AUG-1998; 98US-00134001.

XX

PR 14-AUG-1997; 97US-0055779P.

PR 08-NOV-1997; 97US-0064964P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Doucette-Stamm LA, Bush D;

XX

DR WPI; 2002-381255/41.

DR N-PSDB; ABN91252.

XX

PT Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.

PT

XX

PS Disclosure; SEQ ID NO 3552; 267pp; English.

XX

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site



```
XX SQ Sequence 418 AA;
Query Match 6.5%; Score 171; DB 5; Length 418;
Best Local Similarity 25.2%; Pred. No. 1.3e-06;
Matches 74; Conservative 46; Mismatches 118; Indels 56; Gaps 13;

QY 114 ILAELGSDPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAW 173
Db 69 LVAEIGSGAP--VLAISGHMDVVDAGDHDWTFPPFELTDKDKLFGRTTDMKGLMAM 126

QY 174 INAVSAFR---ALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNL 230
Db 127 VIAMIELKQSNALKQG--TIRLLATTGEETEYQYGAQLLAD---EGYLDVDSGLIIGE-- 178

QY 231 WISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMDLVALLGSLVDSSGHI 290
Db 179 -----PTSNIAYYA-----HKGS-----MSCVVTAKGKAHSSMPH 209

QY 291 LVPGIYDEVVPLTEEEINTYKAI--HLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLS 348
Db 210 LGTNAVDILVDFVNEMKQYKNIKEHDKVHELDAVPMIEKHLHRKIGEESHYIS---G 265

QY 349 IHGIEGAFDEPGTKTV--IPGRVIGKFSIRLVPHMNVSAVE---KQVTRHL-ED 396
Db 266 FVMLNSVFN--GGKQVNSVPHKATAKYNVRTVPEYDSTFVKDLFEKVIHVGED 317

RESULT 111
ADS05236
ID ADS05236 standard; protein; 418 AA.
XX
AC ADS05236;
XX
DT 04-NOV-2004 (first entry)
XX
DE Staphylococcus epidermis polypeptide seqid 4531.
XX
KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
KW recombinant expression vector; infection; computer readable medium;
KW computer based system.
XX
OS Staphylococcus epidermidis.
XX
PN US2004147734-A1.
XX
PD 29-JUL-2004.
XX
PF 01-DEC-2003; 2003US-00724972.
XX
PR 08-NOV-1997; 97US-0064964P.
PR 13-AUG-1998; 98US-00134001.
PR 29-NOV-1999; 99US-00450969.
XX
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
PI
PI Doucette-Stamm L, Bush D;
XX
DR WPI; 2004-580138/56.
DR N-PSDB; ADS01464.
XX
PT New isolated polypeptide and encoding nucleic acid derived from
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
PT treating an S. epidermidis bacterial infection.
XX
PS Claim 17; SEQ ID NO 4531; 741pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a nucleotide
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
CC given in the specification. Also described are: a recombinant expression
```

```
CC vector; a cell comprising a recombinant expression vector of (1);
CC producing an S. epidermidis polypeptide; an isolated nucleic acid
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
CC vaccine composition for prevention or treatment of an S. epidermidis
CC infection, comprising a nucleic acid cited above and a carrier; treating
CC a subject for S. epidermidis infection; a recombinant or substantially
CC pure preparation of an S. epidermidis polypeptide or its fragment; a
CC vaccine composition for prevention or treatment of an S. epidermidis
CC infection; detecting the presence of a Staphylococcus nucleic acid in a
CC sample; a computer readable medium having recorded in it the nucleotide
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
CC system for identifying fragments of the Staphylococcus genome of
CC commercial importance; a computer based system for identifying fragments
CC of the Staphylococcus plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the Staphylococcus
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the Staphylococcus genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an Staphylococcal epidermidis bacterial
CC infection. This is the amino acid sequence of a S. epidermis protein of
CC the invention.
XX
SQ Sequence 418 AA;
Query Match 6.5%; Score 171; DB 8; Length 418;
Best Local Similarity 25.2%; Pred. No. 1.3e-06;
Matches 74; Conservative 46; Mismatches 118; Indels 56; Gaps 13;

QY 114 ILAELGSDPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAW 173
Db 69 LVAEIGSGAP--VLAISGHMDVVDAGDHDWTFPPFELTDKDKLFGRTTDMKGLMAM 126

QY 174 INAVSAFR---ALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNL 230
Db 127 VIAMIELKQSNALKQG--TIRLLATTGEETEYQYGAQLLAD---EGYLDVDSGLIIGE-- 178

QY 231 WISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMDLVALLGSLVDSSGHI 290
Db 179 -----PTSNIAYYA-----HKGS-----MSCVVTAKGKAHSSMPH 209

QY 291 LVPGIYDEVVPLTEEEINTYKAI--HLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLS 348
Db 210 LGTNAVDILVDFVNEMKQYKNIKEHDKVHELDAVPMIEKHLHRKIGEESHYIS---G 265

QY 349 IHGIEGAFDEPGTKTV--IPGRVIGKFSIRLVPHMNVSAVE---KQVTRHL-ED 396
Db 266 FVMLNSVFN--GGKQVNSVPHKATAKYNVRTVPEYDSTFVKDLFEKVIHVGED 317

RESULT 112
ABP26705
ID ABP26705 standard; protein; 468 AA.
XX
AC ABP26705;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 2586.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
PR 27-OCT-2000; 2000GB-00026333.
PR 24-NOV-2000; 2000GB-00028727.
```



ID XX ABU46620 standard; protein; 469 AA.  
AC ABU46620;  
XX 19-JUN-2003 (first entry)  
DT  
XX Protein encoded by Prokaryotic essential gene #32147.  
DE  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
KW  
XX Streptococcus pyogenes.  
OS  
XX WO200277183-A2.  
PN  
XX 03-OCT-2002.  
PD  
XX 21-MAR-2002; 2002WO-US009107.  
PF  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Walli D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA50490.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 74544; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 469 AA;

Query Match 6.3%; Score 166; DB 6; Length 469;

Best Local Similarity 23.8%; Pred. No. 4.6e-06;  
Matches 77; Conservative 44; Mismatches 111; Indels 92; Gaps 14;  
QY 66 PVPFRQELFRMVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEFGSDPTKG 125  
Db 44 PGPVKALEHFLAMA-----ERDGYKTRNIDNYAGDFEFGQ-----GDEVLG 84  
QY 126 TVCFYGHLDVQPADRGWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQ 185  
Db 85 ---IFGHLDVVP--GSGWDTDPYEPVIKDDRIYARGSSDDKGPMTACYYALKIIEKELGL 139  
QY 186 DLPVNIKFIIIEGMEERAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRPATITGTRG 245  
Db 140 PVSKKVRFIVGTDESG-----WGMDYFYFAHNGL-----KNPDFGFGSP-- 178  
QY 246 NSYFMVEVKCRDQDFHSGTGGILHEPMDLVALGLSLVDSSG----HILVPGIYDEVVP 301  
Db 179 -----DAEF-----PIINGEKGNITEYLHFAGDNKGAFVLRHQGLRENMPV 221  
QY 302 LTEEEINTYKAIH-LDLEEYRNSSRVEKFLFDTKEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 222 ESATAVIT--APHDLDLVLE---AALEQF-----LSEHGKVGSM--KA 256  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVS 384  
Db 257 TDGKIEVTIIGKSAHGSTPEAGVN 280

RESULT 115

ABP26706

ID ABP26706 standard; protein; 486 AA.

XX AC ABP26706;

XX AC ABP26706;

DT 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 2588.

DE Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX group A streptococcus; Streptococcus pyogenes; antibacterial;

KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus pyogenes.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;

PI Tettelin H;

XX WPI; 2002-352536/38.

DR N-PSDB; ABN67337.

XX New Streptococcus protein for the treatment or prevention of infection or

PT disease caused by Streptococcus bacteria, such as meningitis, and for

PT detecting a compound that binds to the protein.

XX Claim 1; Page 3408; 4525pp; English.

PS The invention relates to a protein (ABP25413-ABP30895) from group B

XX streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory



CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 486 AA;

Query Match 6.3%; Score 166; DB 5; Length 486;  
Best Local Similarity 23.8%; Pred. No. 4.9e-06;  
Matches 77; Conservative 44; Mismatches 111; Indels 92; Gaps 14;  
QY 66 PVPRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPPIPPVILAEELGSDPTKG 125  
Db 61 PGPVKALEHFLAMA-----ERDGYKTRNIDNYAGDFEQ-----GDEVLG 101  
QY 126 TVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQ 185  
Db 102 ---IFGHLDVVPA--GSGWTDTPYEPVIKDDRIYARGSSDDRGPTWACYALKIikelGL 156  
QY 186 DLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRG 245  
Db 157 PVSKKVRPIVGTDESG-----WGMDYFFAHNGL-----KNPDFGFSP-- 195  
QY 246 NSYFMEVVKCRDQDFHSGTGGILHBPMAADLVALLGSLVDSG-----HILVPGIYDEVVP 301  
Db 196 -----DAEF-----PIINGEKGNITEYLHPAGDNKGAFVLRFGGLRENWVP 238  
QY 302 LTEEEINTYKAIH-LDLEEYRNSRVEKFLFDTKEEILHLWRYPSLSIHGIEGAFDEPG 360  
Db 239 ESATAVIT--APHDLVLE---AALQF-----LSEHGKGSMA--KA 273  
QY 361 TKTVIPGRVIGKFSIRLVPHMNV 384  
Db 274 TDGKIEVTIIGKSAHGSTPEAGVN 297

RESULT 116  
ABU43262  
ID ABU43262 standard; protein; 469 AA.  
XX  
AC ABU43262;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #28789.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA47132.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 71186; 1766pp; English.  
XX

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 469 AA;

Query Match 6.3%; Score 165; DB 6; Length 469;  
Best Local Similarity 23.1%; Pred. No. 5.7e-06;  
Matches 127; Conservative 66; Mismatches 173; Indels 184; Gaps 32;  
QY 36 EKVFQYIDLHQDEFVQTLKEWVAIES---DS-----VQVPFRFRQELFRMMAVAADTL 85  
Db 4 EKVLEY---ENQMIEDLKGLSIESIRDDSKATADAPVGPGR-----EALDYM 49  
QY 86 QRLGARVASVDMGPQQLPDGQSL---PIPPVILAEELGSDPTKGTVCYFVGHLDVQPADRG 141  
Db 50 YNLGKR-----DGFSTHDVDHIAGRIEAGKGED-VLGILC---HVDVVPVPA--G 91  
QY 142 DGWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEA 201  
Db 92 DGWDSNPFQPVVTDNAIARGTLDDKGPPTIAAYAVKILNEMKVDWKKRIHIIIGTDEES 151  
QY 202 GSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI-----TYGTRGNSYF-M 250  
Db 152 D-----WKCTDRYFK-----TEEMPALGFPADAEFFPAIHGEKGITTFDL 190  
QY 251 VEVK-CRDQD-----FHSCTFGG-----ILHEPMADLV-----ALLG 281  
Db 191 VQNEVTEDTDEPDYELLKFFESQRYNMVDPDYAKAEVLVKNMTDVIQNFENFLQNLQG 250  
QY 282 -SLVDSSGHILVPGIYDEVVPLTEEEINTYKAHL-----DLEEYRNSRV 326  
Db 251 ESTVDSG--ILILTIEGKAVHGMDFPSLGNWAGLFLKFLASLNLNKSAKDFVEFN----- 303









Db 103 DPFDPVIKGLYARGASDDKGPTLAAYYALKLIKDL--GLPVNKRIRLILGTDESEWQ 160

QY 205 ALLEELVEKE 213

Db 161 GVHRYLEVE 169

RESULT 120

ADB09474

ID ADB09474 standard; protein; 489 AA.

XX ADB09474;

XX 20-NOV-2003 (first entry)

XX Alloiococcus otitis antigenic protein SEQ ID NO:3414.

KW Alloiococcus otitidis; antigenic protein; immunogenic; immunisation;

KW gene therapy; Gram-positive bacterium; infection.

XX Alloiococcus otitis.

XX WO2003048304-A2.

PN 12-JUN-2003.

PD 25-NOV-2002; 2002WO-US036123.

PF 29-NOV-2001; 2001US-0333777P.

XX 18-NOV-2002; 2002US-0426742P.

PR (AMHP ) WYETH HOLDINGS CORP.

XX Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;

PI WPI; 2003-505284/47.

DR N-PSDB; ADB09473.

XX New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.

PS Claim 33; SEQ ID NO 3414; 1019pp; English.

XX The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.

CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I), its complement, degenerate variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polynucleotide that is comprised in the expression vector; (6) a pharmaceutical composition comprising the polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) immunising against Alloiococcus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (10) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polypeptide from the culture. (I) can be used in gene therapy. The polynucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.

CC The polynucleotides are useful for expressing and detecting Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis antigen protein from the present invention.

XX Sequence 489 AA;

Query Match 6.3%; Score 164; DB 6; Length 489;

Best Local Similarity 32.3%; Pred. No. 7.5e-06;

Matches 61; Conservative 24; Mismatches 64; Indels 40; Gaps 9;

QY 36 EKVFQYIDLHQDEFVQTLKEWVAIES-----DSVQPVPRFRQELFRMMAVAADTLQR 87

Db 32 BEVKKY----QDDFLADLKEVLKIDSVRNDDEATDEFPVGGPAKALHKALEIA-----DR 83

QY 88 LGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS-DPTKGTVCFYGHLDVQPADRGDWLT 146

Db 84 DGFTTKQVENWAGHI-----EYSGDETILGIL---GHMDVVPV--GSGWDT 124

QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVN--IKFIIEGMEEAGSV 204

Db 125 DPFDPVIKGLYARGASDDKGPTLAAYYALKLIKDL--GLPVNKRIRLILGTDESEWQ 182

QY 205 ALLEELVEKE 213

Db 183 GVHRYLEVE 191

RESULT 121

ADC96907

ID ADC96907 standard; protein; 450 AA.

XX ADC96907;

AC 01-JAN-2004 (first entry)

XX E. faecium protein sequence SEQ ID 6534.

DE Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;

XX abdominal-pelvic infection.

KW Enterococcus faecium.

XX US6583275-B1.

PN 24-JUN-2003.

PD 30-JUN-1998; 98US-00107532.

PF 02-JUL-1997; 97US-0051571P.

XX 14-MAY-1998; 98US-0085598P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA Doucette-Stamm LA, Bush D;

XX WPI; 2003-799836/75.

DR N-PSDB; ADC93253.

XX New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection.

PT Example 1; SEQ ID NO 6534; 243pp; English.

XX The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to a transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.

CC The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans -

CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.  
XX  
SQ Sequence 450 AA;

Query Match 6.2%; Score 162.5; DB 7; Length 450;  
Best Local Similarity 21.0%; Pred. No. 9.1e-06;  
Matches 105; Conservative 78; Mismatches 177; Indels 139; Gaps 25;

Qy 45 HQDEFVQTLKEWVAI-----ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGP 99  
Db 13 HHEQALESLSELIRIPSVLDEADSGQGHF-FGKKVIEALDKVLEISEKLGFRTF----- 65  
Qy 100 QQLPDGQSLPIPPVILAE LGS-DPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTVEVDGKL 158  
Db 66 -KDPEGY-----YGSEIGSGDELFGILC---HMDVVPAGDENNWETKPPDPTIKDGWL 115  
Qy 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIEGMEEAGSVALEELVEKEKDRFF 218  
Db 116 VGRGSQDDKGFSIAAMYAVKAL-----IDAGVEF-----KTRIRFI 151  
Qy 219 SGVDYIVISDNLW-----ISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM 273  
Db 152 FGTD-----EENLWRCLKYNEKEGITOQGPAPDAEFPLIYA-----EKGLLQAYLTGPG 201  
Qy 274 ADLVALGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAIHLDLEEYRNSRVEKFLFDT 333  
Db 202 TNEFS-----VKAGGAL---NVVPDAAPYSGEK-----LSEVKEALKKHEPDFEE 243  
Qy 334 KEEILMHLWRYPSSLHIGIEGA-----FD-----EPGTKTVI 365  
Db 244 QGEGIVVLGK----SIHAKDAAQGVNAISRLAIALSEVDFGPINFLGKLVQENATGEAV 299  
Qy 366 PGRVIGKFSIRLVPHMNVSAVE---KQ-----VTRHLEDVFSKRNSNMVVSMTLGLHPW 418  
Db 300 VGKTEDEQSGELT--MNFASLEITPEQTIGVDMRIPVTFKK---DDLVAKLTKTAEKY 353  
Qy 419 IANIDDTQYLAA-----KRAIRTVFGTEPDMIRDGSTIPIAKMEQEIIVHKSVLILPGA 472  
Db 354 GLTYEEFDFLDSLVLPLDSELVKNLLGIYRDTIGD-MTEPFVSGGATFARTMQCVAFGA 412  
Qy 473 V----DDGEHSQNEKINRW 487  
Db 413 MFPDTPDFMEHQANE---RW 428

RESULT 122  
ABU43726  
ID ABU43726 standard; protein; 469 AA.

XX AC ABU43726;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #29253.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Staphylococcus haemolyticus.

XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US0009107.

XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.  
XX PA  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Walli D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA47596.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 71650; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 469 AA;

Query Match 6.1%; Score 161; DB 6; Length 469;  
Best Local Similarity 21.1%; Pred. No. 1.3e-05;  
Matches 119; Conservative 52; Mismatches 181; Indels 212; Gaps 24;

Qy 36 EKVFOYIDLHQDEFVQTLKEWVAIE-----SDSVQVPVPRFRQELFRMMAVAADTLQR 87  
Db 4 EKVQEY---EGQIIDD LKGLLSIESVRDDSKASDETPVGPGRQALDYMIEIA---QR 55  
Qy 88 LGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS DPTKGTVCYGHLDVQPADRGDGLWLT 147  
Db 56 DGFSTHDVDHIAGRIEAGK-----GDDVLGVLC---HVDVVPA--GDGWDSD 97  
Qy 148 PYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIEGMEEAGSVALE 207  
Db 98 PFNPVVTDDAIIARGTLDDKGPTIAAYYAVKILNDMKVDWKRIHIIIGTDESDWKCTE 157  
Qy 208 ELVEKEK-----DRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYF--MVEVKCRD 257  
Db 158 RYFQTEEMPTLGFAPDAEF-----PAI-HGEKGITTFDLVQNSTSED 198  
Qy 258 QD-----FHSGTFGGI-----LHEPMADLV-----ALLGSLVDSSGH 289  
Db 199 QDEPDYELISFESGQRYNMVPDHAQARVFKENMTDVVQHFEBHYLDQHKLQGESVVDSGE 258

QY 290 ILVPGIYDEVVPLTEEEINTYKAH-----LDLEEYRNSSRVEKFLPDTKE 335  
Db 259 LV-----LTLEG-----KAVHGMPSLGVNAGLYLLDFISTLNLNQTAREFVDFSN 304  
QY 336 EIL--MHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVI-----GKFSIRL----- 377  
Db 305 RYLHSHFGEKMGKFH-----TDVMGDVTTNVGIIISYDNKQGRFGINLRYPQKEEEE 359  
QY 378 -----VPHM---NVSAREKQVTRHLEDVFSKRNSSNMVVSMT 412  
Db 360 AIQRTKEIKAYGFDLELGKVVQPHFVDKNDPFVQKLVKAY-----RNQTGMSEPYT 412  
QY 413 LGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGA 472  
Db 413 IGGTYARNLD-----KGVAFGAMFED----- 434  
QY 473 VDDGEHSQNEKINRWNYIEGTKLF 496  
Db 435 SEDLMHQKNEYITKKQLFNATSIY 458

RESULT 123  
ADS06743  
ID ADS06743 standard; protein; 471 AA.  
XX  
AC ADS06743;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Staphylococcus epidermis polypeptide seqid 6038.  
XX  
DE antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
KW recombinant expression vector; infection; computer readable medium;  
KW computer based system.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN US2004147734-A1.  
XX  
PD 29-JUL-2004.  
XX  
PF 01-DEC-2003; 2003US-00724972.  
XX  
PR 08-NOV-1997; 97US-0064964P.  
PR 13-AUG-1998; 98US-00134001.  
PR 29-NOV-1999; 99US-00450969.  
XX  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
XX  
XX Doucette-Stamm L, Bush D;  
XX  
XX WPI; 2004-580138/56.  
DR N-PSDB; ADS02971.  
XX  
PT New isolated polypeptide and encoding nucleic acid derived from  
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
PT treating an S. epidermidis bacterial infection.  
XX  
PS Claim 17; SEQ ID NO 6038; 741pp; English.  
XX  
XX The invention describes an isolated nucleic acid comprising a nucleotide  
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
CC given in the specification. Also described are: a recombinant expression  
CC vector; a cell comprising a recombinant expression vector of (1);  
CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection, comprising a nucleic acid cited above and a carrier; treating  
CC a subject for S. epidermidis infection; a recombinant or substantially  
CC pure preparation of an S. epidermidis polypeptide or its fragment; a

CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
CC sample; a computer readable medium having recorded in it the nucleotide  
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
CC system for identifying fragments of the Staphylococcus genome of  
CC commercial importance; a computer based system for identifying fragments  
CC of the Staphylococcus plasmids of commercial importance; identifying  
CC commercially important nucleic acid fragments of the Staphylococcus  
CC genome and/or plasmids; and identifying an expression modulating fragment  
CC of the Staphylococcus genome and/or plasmids. The methods and  
CC compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of an Staphylococcus epidermidis bacterial  
CC infection. This is the amino acid sequence of a S. epidermis protein of  
CC the invention.  
XX  
SQ Sequence 471 AA;  
Query Match 6.1%; Score 160; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 1.7e-05;  
Matches 128; Conservative 64; Mismatches 184; Indels 164; Gaps 32;  
QY 36 EKVFQYIDLHQDEFVQTLKEWVAIES---DS-----VQVPVFRQELFRMMAVAADTL 85  
Db 6 EKVLEY---ENQMIEDLKGLLSIESIRDSDSKATADAPVGPGR-----EALDYM 51  
QY 86 QRLGARVASVDMGPPQLPDGQSL----PIPPVILAEGLSDPTKGTVCYFGLHDVQPADRG 141  
Db 52 YNLGKR-----DGFSTHDVDHIAGRIEACKGED-VLGILC---HVDVVVEA--G 93  
QY 142 DGWLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEA 201  
Db 94 DGWDSNPFQPVVTDNAIARGTLDDKGPTIAAYAVKILNEMKVDWKRIHIIIGTDEES 153  
QY 202 GSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYTRGNSYF-MVEVK-CRDQD 259  
Db 154 D-----WKCTDRYFKTEEMPTL--GFAPDAFPPAI-HGEKGITTFDLVQNEVTEDTD 202  
QY 260 -----FHSGTFGG-----ILHEPMADLV-----ALLG-SLVDSSGHI 290  
Db 203 EPDYELLKFESGQRYNMVDPDYAKAEVLVKENMTDVIQNFENFLOQNQLQGESTVDSG--I 260  
QY 291 LVPGIYDEVVPLTEEEINTYKAHL-----DLEEYRNSSRVEKFLPDTKEE 336  
Db 261 LILTIEGKAVHGMDPSSLGVNAGLFLLLKFLASLNLNKSADFVEFN-----ERYLFES--- 312  
QY 337 ILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRV-----IGKFSIRLVPHMVNSAVEKQV 390  
Db 313 ---HFGEKMGKFH-----TDIMGDVTTNIGVISYDKEKAGSYGINL----- 351  
QY 391 TRH-----LEDVFSK-RNSSNMVVSMTLG--LHPWIANIDDTQYLAAKRAIRTVFG--T 440  
Db 352 -RYPEGKFKFEDAIDRFRSEINELGFNLGLKGVQKPHYVDKNDPFVKTLVNAVYRNQTGDMT 410  
QY 441 EPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAV-----DDGEHSQNEKINRWNYIEGTKLF 496  
Db 411 EPTYTIGGGT-----YARNLDKGVA---FGAMFADSEDLMHQKNEYITKKQLINATSIY 460  
RESULT 124  
AAU37944  
ID AAU37944 standard; protein; 466 AA.  
XX  
AC AAU37944;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Streptococcus pneumoniae cellular proliferation protein #373.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Streptococcus pneumoniae.  
XX





Db 255 -ISNIRSGTGATNVIGGTCHEILFNFR---YCTENTAENLMAK-THAIFDKHFRHTDATYQ 309

QY 409 VSMTLGLHPWIANIDDTQVLAA-KRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYHKSUVL 467

Db 310 IEWTLGVPFLT--EKGEFVSACIDAIAKTVTGTNAQLSTSGGTSD-GRFIAPIMNAQVV- 365

QY 468 IPLGAVDGGEHSQNEKINRWNYIEGTKLFAPAAFFLEMAQ 505

Db 366 -ELGVLNTTIHQVDESVDIEDLEQLTQIYEILISLIE 402

RESULT 126

AAAY81712

ID AAY81712 standard; protein; 466 AA.

XX

AC AAY81712;

DT 02-JUN-2000 (first entry)

XX

DE Streptococcus pneumoniae protein sequence ID7.

XX

KW Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;

KW bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;

KW kidney disease; diabetes; immunosuppressive disorder; otitis media;

KW pneumococcal.septicaemia; sinusitis; meningitis; therapy.

XX

OS Streptococcus pneumoniae.

XX

PN WO200006738-A2.

XX

PD 10-FEB-2000.

XX

PF 27-JUL-1999; 99WO-GB002452.

XX

PR 27-JUL-1998; 98GB-00016336.

PR 19-MAR-1999; 99US-0125329P.

XX

PA (MICR-) MICROBIAL, TECHNICS LTD.

XX

PI Le Page RWF, Wells JM, Hanniffy SB, Hansbro PM;

XX

DR WPI; 2000-195301/17.

DR N-PSDB; AAZ91808.

XX

PT Streptococcal proteins and polynucleotides useful for diagnosis,

PT treatment and prophylaxis of bacterial infections.

XX

PS Claim 2; Page 42; 76pp; English.

XX

CC This sequence represents a Streptococcus pneumoniae protein of the

CC invention. The proteins (or their homologues, derivatives and/or

CC fragments)are useful as immunogens or antigens. Immunogenic or antigenic

CC compositions comprising the proteins are useful as vaccines and also in

CC diagnostic assays. The sequences are useful for the detection or

CC diagnosis of S. pneumoniae infection, by contacting a sample to be tested

CC with them. Agents capable of antagonising, inhibiting or interfering with

CC the function or expression of the protein or polypeptide are useful in

CC medical compositions in the treatment or prophylaxis of S. pneumoniae

CC infection. As the sequences can be used to treat S. pneumoniae infection,

CC they can be used to treat bacterial pneumonia, which has high rates in

CC young children, the elderly, and in patients with predisposing conditions

CC such as asplenia, heart, lung and kidney disease, diabetes, alcoholism,

CC or with immunosuppressive disorders, especially AIDS. They can also be

CC used to treat pneumococcal septicaemia, otitis media, sinusitis, and

CC meningitis

XX

SQ Sequence 466 AA;

Query Match 6.0%; Score 157.5; DB 3; Length 466;

Best Local Similarity 23.8%; Pred. No. 2.8e-05;

Matches 80; Conservative 40; Mismatches 115; Indels 101; Gaps 14;

QY 130 YGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPV 189

Db 86 FAHMDVWPA--GSGWDTDPYPTIKDGRLYARGASDDKGPTTACYYGLKIINKELGLPTSK 143

QY 190 NIKFIIEGMEEAGSVALBELVE-----KEKDRFFSGVDYIVIS-----DNL 230

Db 144 KVRFIVGTDEESGWADMDYFVEHVGLAKPDFGFSPPAEFPIINGEKGNITEYLHFAGENT 203

QY 231 WISQRKPAITYGTRGN-----SYFMVEVKCRDQ-----DFHSG 263

Db 204 GVA-RLHSFTGGLRENMPVESATAVVSGDLADLQAKLDAFVAEHLRGELQEEAGKYKV 262

QY 264 TFGGILHEPM-----ADLVALLGS-----LVDSSGHILVPGIYDEVVPLTEEE 306

Db 263 IIGKSAHGAMPASGVNCATYLAFLSQFGFAGPAKDYLDIAGKIL-----LNDHE 312

QY 307 INTYKAIHLDLEEYRNSSRVEKFLFD---TKEEILMHLWRYPSLSIHGIEGAFDEPQTKT 363

Db 313 GENLKIAHVDERKMGALSMNAGVHFHDETSADNTIALNI-RYP-----KG 355

QY 364 VIPGRVIGKFSIRLVPHMNVSAVEKQVTRH---LED 396

Db 356 TSPEQI--KSILENLPVVSLSSEHGHTPHYVPMED 389

RESULT 127

ABU00999

ID ABU00999 standard; protein; 466 AA.

XX

AC ABU00999;

XX

DT 23-OCT-2003 (revised)

DT 11-FEB-2003 (first entry)

XX

DE S. pneumoniae type 4 strain protein from coding region #568.

XX

KW Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;

KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;

KW gene therapy; vaccine.

XX

OS Streptococcus pneumoniae; type 4 strain.

XX

PN WO200277021-A2.

XX

PD 03-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-IB002163.

XX

PR 27-MAR-2001; 2001GB-00007658.

XX

PA (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX

PI Massignani V, Tettelin H, Fraser C;

XX

DR WPI; 2003-040579/03.

DR N-PSDB; ABX06280.

XX

PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,

PT useful as medicaments for treating or preventing a disease or infection

PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or

PT ear infection.

XX

PS Claim 1; SEQ ID NO 1136; 56pp; English.

XX

CC The invention relates to a protein comprising or having at least 50%

CC identity to any of the 2469 amino acid sequences, identified in the

CC specification (available on a computer readable format), or its fragment,

CC expressed from 2469 of 2489 identified DNA coding regions from the

CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as

CC ABS56454. Also included are an antibody which binds one of the proteins,

CC treating a patient by administering the protein, DNA or antibody (in a

CC composition), a kit comprising first and second primers, which are the

CC nucleic acid cited above or fragments between nucleotides 8-100 of a















PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.

PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match

Best Local Similarity 5.8%; Score 153; DB 3; Length 451;

Matches 104; Conservatve 95; Mismatches 197; Indels 132; Gaps 25;

QY 8 MAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLH-----QDEFVQTLKEWVAIES 61  
Db 1 ICCSVVEVVVVVAB---ESESNSMSLLRLVVVVHLHAVAGDDAIVSRFQYLR|-- 55  
QY 62 DSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGSD 121  
Db 56 NTVQPNPEYYKAVDFIIS-----QAKPLSLESQTIEFVKGK----PLLLKKWVGSD 102  
QY 122 PTKGTVCFYGHLDVQPADRGDWLTDPYVLTVD--GKLYGRGATDNKGPVLAWINAV-- 177  
Db 103 PTLPAFLNLSHTDVPFE-DSKWTTHP-LQAHMDHGDYIYARGSDMKCVGMQYLEAIRK 160  
QY 178 ---SAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDY-IVISDNLWIS 233  
Db 161 LQASGFKPLRS---VYLSFVPD-EEIGGHGDAEKFAESQ---LFKSLNIAIVLDEGLPSP 213  
QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHSHTFGGILHEPMADLVALLGSLVDSSGHILVP 293  
Db 214 TESYRVFYGER--SPWNLVIKAKGPPGH-----GAKLYDNSA-MENLKSI----- 256  
QY 294 GIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILHLWRYPSPLSIHGI- 352  
Db 257 -----ESIRRRFRASQFDL-----LKAGGIA 276





PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
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PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
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PR 21-OCT-1999; 99US-0160814P.  
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PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 5.8%; Score 152; DB 3; Length 446;  
Best Local Similarity 22.9%; Pred. No. 8.5e-05;

Matches 123; Conservative 71; Mismatches 198; Indels 144; Gaps 30;  
QY 23 GMFSSPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQ--PVPRFRQELFRMAV 80  
Db 3 GVTKMSSSKALIESIG---SLDKDSYVSLLSKLG-ESKFVQNNPPELIPQEDLIVKHV 58  
QY 81 AADTLQRLGARVASVDMGPQQLPDGQSLPIPPV-----LLAELGSDPTKGTVCVYG 131  
Db 59 -LDSL-----RPYSTETG-----GGPLVINHVAYHSGRGNLIVEYPGSVPGK-ILSFVG 105  
QY 132 -HLDVQPADRGDWLTDPYVLTEVDG-KLYGRGATNKGPPVLAWINAVSAFRALEQDLPV 189  
Db 106 MHMDVVVTAN-PDDWEFDPFSLs-IDGDKLRGRGTTDCLGHVALVTELMKKLGEAKPALKS 163  
QY 190 NIKFIIEGMEEAGS---VALEELV-EKEKDRFFSGVDYIVISDNLWI--SQRKPAITYGT 243  
Db 164 TVSVFIASEENSSIPGVGVDMLVKDLLDKLKSPLY-----WIDTADKQPCV--GT 214  
QY 244 RGNsyFMVEVKCR--DQDFHSGTGGILHEPMADLVALLSLVDSSGHILVPGIYDEVVP 301  
Db 215 GG---MIPWKLQFTGKLFHS-----GLAHKAINAMEGLKEIQAR-----FYRDFPP 261  
QY 302 LTEEEINTYKAHLDLEBYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEEPT 361  
Db 262 HPQEEV-----YGFATPSTMKPTQWCYPA-----GG 287  
QY 362 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVV----- 409  
Db 288 INQIPGECTVSGDVRLTFFYDVKEVMTKLQEYVDDINSNIEKLETRGVPVSKYVLPDENLR 347  
QY 410 -SMTLGLHPWIA---NIDDTQYLAAKRAIRTVFG-TEPDMIRDGSTIPIAKMFQEI VHK 463  
Db 348 GRLTLSFDEASAGVACNLDSPGFHVLCATEEVVGHVKPYSIT--GTLPLRLDLQ----- 400  
QY 464 SVVLIPLGAVDG-----EHSQNEKINPNWNYIEGKTLFAAFFLEMAQL 506  
Db 401 -----DEGEDVQTSGYGLMATYHAKNEYCLLTDMCQGFDFVRIISQLEQV 446  
RESULT 136  
AAW21016  
ID AAW21016 standard; protein; 391 AA.  
XX  
AC AAW21016;  
XX  
DT 22-JUL-1997 (first entry)  
XX  
DE H. pylori cytoplasmic protein, hp5el521lorf22.  
XX  
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;  
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;  
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope;  
KW amino acid; metabolism.  
XX  
OS Helicobacter pylori.  
XX  
PN WO9640893-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009122.  
XX  
PR 07-JUN-1995; 95US-00487032.  
PR 01-APR-1996; 96US-00630405.  
XX  
PA (ASTR ) ASTRA AB.  
XX  
PI Smith D, Berglin dh OT, Mellgaard BL;  
XX  
DR WPI; 1997-052306/05.  
DR N-PSDB; AAT68269.  
XX  
PT Helicobacter pylori nucleic acid sequences and related polypeptide(s) -



Db 153 ---WKCTDRYFK-----TEEMPTLGFAPDAEPPCIHGEKITTDFDLVQNKLT 196  
Qy 256 RDQD-----FHSQTFFG-----ILHEPMADLVA-----LLG-SLVDS 286  
Db 197 EDQDEPDYELITFKSGERYNMVDPDHAEARVLVKENMTDVIQDFEYFLEQNHLQGDSTVDS 256  
Qy 287 SGHILVPGIYDEVVPLTEEEINTYKAIH-----LDLEEYR-----NSSRVE 327  
Db 257 G--ILVLTVEGKAVHGMDPSIGVNAGLYLLKFLASLNDNNAQAFVAFSNRYLFNSDFGE 314  
Qy 328 ----KFLFDTKEEILMHL-----WRYPSLSIHGIEGAFDEPGTKTVIPG 367  
Db 315 KMGMKFHTDVMGDVTTNIGVITYDNENAGLFGINLRYP-----EGFE--FEKAMDRFANEI 368  
Qy 368 RVIGKFSIRL-----VPH---MNVSAVEKQVTRHLEDVFSKRNSSNMVSVMTLGLHPWIA 420  
Db 369 QQYG-FEVKLGKQVPPHYVDKNDPFVQKLVTA-----RNQTNDMTEPTYTIGGGTYAR 420  
Qy 421 NIDDTQYLAAKRAIRTVEGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Db 421 NLD-----KGVAFGAMFSD-----SEDLMHQK 442  
Qy 481 NEKINRWNYIEGTKLF 496  
Db 443 NEYITKKQLFNATSIY 458

RESULT 138  
ABM711197  
ID ABM711197 standard; protein; 469 AA.  
XX ABM711197;  
AC ABM711197;  
XX 20-NOV-2003 (first entry)  
XX  
DE Staphylococcus aureus protein #437.  
XX  
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;  
KW enzymatic assay; antibiotic target.  
XX  
OS Staphylococcus aureus.  
XX WO200294868-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 27-MAR-2002; 2002WO-IB0002637.  
XX  
PR 27-MAR-2001; 2001GB-000007661.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Masignani V, Mora M, Scarselli M;  
XX  
DR WPI; 2003-120786/11.  
DR N-PSDB; ACF72757.  
XX  
PT New Staphylococcus aureus protein, useful as a vaccine for treating or  
PT preventing Staphylococcal infection, specifically an infection caused by  
PT S. aureus, e.g. sepsis.  
XX  
PS Claim 1; SEQ ID NO 874; 49pp; English.  
XX

CC The invention relates to novel genes and encoded proteins from  
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a  
CC nucleic acid encoding the protein, or an antibody to the protein, is  
CC useful as a pharmaceutical, particularly as a vaccine for treating or  
CC preventing infection due to Staphylococcus bacteria, specifically an  
CC infection caused by S. aureus. The composition is particularly useful for  
CC treating or preventing sepsis in a patient. The composition can also be  
CC used for diagnostics. The protein is also used in an assay for enzymatic  
CC studies and as a target for antibiotics. This sequence represents one of

CC the novel S. aureus proteins of the invention  
XX  
SQ Sequence 469 AA;  
Query Match 5.8%; Score 151; DB 6; Length 469;  
Best Local Similarity 22.1%; Pred. No. 0.00011;  
Matches 123; Conservative 66; Mismatches 171; Indels 196; Gaps 31;  
Qy 36 EKVFQYIDLHQDEFVQTLKEWVAIES--DSVQ-----PV-PRRQELFRMMAVAADTLQR 87  
Db 4 EKVQYQY---EDQIINDLKLALAESVRDDAKASADAPVCGPRKALDYMEIA-----HR 55  
Qy 88 LGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTLD 147  
Db 56 DGFTTHDVHDIAGRIEAGK-----GND-VLGILC---HVDVWPA--GDGWDSN 97  
Qy 148 PYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALE 207  
Db 98 PFEVVTEDAIARGILDDKGPTIAAYYAIIKILEDMNVVDWKKRIHMIIGTDESD----- 152  
Qy 208 ELVEKEKDRFFSGVDYIVISDNLWISORKPAI-----TYGTRGNSYF-MVEVK-C 255  
Db 153 ---WKCTDRYFK-----TEEMPTLGFAPDAEPPCIHGEKITTDFDLVQNKLT 196  
Qy 256 RDQD-----FHSQTFFG-----ILHEPMADLVA-----LLG-SLVDS 286  
Db 197 EDQDEPDYELITFKSGERYNMVDPDHAEARVLVKENMTDVIQDFEYFLEQNHLQGDSTVDS 256  
Qy 287 SGHILVPGIYDEVVPLTEEEINTYKAIH-----LDLEEYR-----NSSRVE 327  
Db 257 G--ILVLTVEGKAVHGMDPSIGVNAGLYLLKFLASLNDNNAQAFVAFSNRYLFNSDFGE 314  
Qy 328 ----KFLFDTKEEILMHL-----WRYPSLSIHGIEGAFDEPGTKTVIPG 367  
Db 315 KMGMKFHTDVMGDVTTNIGVITYDNENAGLFGINLRYP-----EGFE--FEKAMDRFANEI 368  
Qy 368 RVIGKFSIRL-----VPH---MNVSAVEKQVTRHLEDVFSKRNSSNMVSVMTLGLHPWIA 420  
Db 369 QQYG-FEVKLGKQVPPHYVDKNDPFVQKLVTA-----RNQTNDMTEPTYTIGGGTYAR 420  
Qy 421 NIDDTQYLAAKRAIRTVEGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Db 421 NLD-----KGVAFGAMFSD-----SEDLMHQK 442  
Qy 481 NEKINRWNYIEGTKLF 496  
Db 443 NEYITKKQLFNATSIY 458

RESULT 139  
ADS30510  
ID ADS30510 standard; protein; 419 AA.  
XX  
AC ADS30510;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #19543.  
XX

KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX

PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX





Db 236 KDLQAAL-EKFVAEHASKNLFDFLEESAGKATIT--LYGKSAHGAM-----PEKGVNGAT 287  
QY 353 -----EGAFDEPQTKTVI---PGRVIGKFSI-RLVPHMNVSA-----V 386  
Db 288 YLTLFLNQFNADGAAAFIKVGAEKLLLEDHEGEKLGTAAYVDELMGNTSMNAGVWSFDENS 347  
QY 387 EKQVTRHLEDVFSKRNSSNM-----VVSMTLGLH-----PWIAN-IDDT 425  
Db 348 EGKIALNFR--FPQGNSPERMQEILAKLDGVVEVELSKLHVPHYVPMSPDLVSTLIDVY 405  
QY 426 QYLAAKRAIRTVFGTEPDMIRDSSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQNEKIN 485  
Db 406 EKHTGLKGYETIIG-----GGT-----FGRLLERGVA---YGAMFEGEPDSMHQAN 448  
QY 486 RWNVIEGTKLFAAFFLE 502  
Db 449 EMKPVENIYKAAVIYAE 465

RESULT 141  
AAW62863  
ID AAW62863 standard; protein; 388 AA.  
XX  
AC AAW62863;

DT 17-OCT-2003 (revised)  
DT 26-OCT-1998 (first entry)  
XX

DE Helicobacter pylori glucose inhibited division protein (GidA).  
XX

KW Glucose inhibited division protein; GidA; dapE gene; vaccine;  
KW immunisation.  
XX

OS Helicobacter pylori; strain 60190.  
XX

PN WO9827819-A1.  
XX

PD 02-JUL-1998.  
XX

PF 23-DEC-1997; 97WO-US024147.  
XX

PR 23-DEC-1996; 96US-0033824P.  
XX

PA (UYVA-) UNIV VANDERBILT.  
XX

XX Blaser MJ, Karita M;  
PI  
XX

WPI; 1998-377287/32.  
DR

DR N-PSDB; AAV42320, AAV42322.  
XX

PT Helicobacter pylori dapE gene and related protein - used to create a  
PT mutant used in immunisation against infection by e.g. HIV, influenza,  
PT respiratory syncytial virus etc.  
XX

PS Example; Page 49-51; 77pp; English.  
XX

CC This polypeptide is a glucose inhibited division protein (GidA) encoded by  
CC the newly isolated gidA gene (see AAV42320 and AAV42322) of Helicobacter  
CC pylori strain 60190. It shows 48.3% identity and 66.5% similarity to the  
CC GidA protein of E. coli. The invention relates to conditionally lethal  
CC dapE- mutant H. pylori strains; a claimed dapE- mutant is deposited as  
CC ATCC 55897. Such mutants can be used in a claimed method of immunising a  
CC subject against H. pylori infection. They can also be used as hosts of  
CC nucleic acids encoding foreign proteins. Such mutants can be used in  
CC claimed methods of immunising against bacterial, viral, fungal or  
CC parasite infections. Sperm antigens may also be expressed for use in  
CC birth control. (Updated on 17-OCT-2003 to standardise OS field)  
XX

SQ Sequence 388 AA;

Query Match 5.7%; Score 150; DB 2; Length 388;  
Best Local Similarity 21.4%; Pred. No. 0.00011;

Matches 81; Conservative 52; Mismatches 133; Indels 112; Gaps 16;  
QY 129 FYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP 188  
Db 81 FAGHIDVVP--GDNWQSDPFKPIIKEGFLYGRGAQDMKGGVGAFLSASLNF---NPKTP 135  
QY 189 VNIKFIIIEGMEEGSV-----ALEELVEK-----EKDRFFSGVDYIIVISDN 229  
Db 136 FLLSILLTSDEEGPGIFGTKLMLEKLEKDLPHMAIVAAPTCEK-----VLGDS 185  
QY 230 LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSGGH 289  
Db 186 IKIGRR-----GSGINGRL-----ILKGVQGH 206  
QY 290 ILVPGIYDEVVPLTEEEINTYKAIHL-DLEEYRNSRVEKFLFDTKEEILMHLWRYP SLS 348  
Db 207 VAYPOKQCNPIDTLASVLPISISGVHLDDGDEY-----FDPSKLVVTNL----- 249  
QY 349 IH-GIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNM 407  
Db 250 -HAGL-----GANNVTPGSVEITFNAR-----HSLKTTKESLKEYLEKVLKDLPHLTLEL 297  
QY 408 VVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDSSTIPIAKMFQEIYVHKS VVL 467  
Db 298 ESSSS---PFITASHSKLTSVLKENILKTCRTTPLLNTKGGTSD-ARFFSA---HGIEV 349  
QY 468 IPLGAVDDGEHSQNEKIN 485  
Db 350 VEEGVINDRIHAIDERSV 367

RESULT 142

ADF08023

ID ADF08023 standard; protein; 396 AA.  
XX

AC ADF08023;  
XX

DT 12-FEB-2004 (first entry)  
XX

DE Bacterial polypeptide #4136.  
XX

KW Proteus mirabilis infection; bacterial infection; antibacterial;  
KW immunostimulant.  
XX

OS Proteus mirabilis.  
XX

PN US6605709-B1.  
XX

PD 12-AUG-2003.  
XX

PF 05-APR-2000; 2000US-00543681.  
XX

PR 09-APR-1999; 99US-0128706P.  
XX

PA (GENO-) GENOME THERAPEUTICS CORP.  
XX

PI Breton GL;  
XX

DR WPI; 2003-895291/82.  
DR

DR N-PSDB; ADF03851.  
XX

PT New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.  
XX

PS Disclosure; SEQ ID NO 8308; 870pp; English.  
XX

CC The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis, a  
CC method for evaluating a compound for the ability to bind a P. mirabilis

CC	polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.									
XX										
SQ	Sequence 396 AA;									
Query Match										
Best Local Similarity 20.9%; Score 149; DB 7; Length 396;										
Matches 85; Conservative 48; Mismatches 138; Indels 136; Gaps 17;										
Qy	36	EKVQYIDLHQDEFVQTLKEWVAIESDSV--QPVRFRQELFRMMAVAADTLQRLGARVA	93							
Db	4	EERLSTVNIKLPTFIELYRQLATPSISATDAKTDQSNELINLLANWLETL-----	55							
Qy	94	SVDMGPQQLPDGQSLPIPPV-----ILAELGSDPTKGTVCFYGHLDVQPADRGDGL	145							
Db	56	-----GFSIEIQVPETRGKFNLLATLGS--TGLLLCGHTDTPVDFEG-RWT	101							
Qy	146	TDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLFPVNIKFIEGMEEAGSVA	205							
Db	102	QDPFTLTEKEGKLYGLGTADMKG-PFAFI--IDALRDIDTSQLTHPLYILATADETSMA	158							
Qy	206	LEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTF	265							
Db	159	-----GARYFAANTAIR-PDF-----	173							
Qy	266	GGILHEP-----MADLVALLGLSDSSGHILVPGIYDEVVPLTEEEINTYKAI	313							
Db	174	-AIIGETSLOPIRAKHGHLNPAIRITG---QSGHSSDPEKGVNAIELMHESIT-----	223							
Qy	314	HLDEEYRNSRVEKFLF-----DTKE-----EILMHLWRYPSLSIHGI	352							
Db	224	HLSTLRDLKTRYNNPAFVIPPYTNFNGYINGGDAANRICACCELHMDIRPLPGLTLQDL	283							
Qy	353	EGAFDEPGTKVIPGRVIGKFSIRLV-----PHMNVSAVEK	388							
Db	284	DDLHE--TLAPVKARWPGRLSVEALHEPIPGYECPTDHKMVAVIEK	328							
RESULT 143										
AAG06550										
ID	AAG06550 standard; protein; 440 AA.									
XX										
AC	AAG06550;									
XX										
DT	17-OCT-2000 (first entry)									
XX										
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 3363.									
XX										
KW	Protein identification; signal transduction pathway; metabolic pathway;									
KW	hybridisation assay; genetic mapping; gene expression control; promoter;									
KW	termination sequence.									
XX										
OS	Arabidopsis thaliana.									
XX										
PN	EP1033405-A2.									
XX										
PD	06-SEP-2000.									
XX										
PF	25-FEB-2000; 2000EP-00301439.									
XX										
PR	25-FEB-1999; 99US-0121825P.									
PR	05-MAR-1999; 99US-0123180P.									
PR	09-MAR-1999; 99US-0123548P.									
PR	23-MAR-1999; 99US-0125788P.									
PR	25-MAR-1999; 99US-0126264P.									
PR	29-MAR-1999; 99US-0126785P.									
PR	01-APR-1999; 99US-0127462P.									
PR	06-APR-1999; 99US-0128234P.									



PR	19-JUL-1999;	99US-01443333P
PR	19-JUL-1999;	99US-01443334P
PR	19-JUL-1999;	99US-01443335P
PR	20-JUL-1999;	99US-01443352P
PR	20-JUL-1999;	99US-0144632P
PR	20-JUL-1999;	99US-0144884P
PR	21-JUL-1999;	99US-0144814P
PR	21-JUL-1999;	99US-0145086P
PR	21-JUL-1999;	99US-0145088P
PR	22-JUL-1999;	99US-0145085P
PR	22-JUL-1999;	99US-0145087P
PR	22-JUL-1999;	99US-0145089P
PR	22-JUL-1999;	99US-0145192P
PR	23-JUL-1999;	99US-0145145P
PR	23-JUL-1999;	99US-0145218P
PR	23-JUL-1999;	99US-0145224P
PR	26-JUL-1999;	99US-0145276P
PR	27-JUL-1999;	99US-0145913P
PR	27-JUL-1999;	99US-0145918P
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PR	05-AUG-1999;	99US-0147192P
PR	05-AUG-1999;	99US-0147260P
PR	06-AUG-1999;	99US-0147303P
PR	06-AUG-1999;	99US-0147416P
PR	09-AUG-1999;	99US-0147493P
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PR	17-AUG-1999;	99US-0149175P
PR	18-AUG-1999;	99US-0149426P
PR	20-AUG-1999;	99US-0149722P
PR	20-AUG-1999;	99US-0149723P
PR	20-AUG-1999;	99US-0149929P
PR	23-AUG-1999;	99US-0149902P
PR	23-AUG-1999;	99US-0149930P
PR	25-AUG-1999;	99US-0150566P
PR	26-AUG-1999;	99US-0150884P
PR	27-AUG-1999;	99US-0151065P
PR	27-AUG-1999;	99US-0151066P
PR	27-AUG-1999;	99US-0151080P
PR	30-AUG-1999;	99US-0151303P
PR	31-AUG-1999;	99US-0151438P
PR	01-SEP-1999;	99US-0151930P
PR	07-SEP-1999;	99US-0152363P
PR	10-SEP-1999;	99US-0153070P
PR	13-SEP-1999;	99US-0153758P
PR	15-SEP-1999;	99US-0154018P
PR	16-SEP-1999;	99US-0154039P
PR	20-SEP-1999;	99US-0154779P
PR	22-SEP-1999;	99US-0155139P
PR	23-SEP-1999;	99US-0155486P
PR	24-SEP-1999;	99US-0155659P
PR	28-SEP-1999;	99US-0156458P
PR	29-SEP-1999;	99US-0156596P
PR	04-OCT-1999;	99US-0157117P
PR	05-OCT-1999;	99US-0157753P
PR	06-OCT-1999;	99US-0157865P
PR	07-OCT-1999;	99US-0158029P
PR	08-OCT-1999;	99US-0158232P
PR	12-OCT-1999;	99US-0158369P
PR	13-OCT-1999;	99US-0159293P
PR	13-OCT-1999;	99US-0159294P

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PR	25-OCT-1999;	99US-0161406P
PR	26-OCT-1999;	99US-0161359P
PR	26-OCT-1999;	99US-0161360P
PR	26-OCT-1999;	99US-0161361P
PR	28-OCT-1999;	99US-0161920P
PR	28-OCT-1999;	99US-0161992P
PR	28-OCT-1999;	99US-0161993P
PR	29-OCT-1999;	99US-0162142P

Query Match      5.7%;    Score 149;    DB 3;    Length 440;

Best Local Similarity 23.0%; Pred. No. 0.00016;

Matches 122; Conservative 70; Mismatches 194; Indels 144; Gaps 30;

QY	29	SPPPALLEKVFQYIDLHODEFVQTLKEWVAIESDSVQ--PVPFRFRQELFRMMVAADTLQ	86
Db	3	SSSKALIESIG---SLDKDSYVSLLSKLG-ESKFVQNNPPELIPQEDLIVKHV-LDSL-	56
QY	87	RLGARVASVDMGPPQLPDGQSLPIPPV-----ILAELGSDPTKGTVCFYG-HLDVQ	136
Db	57	----RPYSTETG-----GGPLVINHVAYHSGRGNLIVEYPGSVPGK-ILSFVGMEHMDVV	105
QY	137	PADRGDGLTDPYVVLTEVDG-KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII	195
Db	106	TAN-PDDWEFPDFSLS-IDGDKLRGRGTTDCLGHVALVTELMKKLGEAKPALKSTVVSVF	163
QY	196	EGMEEAGS---VALEELV-EKEKDRFFSGVDYIVISDNLWI--SQRKPAITYGTRGNSYF	249
Db	164	IASEENSSIPGVGVDMLVKDKLLDKKSGPLY-----WIDTADKQPCV--GTGG----	210
QY	250	MVEVKCR--DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEI	307
Db	211	MIPWKLQFTGKLFS---GLAHKAINAMELAMEGLKEIQAR-----FYRDFPFPQEEV	261
QY	308	NTYKAIHLDLEEYRNSRRVEKFFLDFTKEEILMHLWRYPSPLSIHGIEGAFDEPGTKTVIPG	367
Db	262	-----YGFATPSTMKPTQWCYPA-----GGINQIPG	287
QY	368	RVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVV-----SMTLG	414
Db	288	ECTVSGDVRLLTPFDYVKEVMTKLQEIYVDDINSNIEKLETRGPPVSKYVLPDENLRGLTLS	347
QY	415	LHPWIA----NIDDTQYLAAKRAIRTVFG-TEPDMIRDGSTIPIAKMFQEI VHKSVVLIIP	469
Db	348	FDEASAGVACNLDSFGFHVLCATEEVGHVKPYSIT--GTLPLIRDLQ-----	394
QY	470	LGAVDDG-----EHSQNEKINRWNYIEGTKLFAAFLEMAQL	506
Db	395	----DEGFDVOTSGYGLMATYHAKNEYCLLTDMCQGFDFVFIISQLEQV	440

RESULT 144

AAU36697 standard; protein; 469 AA.

XX

AC AAU36697;

九



PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
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PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
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PR 19-JUL-1999; 99US-0144325P.  
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PR 22-JUL-1999; 99US-0145192P.

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PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
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PR 03-AUG-1999; 99US-0147038P.  
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PR 05-AUG-1999; 99US-0147192P.  
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PR 13-AUG-1999; 99US-0148565P.  
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PR 16-AUG-1999; 99US-0149368P.  
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PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
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PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.



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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      5.7%; Score 148.5; DB 3; Length 430;
Best Local Similarity 19.9%; Pred. No. 0.00017;
Matches 100; Conservative 87; Mismatches 187; Indels 129; Gaps 24;

QY 33 ALLEKVFQYIDLH-----QDFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQ 86
Db 2 SLLRLLLVVVVHLHLSAVAGDDAIVSRFQEYLRI--NTVQNPNEYKAVDFIIS----- 52

QY 87 RLGARVASVDMGPPQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGLT 146
Db 53 --QAKPLSLESQTIEFVKGK---PLLLKMWGSDPTLPAFLNLSHTDVVPFE-DSKWT 105

QY 147 DPYVLTEVD--GKLYGRGATDNKGPVLWINAV-----SAFRALEQDLPVNIKFIIEGME 199
Db 106 HP-LQAHMDHHGDIYARGSQDMKCVGMQYLEAIRKLQASGFKPLRS---VYLSFVPD-EE 160

QY 200 EAGSVALEELVEKEKDRFFSGVDY-IVISDNLWISQRPKPAITYGTRGNSYFMVEVKCRDQ 258
Db 161 IGGHDGAEKFAESQ---LFKSLNIAIVLDEGLPSPTESYRVFYGER--SPWLVVIKAKGP 215

QY 259 DFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIINTYKAIHLDLE 318
Db 216 PGH---GAKLYDNSA-MENLLKSI-----ESIRFRASQFDL- 248

QY 319 EYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGI-EG-----AFDEPGTKT----- 363
Db 249 -----LKAGGIAEGDVVSVNMAFLKAGTPSPPTGFVMN 280

QY 364 VIPGRVIGKFSIRLVPHMNVSAVEKQV-----TRHLEDVFSKRNSSNKMVVVSMTLGLH 416
Db 281 LQPSAEAEAGFDIRVPPSVDAEALERLVEEWAPAARNMSFEF-KQKLTKGQFLTAAADSN 339

QY 417 PWIANIDTQYLAAKRAIR-TVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDD 475
Db 340 PWWGLENVAVKEAGGRTSKPEIFPASTD-----ARYFRKAGVPAFGFSPISNTPS 389

QY 476 GEHSQNEKINRWNYIEGTKLFAA 498
Db 390 LLHDHNEYLGAEBYLGKIEVYVS 412

RESULT 146
AAR30458
ID AAR30458 standard; protein; 407 AA.
XX
AC AAR30458;
XX
DT 06-MAY-1993 (first entry)
DE Pig aminoacylase I.
XX
KW AmA; production; yield; recombinant.
XX
OS Sus scrofa.
XX
PN JP04330279-A.
XX
PD 18-NOV-1992.
XX
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PF 22-MAR-1991; 91JP-00081136.
XX
PR 22-MAR-1991; 91JP-00081136.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1993-003494/01.
DR N-PSDB; AAQ33105.
XX
PT Polypeptide with amino:acylase (I) activity - has specific base sequence
PT and is used for preparing probe, primer and antibody.
XX
PS Claim 1; Page 9; 14pp; Japanese.
XX
CC The protein sequence of aminoacylase I was deduced from the cDNA sequence
CC cloned from pig kidney poly (A) mRNA, clones lambda pKAmA -1 to -10. The
CC sequence may be used to transform Saccharomyces cerevisiae to produce
CC aminoacylase I recombinantly. See also AAR30459
XX
SQ Sequence 407 AA;

Query Match      5.5%; Score 143.5; DB 2; Length 407;
Best Local Similarity 18.2%; Pred. No. 0.00045;
Matches 91; Conservative 74; Mismatches 179; Indels 157; Gaps 19;

QY 50 VOTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQLPDG-QSL 108
Db 13 VTLFRQYLRI--TVQPEPDY-----GAAVAFLEERARQLGLGCQKV 52

QY 109 PIPP----VILAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPYV-LTEVDGKLYGRGA 163
Db 53 EVVPGHVVTVLTWPGTNPILSSILLNSHTDVVPVK-EHWSHDPFEGFKDADGYIYGRGA 111

QY 164 TDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEGAG-----SV 204
Db 112 QDMKCVSIQYLEAVRRLKVEGHHPRTIHMTFVPDEVGHGQGMELFVKRPEFQALPAGF 171

QY 205 ALBELVEKEKDRFFSGVDYIVISDNLWISQRPKPAITYGTRGNSYFMVEVKCRDQDFHSGT 264
Db 172 ALDEGLASPTDAF-----TVFYSERSP-----WWLRVTSTGKPGHGSR 209

QY 265 FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIINTYKAIHLDLEEYRNSS 324
Db 210 F-----IEDTAAEKLHKVINSILAFREKEKQRLQSN 240

QY 325 RVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 384
Db 241 QLKP-----GAVTSVNLTMLEGGV-----AYNVVPATMSACDFRVPDVLK 283

QY 385 AVEKQ-----VTRHLEDVFSKRNSSNKMVVVSMTLGLHPWIANIDDTQYL 428
Db 284 AFEEQLQSWCQAAGEGVTFEFVEKWMETQVTSTDSD-----PWAAAFSGV-FK 331

QY 429 AAKRAIRTVF---GTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKIN 485
Db 332 DMKLALELEICPASTDARYIR-AAGVP-ALGFSPMNHPTPVL-----HDHDERLH 379

QY 486 RWNVIEGTKLFAAFFLEMAQL 506
Db 380 EAVFLRGVDIYTQLLSALASV 400

RESULT 147
AAG06511
ID AAG06511 standard; protein; 450 AA.
XX
AC AAG06511;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3311.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
```







QY 270 HEPMADLVA-LLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA-IHLDLEEYRNSSRVE 327  
Db 211 ---MEDTAAEKLHKVNS-----ILAFREKEWQRLQSNPHL----- 243  
QY 328 KFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 244 -----KEGSV-----TSVNLTKLEGGV-----AYNVIPATMSASFVRVAPDVDFKAFE 287  
QY 388 KQVTRHLEDV-----FSKRNSSNMVSVMTLGLHPWIANIDDTQ--YLAAKRAIRTVF 438  
Db 288 EQLQSWCQAAGEGVTLEFAQK-----WMHPQVTTDDSNPWWAAFSRVCKDMN 335  
QY 439 GT-EPDMI-----RDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIE 491  
Db 336 LTLEPEIMPAATDNRYIRAVGVPAALGFSPMNRTPVLL-----HDHDERLHEAVFLR 386  
QY 492 GTKLPFAAFFLEMAQL 506  
Db 387 GVDIYTRLLPALASV 401

RESULT 149

ABB08103  
ID ABB08103 standard; protein; 408 AA.

AC ABB08103;

DT 10-SEP-2002 (first entry)

DE Human peptidase family member amino acid sequence.

XX Aminoacylase-1; ACY-1; metalloprotein; cytosolic enzyme; human;  
KW cytosstatic; therapeutic; cancer therapy; peptidase; enzyme.

OS Homo sapiens.

XX US6387661-B1.

PN 14-MAY-2002.

XX 23-MAR-2001; 2001US-00814951.

XX 23-MAR-2001; 2001US-00814951.

XX (PEKE ) PE CORP NY.

XX Shao W, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2002-478443/51.

XX Isolated nucleic acid molecules encoding enzymes similar to human  
PT aminoacylase-1, useful as a drug target and diagnostic marker for cancers  
PT e.g. T cell leukemias and ovary, brain or lung cancers.

PS Disclosure; Fig 2A; 43pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding  
CC enzymes similar to human aminoacylase-1 (ACY-1) (EC 3.5.1.14) (a  
CC metalloprotein cytosolic enzyme). The ACY-1 similar polynucleotide and  
CC encoded peptide sequences can be used as models for the development of  
CC human therapeutic targets, aid in the identification of therapeutic  
CC proteins, and serve as targets for the development of human therapeutic  
CC agents that modulate enzyme activity in cells and tissues that express  
CC the enzyme. ACY-1 has been found to be expressed in humans in the  
CC placenta, T cells from T cell leukemia, ovary, brain, lung and leukocyte,  
CC and therefore may be a drug target for cancer therapy and act as a  
CC diagnostic marker for these cancers. The present sequence represents a  
CC human peptidase family member polypeptide used in alignment studies

XX Sequence 408 AA;

Query Match 5.4%; Score 141; DB 5; Length 408;  
Best Local Similarity 18.2%; Pred. No. 0.00078;

Matches 90; Conservative 85; Mismatches 176; Indels 144; Gaps 21;  
QY 50 VQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLP 109  
Db 13 VTLFRQYLRI--TVQPKDDYG---AAVAFFEETARQLGLGCQKVEVAPGYV----- 59  
QY 110 IPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPY-VLTEVDGKLYGRGATDNKG 168  
Db 60 --VTVLTPWGTNPTLSSILLNSHTDVPVFK-EHWSHDPFEAFKDESEGYIYARGAQDMKC 116  
QY 169 PVLAWINAVSAFRALEQDLFPVNIKFIEGMEEAG-----SVALEEL 209  
Db 117 VSIQYLEAVRRLKVEGHRFPRTIHMTFVPDDEEVGHHQGMELFVQRPFEHALRAGFALDEG 176  
QY 210 VEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYPMVEVKCRDQDFHSGTFGGIL 269  
Db 177 IANPTDAF-----TVFYSERSP-----WWVRVTSTGRPGHASRF----- 210  
QY 270 HEPMADLVA-LLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA-IHLDLEEYRNSSRVE 327  
Db 211 ---MEDTAAEKLHKVNS-----ILAFREKEWQRLQSNPHL----- 243  
QY 328 KFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 244 -----KEGSV-----TSVNLTKLEGGV-----AYNVIPATMSASFVRVAPDVDFKAFE 287  
QY 388 KQVTRHLEDV-----FSKRNSSNMVSVMTLGLHPWIANIDDTQ--YLAAKRAIRTVF 438  
Db 288 EQLQSWCQAAGEGVTLEFAQK-----WMHPQVTTDDSNPWWAAFSRVCKDMN 335  
QY 439 GT-EPDMI-----RDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIE 491  
Db 336 LTLEPEIMPAATDNRYIRAVGVPAALGFSPMNRTPVLL-----HDHDERLHEAVFLR 386  
QY 492 GTKLPFAAFFLEMAQL 506  
Db 387 GVDIYTRLLPALASV 401

RESULT 150

ADE59755

ID ADE59755 standard; protein; 408 AA.

XX ADE59755;

XX 29-JAN-2004 (first entry)

XX Human Protein Q03154, SEQ ID NO 5651.

XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PN 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; Q03154.



Db 117 VSIQYLEAVRRLKVEGHRFPRTIHTMTFVPDEEVGGHQGMELFVQRPPEFHALRAGFALDEG 176

Qy 210 VEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGIL 269

Db 177 IANPTDAF-----TVFYSERSP-----WWVRVTSTGRPGHASRF----- 210

Qy 270 HEPMADLVA-LLGSLVDSSGHILVPGIYDEVVPLTBEETINTYKA-IHLDLEEYRNSSRVE 327

Db 211 ---MEDTAAEKLHKVNS-----ILAFREKEWQRLQSNPHL----- 243

Qy 328 KFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVE 387

Db 244 -----KEGSV-----TSVNLTKLEGGV-----AYNVIPATMSASFDFRVAPDVDFKAFE 287

Qy 388 QVTRHLEDV-----FSKRNSSNMVVSMTLGLHPWIANIDDTQ--YLAAKRAIRTVF 438

Db 288 EQLQSWCQAAGEGVTLEFAQK-----WMHPQVTPTDSDSNPWWAAPSVCCKDMN 335

Qy 439 GT-EPDMI-----RDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQNEKINRWNYIE 491

Db 336 LTLEPEIMPAATDNRYIRAVGVPALGFSPMNRTPVLL-----HDHDERLHEAVFLR 386

Qy 492 GTKLFAAFFLEMAQL 506

Db 387 GVDIYTRLLPALASV 401

RESULT 152

ADR40173

ID ADR40173 standard; protein; 408 AA.

XX ADR40173;

XX 18-NOV-2004 (first entry)

DE Human aminoacylase 1 (25584) protein.

XX haematological; cytostatic; erythroid; anaemia; erythrocytosis;

KW bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;

KW T-cells; neutropenia; gene therapy; human; aminoacylase 1; enzyme.

XX Homo sapiens.

OS WO2004072242-A2.

XX 26-AUG-2004.

XX 05-FEB-2004; 2004WO-US003417.

XX 05-FEB-2003; 2003US-0445241P.

PR 18-FEB-2003; 2003US-0448389P.

PR 20-MAR-2003; 2003US-0456320P.

PR 03-APR-2003; 2003US-0460279P.

PR 28-APR-2003; 2003US-0465924P.

PR 13-MAY-2003; 2003US-0470052P.

PR 26-AUG-2003; 2003US-0498106P.

PR 04-SEP-2003; 2003US-0500179P.

PR 15-SEP-2003; 2003US-0502909P.

PR 10-OCT-2003; 2003US-0510351P.

PR 17-OCT-2003; 2003US-0512380P.

XX (MILL-) MILLENNIUM PHARM INC.

PA Kelly LM, Carroll JM, Farlow D, Healy A;

XX WPI; 2004-625850/60.

XX N-PSDB; ADR40172.

XX Identifying a compound capable of treating a hematological disorder

PT comprises combining a compound to be tested with a polypeptide related

PT with the disorder under conditions suitable for binding of the test

PT compound to the polypeptide.

XX Claim 1; SEQ ID NO 54; 321pp; English.

PS The invention relates to a novel method for identifying a compound

XX capable of treating a haematological disorder which comprises combining a

CC compound to be tested with a specific polypeptide under conditions

CC suitable for binding of the test compound to the polypeptide. The method

CC of the invention has haematological and cytostatic applications and may

CC be useful for identifying compounds for treating a haematological

CC disorder associated with erythroid cells e.g. anaemia and erythrocytosis,

CC bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and

CC thrombosis or B-cells and T-cells e.g. neutropenia. The compounds

CC identified may be utilised during gene therapy procedures. The current

CC sequence is that of a human haematological disorder-related protein of

CC the invention.

XX Sequence 408 AA;

SQ Query Match 5.4%; Score 141; DB 8; Length 408;

Best Local Similarity 18.2%; Pred. No. 0.00078;

Matches 90; Conservative 85; Mismatches 176; Indels 144; Gaps 21;

Qy 50 VQTLKEWVAIESDVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSLP 109

Db 13 VTLFRQYLRIR--TVQPKPDYG---AAVAFETARQLGLGCQKVEVAPGV----- 59

Qy 110 IPPVILAEELGSDPTKGTVCYFGHLDVQPADRGDWLTDPY-VLTEVDGKLYGRGATDNKG 168

Db 60 --VTVLTWPGTNPSTLSSILLNSHTDVVPVK-EHWSHDPFEAFKQSEGYIYARGAQDMKC 116

Qy 169 PVLAWINAVSAFRALEQDLPVNIKFIIEGMBEAG-----SVALEEL 209

Db 117 VSIQYLEAVRRLKVEGHRFPRTIHTMTFVPDEEVGGHQGMELFVQRPPEFHALRAGFALDEG 176

Qy 210 VEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGIL 269

Db 177 IANPTDAF-----TVFYSERSP-----WWVRVTSTGRPGHASRF----- 210

Qy 270 HEPMADLVA-LLGSLVDSSGHILVPGIYDEVVPLTBEETINTYKA-IHLDLEEYRNSSRVE 327

Db 211 ---MEDTAAEKLHKVNS-----ILAFREKEWQRLQSNPHL----- 243

Qy 328 KFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVE 387

Db 244 -----KEGSV-----TSVNLTKLEGGV-----AYNVIPATMSASFDFRVAPDVDFKAFE 287

Qy 388 QVTRHLEDV-----FSKRNSSNMVVSMTLGLHPWIANIDDTQ--YLAAKRAIRTVF 438

Db 288 EQLQSWCQAAGEGVTLEFAQK-----WMHPQVTPTDSDSNPWWAAPSVCCKDMN 335

Qy 439 GT-EPDMI-----RDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQNEKINRWNYIE 491

Db 336 LTLEPEIMPAATDNRYIRAVGVPALGFSPMNRTPVLL-----HDHDERLHEAVFLR 386

Qy 492 GTKLFAAFFLEMAQL 506

Db 387 GVDIYTRLLPALASV 401

RESULT 153

ABM80467

ID ABM80467 standard; protein; 408 AA.

XX ABM80467;

AC 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAR) polypeptide PRO81002, SEQ:1173.

DT Tumour-associated antigenic target; TAR; human; overexpression; cancer;

DE tumour; diagnosis; cell proliferative disorder; breast cancer;

XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;

XX central nervous system cancer; bladder cancer; pancreatic cancer;





PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.

PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.





XX (INCY-) INCYTE CORP.  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;  
XX WPI; 2004-329368/30.  
DR N-PSDB; ACN42339.  
DR  
XX  
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 441 AA;  
Query Match 5.4%; Score 140.5; DB 8; Length 441;  
Best Local Similarity 18.3%; Pred. No. 0.00098;  
Matches 94; Conservative 84; Mismatches 187; Indels 149; Gaps 21;  
QY 50 VQTLKEWVAIESDSVQVPRFRQELFRMMVAADTLQRLGARVASVDMGPOQLPDGQSLP 109  
Db 13 VTLFRQYLRI--TVQPKDYG---AAVAFFEETARQLGLGCQKVEVAPGYV----- 59  
QY 110 IPPVILAEGLSDPTKGTGVCYGHLDVQPADRGDGLTDPY-VLTEVDGKLYGRGATDNKG 168  
Db 60 --VTVLTWPGTNPNTLLSILLNSHTDVPVFK-EHWSHDPPEAFKDSEGIYARGAQDMKC 116  
QY 169 PVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD 228  
Db 117 VSIQYLEAVRRLKVEGHRFPRTIHTFTVPDEVG----- 150  
QY 229 NLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHE-----PMADLVA---- 278  
Db 151 -----GHQGMELFV-----QRPEFHARAGFALDEGEQVGKPMSSQAGSRRL 192  
QY 279 LLGS-LVDSSGHILVPGI-----YDEVVPLTEEBEINTYKAHILDLEEYRNSRVE 327  
Db 193 LVGTELLHPLNPLSLGLIANPTDAFTVFYSERSPWWVRVTSTGRPGH-----AS 241  
QY 328 KFLFDTKEEIIMHL-----WRYPSLSIHGIEGAFD-----EPGTK-TVIPGR 368  
Db 242 RFMEDTAAEKLHKVNSILAFREKEWQRLQSNPHLKBSVTSVNLTKLEGGVAYNVIPAT 301  
QY 369 VIGKFSIRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSNKMVMSMTGLHPWIAN 421  
Db 302 MSASFDFRVAPDVFKAPEEQLSWCQAAGEGVTLFEAQK-----WMHPQVTP 349

QY 422 IDDTQ--YLAAKRAIRTVFGT-EPDMI-----RDGSTIPIAKMFQEIIVHKSVVLIPLGA 472  
Db 350 TDDSNPWAAAFSRVCKDMNLTLEPEIMPAATDNRYIRAVGVGPALGFSPMNRTPVLL----- 405  
QY 473 VDDGEHSQNEKINRWNYIEGTKLFFAAFFLEMAQL 506  
Db 406 -----HDHDERLHEAVFLRGVDIYTCLLPALASV 434  
RESULT 157  
ADK47763  
ID ADK47763 standard; protein; 443 AA.  
XX  
AC ADK47763;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Streptococcus pneumoniae protein, Seq ID No 4278.  
XX  
KW Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.  
XX  
OS Streptococcus pneumoniae.  
XX  
PN US6699703-B1.  
XX  
PD 02-MAR-2004.  
XX  
PF 26-MAY-2000; 2000US-00583110.  
XX  
PR 02-JUL-1997; 97US-0051553P.  
PR 12-MAY-1998; 98US-0085131P.  
PR 30-JUN-1998; 98US-00107433.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;  
XX  
DR WPI; 2004-212399/20.  
DR N-PSDB; ADK45102.  
XX  
PT New nucleic acid molecules and polypeptides useful for diagnosing,  
PT preventing and treating pathological conditions resulting from bacterial  
PT infection, e.g. Streptococcus pneumoniae infection, and in drug  
PT screening.  
XX  
PS Disclosure; SEQ ID NO 4278; 301pp; English.  
XX  
CC The invention relates to isolated Streptococcus pneumoniae nucleic acids  
CC and polypeptides. The nucleic acids and proteins are useful for  
CC diagnosing, preventing and treating pathological conditions resulting  
CC from bacterial infection, such as S. pneumoniae infection. These may also  
CC be used for drug screening procedures. The present sequence represents a  
CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence  
CC data for this patent did not appear in the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 443 AA;  
Query Match 5.3%; Score 139.5; DB 8; Length 443;  
Best Local Similarity 21.5%; Pred. No. 0.0012;  
Matches 92; Conservative 61; Mismatches 130; Indels 145; Gaps 21;  
QY 121 DPTKGTVCIFYG-----HLDVQPADRGDGLTDPYVLTEVDGKLYGRGATD 165  
Db 61 DP-KG---YGYABIGQAELLAAILCHLDVPSGDEADWQTPPFEATIKDGVVFGRVQD 116  
QY 166 NKGVPVLWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIV 225  
Db 117 DKGPSLAALYAVKSL-----LDQGIQF-----KKRVRFIPTD--- 149  
QY 226 ISDNLW-----ISQRKP-----AITYGTRGNSYFMVEVKCRDQDFHSGTGGI 268

Db 150 -EETLWRCMARYNTIEEQASMGFAPDSSFPLTYAEKG-----LLQVK----- 190

Qy 269 LHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAHLDLEEYRNSR-- 325

Db 191 LHGPGSDQLELEVGGAFN-----VVPDKANYQGPLYEQVCNDLKEAGYD---YQSTEQTV 242

Qy 326 ----VEKFLFDTK-----EILMHLWRYPSLSIHGIEGAFDEPGTKTV----- 364

Db 243 TVLGVPKHAKDASQGINAVIRLATILAPLQEHFALSFLATQAGDGTGRQIFGDIADEPS 302

Qy 365 -----IPGRVIG-----KFSIRLVPHMNVSAVEKQVTR-----HLEDVFS 399

Db 303 GHLSFNVAGLMINHERSEIRIDIRTPVLADKEELVKLLTRCAQNYQLRYEEFDYLAPLYV 362

Qy 400 KRNSSNMVMVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQE 459

Db 363 AKDSK---LVSTLMQIYQEKTG-DNSPAISSGGA--TFARTMPNCVAFGALFPGAKQTEH 416

Qy 460 IVHKSVVVL 467

Db 417 QANEC AVL 424

RESULT 158

ADR96040

ID ADR96040 standard; protein; 446 AA.

XX ADR96040;

AC ADR96040;

XX 16-DEC-2004 (first entry)

XX Novel S. pneumoniae protein sequence, SEQ ID 4675.

XX Meningitis; bacteraemia; pneumonia; otitis media; vaccine;

KW bacterial infection.

XX Streptococcus pneumoniae.

OS US6800744-B1.

XX PD 05-OCT-2004.

XX 30-JUN-1998; 98US-00107433.

PF 02-JUL-1997; 97US-0051553P.

PR 12-MAY-1998; 98US-0085131P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA Doucette-Stamm LA, Bush D;

XX WPI; 2004-697205/68.

DR N-PSDB; ADR93437.

XX New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection.

PT Disclosure; SEQ ID NO 4675; 151pp; English.

PS

XX

CC The invention relates to an isolated nucleic acid comprising a sequence encoding a Streptococcus pneumoniae ADR91366polypeptide, or its fragments, with any of 9 fully defined sequences (appearing as ADR94308, ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682, ADR96079) or any of the fully defined sequences appearing as ADR91705, ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide sequences, or at least 40, 60 or 300 consecutive nucleotides, which is hybridisable under high stringency conditions to the nucleotide sequence. The nucleic acids and proteins are chosen from 5206 disclosed sequences. CC Also included are a recombinant expression vector comprising the isolated nucleic acid cited above operably linked to a transcription regulatory element, a cell comprising the recombinant expression vector and a probe

CC comprising at least 20 consecutive nucleotides of the nucleotide sequences as cited above. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of pathological conditions resulting from bacterial infection by Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and otitis media. The present sequence is one of the 2603 disclosed S. pneumoniae protein sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6800744B1.

XX Sequence 446 AA;

SQ

Query Match 5.3%; Score 139.5; DB 8; Length 446;

Best Local Similarity 21.5%; Pred. No. 0.0012;

Matches 92; Conservative 61; Mismatches 130; Indels 145; Gaps 21;

Qy 121 DPTKGTVCFYG-----HLDVQPADRGDGLTDPYVLTEVDGKLYGRGATD 165

Db 64 DP-KG--YYGYAEIGQGAELLAILCHLDVWPSGDEADWQTPPFEATIKDGWVFGRGVQD 119

Qy 166 NKGPVLAWINAVSAFRALEQDLVPNIKFIEGMEEGAGSVALEELVEKEXDRFFSGVDYIV 225

Db 120 DKGPSLAALYAVKSL-----LDQGIQF-----KKRVRFIFGTD--- 152

Qy 226 ISDNLW-----ISQRKP-----AITYGTRGNSYFVVEVKCRDQDFHSGTFGGI 268

Db 153 -EETLWRCMARYNTIEEQASMGFAPDSSFPLTYAEKG-----LLQVK----- 193

Qy 269 LHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAHLDLEEYRNSR-- 325

Db 194 LHGPGSDQLELEVGGAFN-----VVPDKANYQGPLYEQVCNDLKEAGYD---YQSTEQTV 245

Qy 326 ----VEKFLFDTK-----EILMHLWRYPSLSIHGIEGAFDEPGTKTV----- 364

Db 246 TVLGVPKHAKDASQGINAVIRLATILAPLQEHFALSFLATQAGDGTGRQIFGDIADEPS 305

Qy 365 -----IPGRVIG-----KFSIRLVPHMNVSAVEKQVTR-----HLEDVFS 399

Db 306 GHLSFNVAGLMINHERSEIRIDIRTPVLADKEELVKLLTRCAQNYQLRYEEFDYLAPLYV 365

Qy 400 KRNSSNMVMVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQE 459

Db 366 AKDSK---LVSTLMQIYQEKTG-DNSPAISSGGA--TFARTMPNCVAFGALFPGAKQTEH 419

Qy 460 IVHKSVVVL 467

Db 420 QANEC AVL 427

RESULT 159

AAB96247

ID AAB96247 standard; protein; 474 AA.

XX AAB96247;

AC AAB96247;

XX 29-OCT-2001 (first entry)

DT Putative P. abyssi diaminopimelate/ornithine desuccinylase/deacetylase.

XX Hyperthermophilic archaeon; hyperthermophilic protein.

OS Pyrococcus abyssi.

XX FR2792651-A1.

XX 27-OCT-2000.

XX 21-APR-1999; 99FR-00005034.

XX 21-APR-1999; 99FR-00005034.

XX (CNRS ) CNRS CENT NAT RECH SCI.

PA









CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 215 AA;  
SQ Query Match 5.2%; Score 137; DB 4; Length 215;  
Best Local Similarity 27.0%; Pred. No. 0.00068;  
Matches 68; Conservative 33; Mismatches 81; Indels 70; Gaps 15;  
Qy 36 EKVFQYIDLHQDEFVQTLKEWVAIES--DSVQ-----PV-PRFRQELFRMMAVAADTLQR 87  
Db 4 EKVOQY----EDQIINDLKGLLAIESVRDDAKASEDAPVGGPRKALDYMEIA-----HR 55  
Qy 88 LGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLTD 147  
Db 56 DGFTTHDVHDIAGRIEAGK-----GND-VLGILC---HVDVVPA--GDGWDSN 97  
Qy 148 PYVLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALE 207  
Db 98 PFEPVVTEDAIARGTLDDKGPPTIAAYYAIKILEDMNVDWKKRIHMIIGTDEESD----- 152  
Qy 208 ELVEKEKDRFFSGVDYIVISDNLWISQKPAI-----TYGTRGNSYF-MVEVK-C 255  
Db 153 ---WKCTDRYFK-----TEEMPTLGFAPDAEFFPCIHGEKGITTFDLVQNKLT 196  
Qy 256 RDQ---DFHSGT 264  
Db 197 EDQDELDYELGT 208

RESULT 163  
ABB66172  
ID ABB66172 standard; protein; 408 AA.  
XX ABB66172;  
AC ABB66172;  
DT 26-MAR-2002 (first entry)  
XX Drosophila melanogaster polypeptide SEQ ID NO 25308.  
DE Drosophila melanogaster polypeptide SEQ ID NO 25308.  
XX Drosophila melanogaster polypeptide SEQ ID NO 25308.  
KW Drosophila melanogaster polypeptide SEQ ID NO 25308.  
KW pharmaceutical.  
XX Drosophila melanogaster.  
OS Drosophila melanogaster.  
XX WO200171042-A2.  
PN 27-SEP-2001.  
PD 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-US009231.  
PF 23-MAR-2001; 2001WO-US009231.  
XX 23-MAR-2001; 2001WO-US009231.  
PR 23-MAR-2001; 2001WO-US009231.  
PR 11-JUL-2000; 2000US-00614150.  
XX (PEKE ) PE CORP NY.  
PA Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
PI N-PSDB; ABL10275.  
DR New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
PT interactions.  
XX Disclosure; SEQ ID NO 25308; 2lpp + Sequence Listing; English.  
PS The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 408 AA;  
SQ Query Match 5.2%; Score 137; DB 4; Length 408;  
Best Local Similarity 20.3%; Pred. No. 0.0018;  
Matches 97; Conservative 79; Mismatches 189; Indels 112; Gaps 23;  
Qy 47 DEFVQTLKEWVAIESDSVQPVPRFRQELF-----RMMVAADTLQRLGARV-ASV 95  
Db 11 DEEIIIFQEYLRI--PSVHPDVEDYSKDLFFRSLDFVIFISLAACVEFLKQANKLNLRV 68  
Qy 96 DMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLTDPY-VLTEV 154  
Db 69 DVVYPVVPVPSK-----PVVIMKWLKHKPELKSIIILNSHMDVVPV-FPEKWTHEPFGAHIDA 122  
Qy 155 DGKLYGRGATDNKGPVLAMINAVSAFRA--LEQDLPVNIKFIIIEGMEEAGSVALEELVE- 211  
Db 123 QGRIYARGAQDMKSVGCQYMAAVRALKASGYQPKRTVYLTVPD-EETGGHMGMAEFVKG 181  
Qy 212 ---KEKDRFFSGVDYIVISDNLWISQKPAI--TYGTRGNSYFEMVEVKCRDQDFHSGT--FG 266  
Db 182 DYFKAMNVGFSLDEGIASEDDTY-----PVFYAER--TLWQLRFK-----FSGTSGHG 227  
Qy 267 GILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTTEEINTYKAIHLDLEEYRNSSRV 326  
Db 228 SLHK-----STAGEKEPHF-----VMDKLMKFRQTV----- 254  
Qy 327 EKFLFDTKKEIIMHLWRYPVPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAV 386  
Db 255 -KLL--AEDSSLQSGDVTTLNLTQLNGGVQ---SNVVPVLEATFDIRIAINQNADAM 306  
Qy 387 EKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQ--YLAAKRAIRTVFGTEPDM 444  
Db 307 ENQIREWCNEV-----GGGVELDTLKCPSVVTIKIDSNPYWLGFKKGLDELGLITHR 360  
Qy 445 IRDGT-----IPIAKMFQEIVHKSIVLPLGAVDDGEHSONEKNRWNVIEG 492  
Db 361 VFPGATDSFYVRQVGIP-ALGFSPINNTPVLL-----HNHDEYLRADTYLHG 406  
RESULT 164  
AAG06512  
ID AAG06512 standard; protein; 429 AA.  
XX AAG06512;  
AC AAG06512;  
XX 17-OCT-2000 (first entry)  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 3312.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3312.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
PN 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
PF 25-FEB-2000; 2000EP-00301439.  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.



PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 24-JUN-1999; 99US-0140354P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
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PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 20-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
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PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.

PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
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PR 18-OCT-1999; 99US-0160741P.  
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PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
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PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 5.2%; Score 137; DB 3; Length 429;  
Best Local Similarity 19.6%; Pred. No. 0.002;  
Matches 99; Conservative 86; Mismatches 185; Indels 136; Gaps 24;

QY 33 ALLEKVFQYIDLH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQ 86  
Db 2 SLRLLLVVVVLHLSAVAGDDAIVSRFQEYLRI--NTVQNPPEYKAVDFIIS----- 52

QY 87 RLGARVASVDMGPPQQLPDGQSLPIPPVILAELGSDPTKGTVCYGHLDVQPADRGDWLT 146  
Db 53 --QAKPLSLESQTIEFVGK-----PLLLKXWVGSDDPTLPAFLNLSHTDVVPFE-DSKWT 105

QY 147 DPVYLTEVD--GKLYGRGATDNKGPVLAWINAV-----SAFRALEQDLPNVNIKFIIEGME 199  
Db 106 HP-LQAHMDRHGDIYARGSQDMKCVGMQYLEAIRKLOASGFKPLRS---VYLSFVPD-EE 160

QY 200 EAGSVALEELVEKEKDRFFSGVDY-IVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQ 258  
Db 161 IGHGDGAEKFABSQ---LFKSLNIAIVLDEGLPSPTESYRVFYGER--SPWWLVIKAKGP 215

QY 259 DFHSGTFFGGILHEPMAIDLVALGLSLVDSSGHILVPGIYDEVVPLTETEEINTYKAIHLDLE 318  
Db 216 PGH----GAKLYDNSA-MENLLKSI-----ESIRRFRAEQFDL- 248

QY 319 EYRNSRVEKEFLDFTKEEILMHLWRYPSLSIHGI-EG-----APDEPGTKT----- 363  
Db 249 -----LKAGGIAEGDVVSVMNAFLKAGTPSPPTGFVMN 280

QY 364 VIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFS-----KRNSSNKWVVSMTL 413  
Db 281 LQPSAEAGFDIRVPP-----SVDEALERLVEEWAPAAARNMPFEFKQLTGKQFLTAAD 335

QY 414 GLHPWIANIDTQYLAAKRAIR-TVFGTEPDMIRDGSTIPIAKMFOEIVHKSVLIPLGA 472  
Db 336 DSNPWWGLENNAVKEAGGRTSKPEIFPASTD-----ARYFRKAGVPAGFSPISN 385

QY 473 VDDGEHSQNEKINRWNYIEGTKLFAA 498  
Db 386 TPSLLHDHNEYLKAEYLGKIEVYVS 411

RESULT 165  
ABU40289  
ID ABU40289 standard; protein; 576 AA.

XX ABU40289;  
XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #25816.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Pseudomonas putida.  
XX WO200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
XX 06-SEP-2001; 2001US-00948993.  
XX 25-OCT-2001; 2001US-0342923P.  
XX 08-FEB-2002; 2002US-00072851.  
XX 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX N-PSDB; ACA44159.

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
PS Claim 25; SEQ ID NO 68213; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 576 AA;

Query Match 5.2%; Score 137; DB 6; Length 576;  
Best Local Similarity 25.4%; Pred. No. 0.0031;

Matches	52;	Conservative	34;	Mismatches	79;	Indels	40;	Gaps	9
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QY	51	QTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTL-QRLGARVASVDMGPQQLPDGQSLP	109
Db	104	ETLRELVAIPTFNVEGTPQYENPEFLKIADKIKALADRFGLAFRNIDNRVVEI-----	156
QY	110	IPPVILAEIGSDPTKGTVCFCYGHLDVQPAD-----RGDGWLTDPYVLTEVDGKLYGRGAT	164
Db	157	-----SLGSG--KEVIGIHADVVVVPNDWNKADGTRLDPEKVTLVGDRMYGRGTE	207
QY	165	DNKGPVLAWINAVSAFRALEQDLPV--NIKFIIEGMEEBAGSVALEELVEKEKDRFFSGVD	222
Db	208	DDKNGIVVAMYALKV--AKDENLPLARQFKLLIDTTETSGDAIPYYFFERNPT-----PD	260
QY	223	YIVISDNLWISQRKPAIT-----YGT	243
Db	261	Y-----NLALDGGYPVIVIAEKG YGT	280

  

RESULT	166
ABP40280	
ID	ABP40280 standard; protein; 446 AA.
XX	
AC	ABP40280;
XX	
DT	24-JUL-2002 (first entry)
DE	
XX	Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5125.
KW	Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW	antibacterial; gene therapy.
XX	
OS	Staphylococcus epidermidis.
XX	
PN	US6380370-B1.
XX	
PD	30-APR-2002.
XX	
PF	13-AUG-1998; 98US-00134001.
XX	
PR	14-AUG-1997; 97US-0055779P.
PR	08-NOV-1997; 97US-0064964P.
XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.
XX	
PI	Doucette-Stamm LA, Bush D;
XX	
DR	WPI; 2002-381255/41.
DR	N-PSDB; ABN92825.
XX	
PT	Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT	polypeptide, useful for diagnosing and treating bacterial infections.
XX	
PS	Disclosure; SEQ ID NO 5125; 267pp; English.
XX	
CC	ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC	frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC	given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC	antibacterial activity and can be used in gene therapy. The sequences can
CC	also be used in the diagnosis and treatment of bacterial infections,
CC	particularly S. epidermidis infections. The sequences can be used to
CC	screen for compounds able to interfere with the S. epidermidis life cycle
CC	or inhibit S. epidermidis infection. N.B. The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from the USPTO web site
XX	
SQ	Sequence 446 AA;

  

Query Match	5.2%;	Score	136.5;	DB	5;	Length	446;
Best Local Similarity	23.3%;	Pred.	No.	0.0023;			
Matches	120;	Conservative	57;	Mismatches	181;	Indels	157;
Gaps	30;						

  

QY	58	AIESDS-----VQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSL--	108
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PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 5877; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 190 AA;

Query Match 5.2%; Score 136; DB 4; Length 190;

Best Local Similarity 29.8%; Pred. No. 0.00069;

Matches 57; Conservative 24; Mismatches 68; Indels 42; Gaps 10;

QY 36 EKVFQYIDLHQDEFVQTLKEWVAIES--DSVQ-----PV-PRFQELFRMMAVAADTLQR 87

DB 3 EKVQYQY----EDQIINDLKGLLAIESVRDDAKASEDAPVGPGRKALDYMVEIA-----HR 54

QY 88 LGARVASVDMGPPQLPDGQSLPIPPVILAEKSGDPTKGTVCVFGYHLDVQPADRGDGLTD 147

DB 55 DGFTHDVEDHIAGRIEAGK-----GND-VLGILC---HVDVVPVPA--GDGWDN 96

QY 148 PYVLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPVNIKPIIEGMEEGAGSVALE 207

DB 97 PFEPVVTEDAIARGTLDDKGPTIAAYVAIKILEDMNVWDVKKRIHMIIGTDESD----- 151

QY 208 ELVEKEKDRFF 218

DB 152 ---WKCTDRYF 159

RESULT 168

ADN47750

ID ADN47750 standard; protein; 442 AA.

XX AC ADN47750;

XX 01-JUL-2004 (first entry)

DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1628.

XX gene disruption; gene targeting; marker gene; transformation;  
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;  
KW gene structure; gene function; enzyme activity; medicine;  
KW forensic science; food; drug inspection; molecular biology; immunology.

XX Thermococcus kodakaraensis.

OS WO2004022736-A1.

PN 18-MAR-2004.

PF 29-AUG-2003; 2003WO-IB003597.

XX 30-AUG-2002; 2002JP-00319011.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Imanaka T, Atomi H;

XX WPI; 2004-257583/24.

PT Method for disrupting targeted gene in genome of organism particularly  
PT thermostable bacterium and with genome chips for analysis, applicable in  
PT studying gene structure and functions.

PS Claim 9; SEQ ID NO 1628; 598pp; Japanese.

XX This invention relates to a novel method for targeting disruption of an  
CC arbitrary gene in a genome of an organism which comprises providing the  
CC whole sequential data of the genome of such organism, selecting at least  
CC 1 arbitrary region in the sequence, providing a vector that contains a  
CC sequence homologous with the selected region and a marker gene,  
CC transfection, and homologous recombination. The genome is preferably  
CC the genome of a hyperthermostable archaeobacterium, particularly  
CC Thermococcus kodakaraensis KOD1. The method is for targeting the  
CC disruption of a gene in the genome of an organism, which is applicable in  
CC studying gene structure and functions as well as enzyme activities of  
CC encoded proteins and useful in medicine, forensic science, food or drug  
CC inspection, molecular biology and immunology. With this method, the  
CC disruption of a gene at an arbitrary position in a genome can be achieved  
CC efficiently and reliably. The present sequence is that of a protein  
CC encoded by the genome of Thermococcus kodakaraensis which was derived  
CC using the method of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 442 AA;

Query Match 5.1%; Score 135; DB 8; Length 442;

Best Local Similarity 19.9%; Pred. No. 0.0032;

Matches 88; Conservative 73; Mismatches 168; Indels 114; Gaps 22;

QY 114 ILAELGSDPTKGTVCVFGYHLDVQPADRGDGLTDPPYVLTEVDGKLYGRGATDNKGPVLAW 173

DB 58 VYGEIGEGKPK--LLFMAHFDVVPVNR-EEWETDPFKLTVKGDRAVGRGSADDKG----- 109

QY 174 INAVSAFRAJL---EQDLPVNIKPIIEGMEEG-----SV 204

DB 110 -NVASIMLALKELSKELDKGVLFVFAFTGDEEIGRMAMHIAERLAQEGKLPYMYVNADGI 168

QY 205 ALEELVEKEKDRFFSGVDYIVISDNLWISQ-----RKPAITYGTRGNSYFMVEVKC 255

DB 169 GMKPIIRRRKG---FGVTVRVPSEKTMVKGTIKREIFRIRTPVLE--TRHAAVFLPGV-- 221

QY 256 RDQDFHSGTGG-ILHEPMADLVALLGSLVDSS---GHI-----LVPGIYDEVVPLTEEEI 307

DB 222 ---DTHPLIAASHFLRSREAFVSLGKFLKGNVVPGEVTLTYVVPGEDEV-----EVDV 274

QY 308 NTYKAHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPG 367

DB 275 GLTRLLKAVVPFVRAPIKAEKY-----SDYGVS---ITPNLYSIKDG 313

QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRHLEDV--FSKRNSNKNMNVSMTLG---LHPWIANI 422

DB 314 KHILKFDVRA----MSRLKDEIEQAMREVAEFNLPKAEIEVATNEKAGYLFTHP----- 363

QY 423 DDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGHSQNE 482

DB 364 -EEKIVRVTVLEVLGEELGEKAEPV-EGPGAADSRFFTPYGVKAIDFGPRGG---NIHGPNE 418

QY 483 KINRWNYIEGTKLFAAFFLEMAQ 505

DB 419 YVE-----IDSLRKMPPALYAEAR 437

RESULT 169

AAG43831

ID AAG43831 standard; protein; 341 AA.

XX AAG43831;  
AC  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54830.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
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PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
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PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
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PR 21-MAY-1999; 99US-0135353P.  
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PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
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PR 18-JUN-1999; 99US-0139460P.  
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PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
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PR 08-JUL-1999; 99US-0142803P.  
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PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
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PR 19-JUL-1999; 99US-0144333P.  
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PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.

PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 5.1%; Score 134.5; DB 3; Length 341;  
Best Local Similarity 21.4%; Pred. No. 0.0024;  
Matches 89; Conservative 59; Mismatches 152; Indels 115; Gaps 21;

QY 132 HLDVQPADRGDWLTDPYVLTEVDG-KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVN 190  
Db 2 HMDVVTAN-PDDWEFDPFSLs-IDGDKLRGRGTTDCLGHVALVTLMKKLGQAKPALKST 59  
QY 191 IKFIIEGMEEAGS---VALEELV-EKEKDRFFSGVDYIVISDNLWI--SQRKPAITYGTR 244  
Db 60 VVAVFIASEENSSIPGVGVDMLVKDKLLDXLKSGPLY-----WIDTADKQPCV--GTG 110  
QY 245 GNSYFMVEVKCR--DQDFHSGTFGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPL 302  
Db 111 G-----MIPWKLQFTGKLFHS-----GLAHKAINAMELAMEGLKEIQAR-----FYRDFPPH 157  
QY 303 TEEENYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTK 362  
Db 158 PQEEV-----YGFATPSTMTKPTQWCYPA-----GGI 183

QY 363 TVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNMVV----- 409  
Db 184 NQIPGECTVSGDVRLTFFYDVKEVITKLEQYVDDINGNIERLETRGVPVSKYVLPDENLRG 243  
QY 410 SMTLGLHPWIA---NIDDTQYLAAKRAIRTVFG-TEPDMIRDGSTIPIAKMFQEI VHKS 464  
Db 244 RLTLSFDEASAGVACNLDSPGFHVLCCKATEEVVGHVKPYSIT--GTLPLIRDLQ----- 295  
QY 465 VVLPLGAVDDG-----EHSQNEKINRWNYIEGTKLFAAFFLEMAQL 506  
Db 296 -----DEGFDVQTSGYGLMATYHAKNEYCLLTDMCQGFDFVIRIISQLEQV 341

RESULT 170  
ADS21973  
ID ADS21973 standard; protein; 391 AA.

XX ADS21973;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #11006.

XX KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX OS Bacteria.  
XX PN US2003233675-A1.

XX PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 11006; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of







QY 77 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS DPTKGTVC FYGHLDVQ 136  
Db 64 ML-----ASIGQ-----AGLLLAGHTDTV 84  
QY 137 PADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 196  
Db 85 PFDDG-RWTRDPFTLT EHDGKLYGLGTADMKG-FFAFI--LDALRDVDVT KLKPLYLILA 140  
QY 197 GMEEAGSVALEELVEKEKDRFFSGV-----DYIVISDNLMWISQRKPAITYGTRGN-SYFM 250  
Db 141 TADEETSMA-----GARYFAET TALRPDCAIIGE-----PTSLQPVRAHKGHS 184  
QY 251 VEVKCRDQDFHSGT FGGILHEPMA DLVALLGSLVDSSGHILVPGIYDEVVPLTBE EINTY 310  
Db 185 NAIRIQQSGHSS-----DP-ARGVNAIELMHDAIGHIL--QLRDNLKERYHVEAFTV 234  
QY 311 KAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDE-----PGT 361  
Db 235 PYPTLNLGHIHGGDASNRICACC--ELHMDIRPLPGMTLNELNGLNDALAPVSRWPGR 292  
QY 362 KTV-----IPGRVIGKFSIRLVP-HMNVSAVEK 388  
Db 293 LTVDELHPPPIPG-----YECPPNHQLVEVVEK 319

RESULT 174  
ADK13774  
ID ADK13774 standard; protein; 383 AA.

XX ADK13774;  
AC ADK13774;  
XX ADK13774;  
DT 20-MAY-2004 (first entry)  
XX  
DE E. coli iron transport and metabolism protein SEQ ID NO:69.

XX Escherichia coli.  
OS Escherichia coli.  
XX WO2004018638-A2.

PN WO2004018638-A2.  
XX  
XX 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-US026488.

XX  
PR 21-AUG-2002; 2002US-0405331P.  
XX  
PA (MINU ) UNIV MINNESOTA.  
PA (KAPU/) KAPUR V.  
PA (GADG/) GADGIL M.

XX Kapur V, Gadgil M;  
PI WPI; 2004-238974/22.  
XX N-PSDB; ADK13710.  
DR  
DR  
XX New isolated and purified iron transport and metabolism polypeptides and  
PT encoding polynucleotides, useful in identifying potential targets for  
PT agents against pathogenic bacteria.  
XX  
PS Claim 1; SEQ ID NO 69; 185pp; English.  
XX

CC The present sequence represents an Escherichia coli iron transport and  
CC metabolism protein. Also described: (1) an isolated and purified  
CC polynucleotide comprising a nucleic acid sequence encoding an Escherichia  
CC coli iron transport and metabolism protein; and (2) an expression  
CC cassette comprising a nucleic acid sequence encoding a promoter operably  
CC linked to at least one of the polynucleotide sequences of (1). The  
CC Escherichia coli iron transport and metabolism proteins have  
CC antibacterial activity. The methods and compositions of the present  
CC invention are useful in identifying genes and proteins involved in  
CC bacterial iron transport and metabolism, and using such as potential

CC targets for agents against pathogenic bacteria.  
XX  
SQ Sequence 383 AA;  
Query Match 5.0%; Score 132; DB 8; Length 383;  
Best Local Similarity 22.3%; Pred. No. 0.0048;  
Matches 88; Conservative 49; Mismatches 143; Indels 114; Gaps 21;

QY 22 RGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVA-----IESDSVQVPRFRQELFR 76  
Db 13 RALIATPS-----ISATEEALDQSNADLITLLADWFKDLGFNVE---VQPVPGTRNK-FN 63  
QY 77 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS DPTKGTVC FYGHLDVQ 136  
Db 64 ML-----ASIGQ-----AGLLLAGHTDTV 84

QY 137 PADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 196  
Db 85 PFDDG-RWTRDPFTLT EHDGKLYGLGTADMKG-FFAFI--LDALRDVDVT KLKPLYLILA 140  
QY 197 GMEEAGSVALEELVEKEKDRFFSGV-----DYIVISDNLMWISQRKPAITYGTRGN-SYFM 250  
Db 141 TADEETSMA-----GARYFAET TALRPDCAIIGE-----PTSLQPVRAHKGHS 184

QY 251 VEVKCRDQDFHSGT FGGILHEPMA DLVALLGSLVDSSGHILVPGIYDEVVPLTBE EINTY 310  
Db 185 NAIRIQQSGHSS-----DP-ARGVNAIELMHDAIGHIL--QLRDNLKERYHVEAFTV 234

QY 311 KAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDE-----PGT 361  
Db 235 PYPTLNLGHIHGGDASNRICACC--ELHMDIRPLPGMTLNELNGLNDALAPVSRWPGR 292

QY 362 KTV-----IPGRVIGKFSIRLVP-HMNVSAVEK 388  
Db 293 LTVDELHPPPIPG-----YECPPNHQLVEVVEK 319

RESULT 175  
AAU72909  
ID AAU72909 standard; protein; 473 AA.  
XX AAU72909;  
AC AAU72909;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Human metalloprotease partial protein sequence #21.

XX Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;  
KW vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;  
KW hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;  
KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;  
KW metalloprotease; serine protease; cancer; haematopoietic; breast; colon;  
KW lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain;  
KW immune-related disease; cardiovascular disease; neuronal disease;  
KW migraine; sexual dysfunction; mood disorder; attention disorder;  
KW cognition disorder; hypotension; hypertension; psychotic disorder;  
KW dyskinesia; metabolic disorder; inflammatory disorder.

XX Homo sapiens.  
OS  
XX WO200183782-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 04-MAY-2001; 2001WO-US014431.  
XX  
PR 04-MAY-2000; 2000US-0201879P.  
XX  
PA (SUGE-) SUGEN INC.

XX Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;  
PI Payne V;  
XX













SQ	Sequence 258 AA;	
	Query Match	4.9%; Score 128.5; DB 7; Length 258;
	Best Local Similarity	26.0%; Pred. No. 0.0055;
	Matches	45; Conservative 32; Mismatches 69; Indels 27; Gaps 6;
QY	44 LHQDEFVQTLKEWVAIES--DSVQVPFRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ 101	
Db	34 MEKSEKISILQDVKIKSVNGNEBEVAIYLQNLLKKYIPELSLV-----SY 79	
QY	102 LPDGQSLPIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTVEVDGKLYGR 161	
Db	80 APNRSSL-----VAYLGENREK-VLGFSGHMDVVSEGDESQWTFPPFAAHIEGNKLYGR 132	
QY	162 GATDNKGPVLAWINAVSAFRALEQDLPVN--IKFIIEGMEEAGSVALEELVEK 212	
Db	133 GATDMKSLVAMVLAMIELK--EKKVPLNGAVKFLGTVGEEVGELGAGQLTEK 183	
RESULT 182		
ADN46443		
ID	ADN46443 standard; protein; 372 AA.	
XX		
AC	ADN46443;	
XX		
DT	01-JUL-2004 (first entry)	
XX		
DE	Thermococcus kodakaraensis KOD1 protein sequence SeqID321.	
XX	gene disruption; gene targeting; marker gene; transformation;	
KW	homologous recombination; hyperthermostable archaeobacterium; KOD1;	
KW	gene structure; gene function; enzyme activity; medicine;	
KW	forensic science; food; drug inspection; molecular biology; immunology.	
XX		
OS	Thermococcus kodakaraensis.	
XX		
PN	WO2004022736-A1.	
XX		
PD	18-MAR-2004.	
XX		
PF	29-AUG-2003; 2003WO-IB003597.	
XX		
PR	30-AUG-2002; 2002JP-00319011.	
XX		
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.	
XX		
PI	Imanaka T, Atomi H;	
XX		
DR	WPI; 2004-257583/24.	
XX		
PT	Method for disrupting targeted gene in genome of organism particularly	
PT	thermostable bacterium and with genome chips for analysis, applicable in	
PT	studying gene structure and functions.	
XX		
PS	Claim 9; SEQ ID NO 321; 598pp; Japanese.	
XX		
CC	This invention relates to a novel method for targeting disruption of an	
CC	arbitrary gene in a genome of an organism which comprises providing the	
CC	whole sequential data of the genome of such organism, selecting at least	
CC	1 arbitrary region in the sequence, providing a vector that contains a	
CC	sequence homologous with the selected region and a marker gene,	
CC	transformation, and homologous recombination. The genome is preferably	
CC	the genome of a hyperthermostable archaeobacterium, particularly	
CC	Thermococcus kodakaraensis KOD1. The method is for targeting the	
CC	disruption of a gene in the genome of an organism, which is applicable in	
CC	studying gene structure and functions as well as enzyme activities of	
CC	encoded proteins and useful in medicine, forensic science, food or drug	
CC	inspection, molecular biology and immunology. With this method, the	
CC	disruption of a gene at an arbitrary position in a genome can be achieved	
CC	efficiently and reliably. The present sequence is that of a protein	
CC	encoded by the genome of Thermococcus kodakaraensis which was derived	
CC	using the method of the invention. Note: The sequence data for this	
CC	patent did not form part of the printed specification, but was obtained	

CC	in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 372 AA;	
	Query Match	4.9%; Score 128.5; DB 8; Length 372;
	Best Local Similarity	22.9%; Pred. No. 0.0098;
	Matches	84; Conservative 57; Mismatches 141; Indels 85; Gaps 19;
QY	47 DEFVQTLKEWVAIESDSVQVPFRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQ 106	
Db	2 DEF-ELLKRLVSIKSP-----FGEE-----HEISEFIAS-----LLEEN 34	
QY	107 SLPIPPVILAEELGSDPT-----KG-TVCFYGHLDVQPADRGDWLTDPYVLTVEVDG-KLY 159	
Db	35 GIPVETVPVEGFGDDVVAYLKGKGTVVVLNGHMDT--VHLSQGWTKNPW--GELDGDRFY 90	
QY	160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFS 219	
Db	91 GLGSADMKGGLAALLSAFLELSELPKNERPNVIFTAVSDEEGFSRGSWELIKSGR---LD 147	
QY	220 GVDYIVISDNLWISQRKPAITYGTRGNSYFVVEVKCRDQDFHSGT--FGGILHEPMDLV 277	
Db	148 KADLVLVGE-----PTNEKIMLGARGR--FVIEVGAKGKKAHAARPYLGINAIEELAKLV 200	
QY	278 ALLGSLVDSSGHILVPGIY-----DEVVPLTEEEINTYKAHLDLEE--- 319	
Db	201 SNLNRIRMKKHPKLGKSYCTLYFSGSADGLSVDPDEAIAI----IDRHVVVGDEWEKVRG 256	
QY	320 --YRNSSRV-----EKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTV--IPG 367	
Db	257 ELYRLAERVGVRAELEIEKYRRPT-PEMLPYVVKENNRFRVRRFKEAYREVERKSVEITYG 315	
QY	368 RVIGKFS 374	
Db	316 ASVGDFN 322	
RESULT 183		
ABU92042		
ID	ABU92042 standard; protein; 361 AA.	
XX		
AC	ABU92042;	
XX		
DT	15-JUL-2003 (first entry)	
XX		
DE	Human protein modification and maintenance molecule-22 (PMMM-22).	
XX	Human; protein modification and maintenance molecule; PMMM; cancer;	
KW	cell proliferation disorder; atherosclerosis; neurological disorder;	
KW	epilepsy; Huntington's disease; stroke; immune disorder; allergy;	
KW	inflammatory disorder; AIDS; developmental disorder; hypothyroidism;	
KW	Cushing's syndrome; gastrointestinal disorder; epithelial disorder;	
KW	infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;	
KW	neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnery;	
KW	antiinflammatory; thyromimetic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003031939-A2.	
XX		
PD	17-APR-2003.	
XX		
PF	11-OCT-2002; 2002WO-US032850.	
XX		
PR	12-OCT-2001; 2001US-0329689P.	
PR	25-OCT-2001; 2001US-0335703P.	
PR	09-NOV-2001; 2001US-0348887P.	
PR	28-NOV-2001; 2001US-0334145P.	
PR	06-DEC-2001; 2001US-0337451P.	
PR	14-DEC-2001; 2001US-0340584P.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA		

XX Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY;  
PI Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;  
PI Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue H;  
PI Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;  
PI Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;  
XX WPI; 2003-430274/40.  
DR N-PSDB; ACA92437.

XX New human protein modification and maintenance molecules (PMMM), useful  
PT for diagnosing, treating and preventing diseases or conditions associated  
PT with the aberrant PMMM expression e.g. cancer, atherosclerosis, or  
PT infections.

XX Claim 1; Page 262; 311pp; English.

XX The present invention relates to the isolation of human protein  
CC modification and maintenance molecules (PMMM), and the polynucleotide  
CC sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM  
CC -1 to PMMM-40) are disclosed. The sequences of the invention are useful  
CC for diagnosing a condition or disease associated with the expression of  
CC PMMM in a subject, preparing a polyclonal or monoclonal antibody, and  
CC generating an expression profile of a sample containing the  
CC polynucleotides. The diseases or conditions associated with decreased  
CC expression or overexpression of PMMM are cell proliferation disorders  
CC (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,  
CC Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS,  
CC allergies), developmental disorders (e.g. hypothyroidism, Cushing's  
CC syndrome), gastrointestinal disorders (e.g. hypothyroidism, and infections. The  
CC PMMM polypeptides or their fragments are useful in screening compounds  
CC for effectiveness as agonists or antagonists of the polypeptides, or in  
CC altering the expression of the target polynucleotide and compounds that  
CC specifically bind to, or modulate the activity of the polypeptide.  
CC ABU92021-ABU92060 represent the human PMMM polypeptides of the invention

XX Sequence 361 AA;

Query Match 4.9%; Score 127.5; DB 6; Length 361;  
Best Local Similarity 25.9%; Pred. No. 0.012;  
Matches 53; Conservative 32; Mismatches 89; Indels 31; Gaps 9;

QY 119 GSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTETVDGKLYGRGATDNKGPVLAWINAVS 178  
DB 112 GSDPSLQPYLLMAHFDVVPAPPE-EGWEVPPFSGLELDGVIYGRGTLDKNSVMALLQALE 170  
QY 179 AFRALQDLPVNIKFIIEGMEE---AGSVALEELVEKEKDRFFSGVD--YIV-----IS 227  
DB 171 LL-LIRKIYIPRRSFFISLGHDESSGTGAQRISALLQSR-----GVQLAFIVDEGGFIL 223  
QY 228 DNLWISQRKP--AITYTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVD 285  
DB 224 DDFIPNFKKPIALIAVSEKGSNMMLQVNM-----TSGHSSAPPKETSIGILAAAVS 275  
QY 286 SSGHILVPGIYDE--VVPLTEEEIN 308  
DB 276 RLEQTPMPIIFGSGTVTVLQQLAN 300

RESULT 184

ABM83692  
ID ABM83692 standard; protein; 372 AA.  
XX  
AC ABM83692;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3941.  
XX  
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX  
OS Homo sapiens.  
XX

PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
XX  
PR 12-SEP-2002; 2002US-0410259P.  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
PA (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RS, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.  
DR N-PSDB; ACN42344.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 372 AA;

Query Match 4.8%; Score 127; DB 8; Length 372;  
Best Local Similarity 17.8%; Pred. No. 0.013;  
Matches 85; Conservative 86; Mismatches 161; Indels 146; Gaps 22;

QY 50 VQTLKEWVAIESDSVQVPFRERQELFRMMAVAADTLQRLGARVASVDMGQQQLPDGQSLP 109  
DB 13 VTLFRQYLRIR--TVQPKPDYG---AAVAFFEETARQLGLGCQKVEVAPGVV----- 59  
QY 110 IPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLTDPY-VLTEVDGKLYGRGATDNKG 168  
DB 60 --VTVLTWPGTNPRTLSSILLNSHTDVVPVFK-EHWSHDPFEAFKDSGVIYARGAQDMKC 116  
QY 169 PVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD 228  
DB 117 VSIQYLEAVRRLK-----VEG-----HRFPRTIHMFTVFXD 146

QY 229 --NLWISQRKPAITYTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVA-LLGSLVD 285  
DB 147 AFTVIFYSERSP-----WWVRVTSTGRPGHASRF-----MEDTAAEKLHKVNV 188  
QY 286 SSGHILVPGIYDEVVPLTEEEINTYKA-IHLDLEEYRNSRVEKFLFDTKKEILMHLWRY 344  
DB 189 S-----ILAFREKEWQRLQSNPHL-----KEGSV----- 212



Qy 345 PSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV----- 397  
Db 213 TSVNLTKLEGGV-----AYNVIPATMSASFDFRVPADVDFKAFEEQLQSWCQAAGEGVILE 268  
Qy 398 FSKRNSNKMVWSMTLGLHPWIANIDDTQ--YLAAKRAIRTVFGT-EPDMI-----RDG 448  
Db 269 FAQK-----WMHPQVTPTDSDSNPWWAASF RVCKDMNLTLEPEIMPAATDNRYI 316  
Qy 449 STIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEG TKLFAAFFLEMAQL 506  
Db 317 RAVGVPALGFSPMNRTPVLL-----HDHDERLHEAVFLRGVDIYTCLLPALASV 365

RESULT 185  
ABM83691  
ID ABM83691 standard; protein; 378 AA.  
XX  
AC ABM83691;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3940.  
XX  
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004023973-A2.  
PN  
XX  
PD 25-MAR-2004.  
XX  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
XX  
XX  
PR 12-SEP-2002; 2002US-0410259P.  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;  
XX  
DR WPI; 2004-329368/30.  
DR N-PSDB; ACN42343.  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 378 AA;  
SQ  
Query Match 4.8%; Score 127; DB 8; Length 378;  
Best Local Similarity 17.6%; Pred. No. 0.014;  
Matches 84; Conservative 89; Mismatches 167; Indels 136; Gaps 21;  
Qy 50 VQTLKEWVAIESDVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPFQQLPDGQSLP 109  
Db 13 VTLFRQYLRI--TVQPKPDYG---AAVAFFEETARQLGLGCQKVEVAPGYV----- 59  
Qy 110 IPPVILAELGSDPTKGTVCYFYGHLDVQPADRGDGLWLTDPY-VLTEVDGKLYGRGATDNKG 168  
Db 60 --VTVLTPGNTPTLSSILLNSHTDVVPVFK-EHWSHDPF EAFK DSEGYIYARGAQDMKC 116  
Qy 169 PVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD 228  
Db 117 VSIQYLEAVRRLK-----VEGHRFPRTIHM-----TFVPGIANPTDAF 154  
Qy 229 NLWISQRPKITTYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVA-LLGSLVDSS 287  
Db 155 TVFYSERSP-----WWVRVTSTGRPGHASRF-----MEDTAAEKLHKVVNS- 195  
Qy 288 GHILVPGIYDEVVPLTEEBEINTYKA-IHLDLEBYRNSRVEKFLDFTKEEILMHLWRYPS 346  
Db 196 -----ILAFREKEQWRLQSNPHL-----KEGSV-----TS 220  
Qy 347 LSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV-----FS 399  
Db 221 VNLTKLEGGV---AYNVIPATMSASFDFRVPADVDFKAFEEQLQSWCQAAGEGVILEFA 276  
Qy 400 KRNSSNKMVWSMTLGLHPWIANIDDTQ--YLAAKRAIRTVFGT-EPDMI-----RDGST 450  
Db 277 QK-----WMHPQVTPTDSDSNPWWAASF RVCKDMNLTLEPEIMPAATDNRYIRA 324  
Qy 451 IPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEG TKLFAAFFLEMAQL 506  
Db 325 VGVPALGFSPMNRTPVLL-----HDHDERLHEAVFLRGVDIYTCLLPALASV 371

RESULT 186  
AAG43832  
ID AAG43832 standard; protein; 339 AA.  
XX  
AC AAG43832;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54831.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
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PR 14-MAY-1999; 99US-0134370P.  
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PR 21-MAY-1999; 99US-0135353P.  
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PR 27-MAY-1999; 99US-0136392P.  
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PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
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PR 08-JUN-1999; 99US-0138094P.  
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PR 27-JUL-1999; 99US-0145913P.  
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PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
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PR 09-AUG-1999; 99US-0147493P.  
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PR 11-AUG-1999; 99US-0148319P.  
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PR 13-AUG-1999; 99US-0148565P.  
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PR 23-AUG-1999; 99US-0149930P.  
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PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.

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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
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PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.8%; Score 126.5; DB 3; Length 339;
Best Local Similarity 21.3%; Pred. No. 0.013;
Matches 88; Conservative 59; Mismatches 152; Indels 115; Gaps 21;

QY 133 LDVQPADRGWLTDPYVLTEVDG-KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191
Db 1 MDVVVTAN-PDDWEFDPFSLs-IDGDKLRGRGTTDCLGHVALVTLMKKLGOAKPALKSTV 58

QY 192 KFIIEGMEEAGS---VALEELV-EKEKDRFFSGVDYIVISDNLWI--SQRKPAITYGTRG 245
Db 59 VAVFIASEENSIPGVGVMDLVKDKLDKLSGPLY-----WIDTADKQPCV--GTGG 109

QY 246 NSYFMVEVKR--DQDFHSGTFGGIILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLT 303
Db 110 ---MIPWKLQFTGKLFHS---GLAHKAINAMELAMEGLKEIQAR-----FYRDFPPHP 156

QY 304 EEEINTYKAHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKT 363
Db 157 QEEV-----YGFATPSTMKPTQWCYPA-----GGIN 182

QY 364 VIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSNKMVV-----S 410
Db 183 QIPGECTVSGVRLTPFYDVKEVITKQLQEVDDINGNIERLETRGFSKYLVDENLRGR 242

QY 411 MTLGLHPWIA-----NIDDTQYLAAKRAIRTVFG-TEPDMIRDGSTIPIAKMFOEIVHKS 465
Db 243 LTLSFDEASAGVACNLDSPGFHVLCATEEVVGHVKPYSIT--GILPLRDLQ----- 293

QY 466 VLIPLGAVDDG-----EHSQNEKINRWNYIEGTKLFAAFFLEMAQL 506
Db 294 -----DEGFDVQTSQGYGLMATYHAKNEYCLLTDMCQGFDFVIRIISQLEQV 339

RESULT 187
ABU51393
ID ABU51393 standard; protein; 203 AA.
XX
AC ABU51393;
XX
DT 07-MAY-2003 (first entry)
XX
DE Helicobacter pylori selected interacting domain (SID) protein #737.
XX
KW Protein-protein interaction; ulcer; selected interacting domain; SID.
XX
OS Helicobacter pylori.
PN WO200266501-A2.
XX
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PD 29-AUG-2002.
XX
PF 28-DEC-2001; 2001WO-EP015428.
XX
PR 02-JAN-2001; 2001US-0259302P.
XX
PA (HYBR-) HYBRIGENICS.
PA (INSP ) INST PASTEUR.
XX
PI Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX
DR WPI; 2002-674910/72.
DR N-PSDB; ABX66138.
XX
PT New complexes of protein-protein interactions in Helicobacter pylori,
PT useful for identifying modulating compounds for treating or preventing
PT ulcers in mammals.
XX
PS Claim 6; Page 265; 642pp; English.
XX
CC The invention describes a complex of protein-protein interactions in
CC Helicobacter pylori selected from 421 complexes given in the
CC specification. The complex of protein-protein interactions are useful for
CC screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This is the
CC amino acid sequence of a selected interacting domain (SID), identified
CC via protein-protein interactions. Note: Where the patent number printed
CC at the top of the pages in the specification has obscured areas of
CC protein sequence, the indexer has replaced the residue with an X to
CC represent an illegible residue
XX
SQ Sequence 203 AA;

Query Match 4.8%; Score 126; DB 5; Length 203;
Best Local Similarity 36.3%; Pred. No. 0.0065;
Matches 33; Conservative 14; Mismatches 34; Indels 10; Gaps 3;

QY 128 CFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL 187
Db 16 CFAGHIDVVP--GNHWQSDPFKPKVIKEGFLYGRGAQDMKGGVGAFLSASLNF---NPKT 70

QY 188 PVNIKFIIIEGMEEAGSV-----ALEELVEKE 213
Db 71 PFLLSILLTSDEEGPGIFGTRLMLEKLEKD 101

RESULT 188
ADP43682
ID ADP43682 standard; protein; 373 AA.
XX
AC ADP43682;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PMMM-39 protein SEQ ID NO:39.
XX
KW human; protein modification and maintenance molecule; PMMM;
KW gastrointestinal; cardiovascular; immunosuppressive; antiinflammatory;
KW cytostatic; neuroprotective; gynaecological; gene therapy;
KW gastrointestinal disorder; cardiovascular disorder; autoimmune disorder;
KW inflammatory disorder; cell proliferative disorder;
KW developmental disorder; epithelial disorder; neurological disorder;
KW reproductive disorder.
XX
OS Homo sapiens.
XX
PN WO2004053068-A2.
XX
PD 24-JUN-2004.
XX
PF 03-DEC-2003; 2003WO-US038573.
XX
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CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present  
CC for SEQ ID NO:4455 to 4464  
XX  
SQ Sequence 418 AA;  
Query Match 4.8%; Score 126; DB 4; Length 418;  
Best Local Similarity 24.8%; Pred. No. 0.02;  
Matches 67; Conservative 31; Mismatches 98; Indels 74; Gaps 13;  
QY 100 QQLPDGOSLPPIPPVILAEI-GSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKL 158  
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QY 159 YRGATDNKGPVLAWINAVSAFRALEQDLVPVNIKFIIIEGMEAEAGSVALEELVEKEKDRFF 218  
Db 105 YGRGVSDMKG-----GMSSLFYVLEQ-----LHQEGORPEGDIIVQSVVGEEVGE-- 149  
QY 219 SGV-----DYIVISDNLWISQKPAITYGTRGNSYFMEVK-----CRDQDFHS 262  
Db 150 AGTKRACEIGPKGDLALVLD-----TSENQALQGQGVITGWITVKSNTIHDGARSQTIHA 205  
QY 263 --GTFGGILHEPMADLVALGSL-----VDSSGHILVPG-----IYDE 298  
Db 206 GGGFLGASAIETKTKVIOQSLNELERHVAVMKSPGMPPGANTINPAVIEGGRHPAFIAD 265  
QY 299 -----VVPLTETEEINTYKAHLDLEEYRN 322  
Db 266 CRLWITVHYLPNE---SYESVNVNEIEQYLN 292  
RESULT 190  
AAU33879  
ID AAU33879 standard; protein; 449 AA.  
XX  
AC AAU33879;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Staphylococcus aureus cellular proliferation protein #155.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US0009180.  
XX  
PR 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS51738.  
XX  
PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 5375; 511pp; English.  
XX

CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 449 AA;  
Query Match 4.8%; Score 126; DB 4; Length 449;  
Best Local Similarity 21.7%; Pred. No. 0.022;  
Matches 117; Conservative 63; Mismatches 167; Indels 192; Gaps 30;  
QY 53 LKEWVAIES--DSVQ-----PV-PRFRQELFRMMAVAADTLQRLGARVASVDMGPQLPD 104  
Db 1 LKGLLAIESVRDDAKASEDAPVGPGRKALDYMEIA---HRDGFTHDVEDIARGT 56  
QY 105 QOSLPPIPPVILAEI-GSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYRGAT 164  
Db 57 GK-----GND-VLGILC---HVDVVPA--GDGWDSPFEPVVTEDAIARGTL 98  
QY 165 DNKGPVLAWINAVSAFRALEQDLVPVNIKFIIIEGMEAEAGSVALEELVEKEKDRFFSGVDYI 224  
Db 99 DDKGPTIAAYAIKILEDMNVWDKKRIHMIIGTDESD-----WKCTDRYFK----- 145  
QY 225 VISDNLWISQKPAI-----TYGTRGNSYF-MVEVK-CRDQD-----FHSQT 264  
Db 146 -----TEEMPTLGFAPDAEFPPIHGEKGITTFDLVQNKLTEDQDEPDYELTFKSGE 197  
QY 265 FGG-----ILHEPNADLVA-----LLG-SLVDSSGHILVPGIYDEVVPLT 303  
Db 198 RYNMVPDHAEARVLVKENMTDVIQDFEYFLEQNHLOQDSTVDSG--ILLVLTVEGKAVHGM 255  
QY 304 EEEINTYKAH-----LDLEEYR-----NSSRVE---KFLFDTKEEILMH 340  
Db 256 DPSIGVNAGLYLLKFLASLNLDNNAQAFVAFSNRYLFNSDFGEKMGKMFHTDVMGDTV 315  
QY 341 L-----WRYPSLSIHGIEGAFDEPGTKTIVPGRVIGKFSIRL----VPH 380  
Db 316 IGVTYDYNENAGLFGINLRP---EGFE--FEKAMDRFANEIQYQY--FEMKLGKVQPPH 368  
QY 381 ---MNVSAREKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTV 437  
Db 369 YVDKNDPQKLVYAY-----RNQTNMTPEPTIGGGTVARNLD----- 407  
QY 438 FGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGGEHSONEKNRWNYYIEGTKLF 496  
Db 408 -----KGVAFGAMFSD-----SEDLMHQKNEYITKKQLFNATSIY 442  
RESULT 191  
ABB62632  
ID ABB62632 standard; protein; 359 AA.  
XX  
AC ABB62632;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 14688.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;







Db 26 QNITSYIDSHGTEQIALLEKLVNINSGTDNVEGV-----VKVGNLIKPELEALGFETA 78  
QY 94 SVDMPGQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFGHLD-VQPADRGDGNLTDPPVLT 152  
Db 79 WHDL-PSAMNHAGSL-----VAVHDGSKSAK-RILLIGHLDTVFP--QTSRFQTFAY--- 126  
QY 153 EVDG--KLYGRGATDNKGPVLAWINAVSAFR---ALEQDLPVNIKFIIEGMEEAGS---- 203  
Db 127 -LDGGKKAKGPGVIDDKGGVVTMLYALQALKHSGALEK---MNISVVLIIGDELAAPTE 182  
QY 204 VALEELV-EKEKDRFFSGVDYIVISDNLWISQKPAITYGTRG-NSYFMVEVKCRDQDFH 261  
Db 183 ISREWLIAEAKRSDIALGFEP-ALSPNQLITER-----RGLSEWFLTSTGI---DKH 230  
QY 262 SGTG-----GGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 231 SATIFQPETGFGAMYESARVLDEIRQKLSNEQGLTINPGLILGGSTAVEDSASGQGTASG 290  
QY 307 ----INTYKAIHLDEEYRNSSRVEKFLFDTKEEILMHLWRYPSPSLSIHGIEGAFDEPGTK 362  
Db 291 RKTTVARITSVHGD---RFSSDQORASAET-----RMKDIAHPLPQTNSDLKIK 338  
QY 363 TVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLGLHPWIANI 422  
Db 339 AIMP-----VMADRESNR----- 351  
QY 423 DDTQYLAAKRAIR-----TVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIV--LIPLGAVDD 475  
Db 352 ---QLLAAYSQVSDLDGPALESAPSAERGGADI-----SYVNKYVTASLDGLGAWGA 401  
QY 476 GEHSQNEKINRWNYIEGTKLFAAFL 501  
Db 402 GAHSENETIELGSLPVVTKR-AAIFL 426

RESULT 195  
ADL12114  
ID ADL12114 standard; protein; 432 AA.  
XX  
AC ADL12114;  
XX  
DT 06-MAY-2004 (first entry)  
DE Pseudomonas syringae anti-cancer protein #26.  
XX cytosolic; gene therapy; Avr; Hop; cancer.  
KW Pseudomonas syringae; pv tomato DC3000.  
XX  
PN WO2003068930-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 12-FEB-2003; 2003WO-US004450.  
XX  
PR 12-FEB-2002; 2002US-0356408P.  
XX 10-MAY-2002; 2002US-0380185P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
PA (USDA ) US SEC OF AGRIC.  
PA (UYNE-) UNIV NEBRASKA.  
XX (UNIV ) UNIV KANSAS STATE RES FOUND.  
PI Collmer A, Alfano JR, Cartinhour SW, Schneider DJ, Tang X;  
XX WPI; 2003-679632/64.  
DR N-PSDB; ADL12113.  
XX  
PT New nucleic acid molecule, useful for preparing a composition for  
XX treating cancer.  
PS Claim 15; SEQ ID NO 52; 284pp; English.

XX  
CC The invention relates to novel Pseudomonas Avr and Hop genes, a sequence  
CC that hybridizes with these sequences under stringency conditions  
CC comprising a hybridization medium that includes 0.9 x saline sodium  
CC citrate (SSC) buffer at a temperature of 42 deg C. The nucleic acid  
CC molecule is useful for preparing a composition for treating cancer. This  
CC sequence corresponds to one of the proteins of the invention.  
SQ Sequence 432 AA;  
Query Match 4.8%; Score 125.5; DB 7; Length 432;  
Best Local Similarity 22.5%; Pred. No. 0.023;  
Matches 114; Conservative 68; Mismatches 179; Indels 145; Gaps 27;  
QY 36 EKVFQYIDLHQDEFVQTLKEWVAIES--DSVOPVPRFRQELFRMMAVAADTLQRLGARVA 93  
Db 26 QNITSYIDSHGTEQIALLEKLVNINSGTDNVEGV-----VKVGNLIKPELEALGFETA 78  
QY 94 SVDMPGQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFGHLD-VQPADRGDGNLTDPPVLT 152  
Db 79 WHDL-PSAMNHAGSL-----VAVHDGSKSAK-RILLIGHLDTVFP--QTSRFQTFAY--- 126  
QY 153 EVDG--KLYGRGATDNKGPVLAWINAVSAFR---ALEQDLPVNIKFIIEGMEEAGS---- 203  
Db 127 -LDGGKKAKGPGVIDDKGGVVTMLYALQALKHSGALEK---MNISVVLIIGDELAAPTE 182  
QY 204 VALEELV-EKEKDRFFSGVDYIVISDNLWISQKPAITYGTRG-NSYFMVEVKCRDQDFH 261  
Db 183 ISREWLIAEAKRSDIALGFEP-ALSPNQLITER-----RGLSEWFLTSTGI---DKH 230  
QY 262 SGTG-----GGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 231 SATIFQPETGFGAMYESARVLDEIRQKLSNEQGLTINPGLILGGSTAVEDSASGQGTASG 290  
QY 307 ----INTYKAIHLDEEYRNSSRVEKFLFDTKEEILMHLWRYPSPSLSIHGIEGAFDEPGTK 362  
Db 291 RKTTVARITSVHGD---RFSSDQORASAET-----RMKDIAHPLPQTNSDLKIK 338  
QY 363 TVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLGLHPWIANI 422  
Db 339 AIMP-----VMADRESNR----- 351  
QY 423 DDTQYLAAKRAIR-----TVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIV--LIPLGAVDD 475  
Db 352 ---QLLAAYSQVSDLDGPALESAPSAERGGADI-----SYVNKYVTASLDGLGAWGA 401  
QY 476 GEHSQNEKINRWNYIEGTKLFAAFL 501  
Db 402 GAHSENETIELGSLPVVTKR-AAIFL 426  
RESULT 196  
ABB08102  
ID ABB08102 standard; protein; 373 AA.  
XX  
AC ABB08102;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Enzyme similar to human aminoacylase-1 (ACY-1).  
XX  
KW Aminoacylase-1; ACY-1; metalloprotein; cytosolic enzyme; human;  
KW cytosolic; therapeutic; cancer therapy; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN US6387661-B1.  
XX  
PD 14-MAY-2002.  
XX  
PF 23-MAR-2001; 2001US-00814951.  
XX  
PR 23-MAR-2001; 2001US-00814951.

XX PA (PEKE ) PE CORP NY.

XX PI Shao W, Yan C, Di Francesco V, Beasley EM;

XX DR WPI; 2002-478443/51.

XX DR N-PSDB; ABL60776, ABL60777.

XX

PT Isolated nucleic acid molecules encoding enzymes similar to human

PT aminoacylase-1, useful as a drug target and diagnostic marker for cancers

PT e.g. T cell leukemias and ovary, brain or lung cancers.

XX

PS Claim 1; Fig 2A; 43pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule encoding

CC enzymes similar to human aminoacylase-1 (ACY-1) (EC 3.5.1.14) (a

CC metalloprotein cytosolic enzyme). The ACY-1 similar polynucleotide and

CC encoded peptide sequences can be used as models for the development of

CC human therapeutic targets, aid in the identification of therapeutic

CC proteins, and serve as targets for the development of human therapeutic

CC agents that modulate enzyme activity in cells and tissues that express

CC the enzyme. ACY-1 has been found to be expressed in humans in the

CC placenta, T cells from T cell leukemia, ovary, brain, lung and leukocyte,

CC and therefore may be a drug target for cancer therapy and act as a

CC diagnostic marker for these cancers. The present sequence represents an

CC enzyme similar to human aminoacylase-1 (ACY-1)

XX

SQ Sequence 373 AA;

Query Match 4.8%; Score 125; DB 5; Length 373;  
Best Local Similarity 18.0%; Pred. No. 0.021;  
Matches 83; Conservative 74; Mismatches 158; Indels 146; Gaps 19;

QY 84 TLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEIGSDPTKGTVCYFYGHLDVQPADRGDG 143

Db 14 TLFQRQLRIRTVQPKP-----DYGNTPTLSSILLNSHTDVPVFK-EH 55

QY 144 WLTDPY-VLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG 202

Db 56 WSHDPFEAFKDSEGYIYARGAQDMKCVSIQYLEAVRRLKVEGHRFPRTIHTFVPDEEVG 115

QY 203 -----SVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGT 243

Db 116 GHQGMELFVQRPPEFHALRAGFALDEGIANPTDAF-----TVFYSERSP----- 158

QY 244 RGNYSFMVEVKCRDQDFHSGTGGILHEPMDLVA-LLGSLVDSSGHILVPGIYDEVVPL 302

Db 159 -----WWVRVTSTGRPGHASRF-----MEDTAAEKLHKVVNS-----ILAF 194

QY 303 TEEIINTYKA-IHLDLEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGT 361

Db 195 REKEWQRLQSNPHL-----KEGSV-----TSVNLTKLEGGV-----A 226

QY 362 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNKMVVSMTLG 414

Db 227 YNVIPATMSASFDFRVPADVDFKAFEEQLQSWCQAAGEGVTLFEFAQK-----W 274

QY 415 LHPWIANIDDTQ--YLAAKRAIRTVFGT-EPDMI-----RDGSTIPIAKMFQEIHKSV 465

Db 275 MHPQVTPTDSDNPWWAAFSRVCKDMNLTLEPEIMPAATDNRIRAVGVPAFGFSPMNRTP 334

QY 466 VLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQL 506

Db 335 VLL-----HDHDERLHEAVFLRGVDIYTRLLPALASV 366

RESULT 197

ABU07744

ID ABU07744 standard; protein; 373 AA.

XX

AC ABU07744;

XX

DT 23-MAY-2003 (first entry)

XX Human aminoacylase.

DE

XX Human; enzyme; aminoacylase; gene therapy; leukaemia; metalloprotein;

KW EC 3.5.1.14.

XX Homo sapiens.

OS

XX US2002142421-A1.

PN

XX 03-OCT-2002.

PD

XX 01-APR-2002; 2002US-00109860.

PF

XX 23-MAR-2001; 2001US-00814951.

PR

XX (PEKE ) PE CORP NY.

PA

XX Shao W, Yan C, Di Francesco V, Beasley EM;

PI WPI; 2003-328329/31.

XX N-PSDB; ABX93510, ABX93511.

DR

XX New human aminoacylase enzyme peptides, useful for treating, e.g.,

PT leukemia.

PT

XX Claim 1; Fig 2; 42pp; English.

PS

XX The invention relates to an isolated human aminoacylase polypeptide. The

CC polypeptide is useful for preparing a composition for treating a disease

CC or condition mediated by a human enzyme protein by identifying an agent

CC that modulates or binds to the peptide e.g. leukaemia. The present

CC sequence represents the amino acid sequence of human aminoacylase

XX

SQ Sequence 373 AA;

Query Match 4.8%; Score 125; DB 6; Length 373;  
Best Local Similarity 18.0%; Pred. No. 0.021;  
Matches 83; Conservative 74; Mismatches 158; Indels 146; Gaps 19;

QY 84 TLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEIGSDPTKGTVCYFYGHLDVQPADRGDG 143

Db 14 TLFQRQLRIRTVQPKP-----DYGNTPTLSSILLNSHTDVPVFK-EH 55

QY 144 WLTDPY-VLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG 202

Db 56 WSHDPFEAFKDSEGYIYARGAQDMKCVSIQYLEAVRRLKVEGHRFPRTIHTFVPDEEVG 115

QY 203 -----SVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGT 243

Db 116 GHQGMELFVQRPPEFHALRAGFALDEGIANPTDAF-----TVFYSERSP----- 158

QY 244 RGNYSFMVEVKCRDQDFHSGTGGILHEPMDLVA-LLGSLVDSSGHILVPGIYDEVVPL 302

Db 159 -----WWVRVTSTGRPGHASRF-----MEDTAAEKLHKVVNS-----ILAF 194

QY 303 TEEIINTYKA-IHLDLEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGT 361

Db 195 REKEWQRLQSNPHL-----KEGSV-----TSVNLTKLEGGV-----A 226

QY 362 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNKMVVSMTLG 414

Db 227 YNVIPATMSASFDFRVPADVDFKAFEEQLQSWCQAAGEGVTLFEFAQK-----W 274

QY 415 LHPWIANIDDTQ--YLAAKRAIRTVFGT-EPDMI-----RDGSTIPIAKMFQEIHKSV 465

Db 275 MHPQVTPTDSDNPWWAAFSRVCKDMNLTLEPEIMPAATDNRIRAVGVPAFGFSPMNRTP 334

QY 466 VLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQL 506

Db 335 VLL-----HDHDERLHEAVFLRGVDIYTRLLPALASV 366





OS Drosophila melanogaster.  
XX WO200171042-A2.  
PN 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-US009231.  
XX PF 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
DR N-PSDB; ABL06742.  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX Disclosure; SEQ ID NO 14709; 21pp + Sequence Listing; English.  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 401 AA;  
SQ Query Match 4.7%; Score 124.5; DB 4; Length 401;  
Best Local Similarity 19.3%; Pred. No. 0.026;  
Matches 95; Conservative 77; Mismatches 158; Indels 161; Gaps 25;  
QY 72 QELFRMMAVAADT-----LQRLGARVASVDMGPPQL-PDQSLPIPPVILAEELGSDPTKG 125  
Db 16 REYLRIPTVHPDVDYTACVEFLKROASSLNLFVEVVYPAVQTKPV--VLIKWEGSQPELS 73  
QY 126 TVCFYGHLDVQPADRGDGLTDPYVL-TEVDGKLYGRGATDNKGPVLAWINAVSAFRAL- 183  
Db 74 SIVLNSHTDVPVFR-EKWTHEPFSADIDEEGRIFARGTQDMKSVGTQYLGAIRLLKASG 132  
QY 184 --EQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db 133 FKPKRNLYVT---FVPDEETGGHLGMAEFVK-----TDY----- 163  
QY 241 YGTRGNSYFMVEVKCRDQDFH-----SGTFFGILHEPMDLVALLGSLV 284  
Db 164 YKXNNAGFSLDEGATSESDVHHLFYAERLRWGLKLVSGTSG----- 205  
QY 285 DSSGHILVPGIYDEVVPLTEEEINT--YKAHL--DLEEYRNSRVEKFLFD---TKEEI 337  
Db 206 --HGSLLLP-----NTAGVKNLYLVNKLTEFR-TSQVENLARDSSLSKGDV 248  
QY 338 LMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAREKQVTRHLE-- 395  
Db 249 -----TTVNLTLQSGGVQ----SNVVPPLFEAVFDIRIAITVNVVAFEKQIRDWCEEA 297  
QY 396 -----DVFSKRNSNKMVSMTLGLHPWI--ANIDDTQ--YLAAKRAIRTV----- 437  
Db 298 GGGIEIDFFOK-----EPYIGPTKLDNSNPYWLAVKAAIDELGLKVHPIV 342  
QY 438 --FGTEPDMRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGHSQNEKINRWNYIEGTKL 495  
Db 343 CPGATDSRFIREKGTPAIG--FSPINTMTRI-----HHDFFLQADVLYNGIDV 390

QY 496 FAAFFLEMAQL 506  
Db 391 YKKIIRNLAEV 401  
RESULT 200  
ADM26975  
ID ADM26975 standard; protein; 381 AA.  
XX  
AC ADM26975;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Hyperthermophile Methanopyrus kandleri protein #1581.  
XX  
KW hyperthermophile; protein stability enhancement;  
KW protein activity enhancement.  
XX  
OS Methanopyrus kandleri.  
XX  
PN WO2003076575-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 04-MAR-2003; 2003WO-US006664.  
XX  
PR 04-MAR-2002; 2002US-0361742P.  
PR 14-MAY-2002; 2002US-0380423P.  
PR 16-SEP-2002; 2002US-0410974P.  
XX  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
XX  
PI Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;  
XX  
DR WPI; 2003-748383/70.  
DR N-PSDB; ADM27081.  
XX  
PT New isolated nucleic acids encoding any of about 1700 Methanopyrus  
PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
PT as diagnostic agents.  
XX  
PS Claim 31; SEQ ID NO 1581; 1023pp; English.  
XX  
CC The invention comprises the amino acid sequence of proteins from the  
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the  
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
CC proteins of the invention are useful for enhancing the stability and/or  
CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
CC a variety of diagnostic and analytical methods. The present amino acid  
CC sequence represents a Methanopyrus kandleri protein of the invention.  
XX  
SQ Sequence 381 AA;  
Query Match 4.7%; Score 124; DB 7; Length 381;  
Best Local Similarity 22.0%; Pred. No. 0.027;  
Matches 112; Conservative 63; Mismatches 163; Indels 172; Gaps 28;  
QY 31 PPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFQELFRMMAVAADTLQRLGA 90  
Db 5 PSGALQRV--NDLELDP-IGLLKDAVA-----TPSVTGEHEMTRLLTEVLDEHGV 52  
QY 91 RVASVDMGPPQQLPDGQSLPIPPVILAEELGSDPTKGTVCFCYGHLDVQPADRGDW-LTDPY 149  
Db 53 PYEVDMEG-----NVLADLSG-----LVLNAHLDTVPP--GDGWEVTDPF 91  
QY 150 VLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEEL 209  
Db 92 DPTIRNGKLYGRGAADCKGGLAAATAAV--VQGYVEEMPMLLATVG--EESSS----- 141  
QY 210 VEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGIL 269  
Db 142 ---BED---NGTLHV-----CRTRELEAR--AGIV 163





PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 367 AA;

Query Match 4.7%; . Score 123.5; DB 8; Length 367;  
Best Local Similarity 16.8%; Pred. No. 0.028;  
Matches 81; Conservative 79; Mismatches 163; Indels 159; Gaps 18;

QY 50 VQTLKEWAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLP 109  
Db 13 VTLFRQYLRLR--TVQPKPDYG---AAVAFFEETARQLGLGQKVEVAPGYV----- 59  
QY 110 IPPVILAEUGSDPTKGTVCFCYGHLDVQPADRGDGLWLTDPY-VLTEVDGKLYGRGATDNKG 168  
Db 60 --VTVLTPGNTPTLSSILLNSHTDVPVVFKE-EHWSHDPFEAFKDSGGYIYARGAQDMKC 116  
QY 169 PVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD 228  
Db 117 VSIQYLEAVRLKVEGHRFPRTIHTMFTVPDEVG----- 150  
QY 229 NLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA---DLVALLGS--- 282  
Db 151 -----GHQGMELFV-----QRPEFHALRAGFALDEGIANPTDAFTVFYSERS 192  
QY 283 --LVDSGGHILVPGIYDEVVPLTEEEINTYKAIHLDLLEEYRNSRVEKFLFDTKEEILMH 340  
Db 193 PWXLQSNPH-----LKEGSVT----- 208  
QY 341 LWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV--- 397  
Db 209 -----SVNLTKLEGGV---AYNVIPATMSASFDFRVAPDVFKAPEEQLSWCQAAGEG 259  
QY 398 ----FSKRNSNMVVSMTLGLHPWIANIDDTQ--YLAAKRAIRTVFGT-EPDMI----- 445  
Db 260 VTLEFAQK-----WMHPQVTPDDSNPWWAAFSRVCKDNMLTLEPEIMPAATD 307  
QY 446 -RDGSTIPIAKMFQEIIVHKSIVLILPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMA 504  
Db 308 NRYIRAVGVPAFGSPMNRTPVLL-----HDHDERLHEAVFLRGVDIYTCLLPALA 358  
QY 505 QL 506  
Db 359 SV 360

RESULT 203  
ABO65647  
ID ABO65647 standard; protein; 441 AA.

XX ABO65647;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 12164.  
DE  
XX  
KW Recombinant expression vector; transcription regulatory element;  
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.  
XX  
OS Klebsiella pneumoniae.  
XX  
PN US6610836-B1.  
XX  
PD 26-AUG-2003.  
XX  
PF 27-JAN-2000; 2000US-00489039.  
XX  
PR 29-JAN-1999; 99US-0117747P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton GL, Osborne M;  
XX  
XX WPI; 2003-895346/82.  
DR N-PSDB; ACH99198.  
XX  
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
PS Disclosure; SEQ ID NO 12164; 932pp; English.  
XX  
XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention  
XX  
SQ Sequence 441 AA;

Query Match 4.7%; Score 123.5; DB 7; Length 441;  
Best Local Similarity 19.1%; Pred. No. 0.037;  
Matches 95; Conservative 66; Mismatches 173; Indels 163; Gaps 25;

QY 22 RGMFSSPPPPALLEKVFQVIDLHQDEFVQTLKEWVA-----IESDSVQVPVPRFRQELFR 76  
Db 71 RALIATPS-----ISATEEALDQSNESLINLLAGWFRDLGFNVE---IQVP----- 114  
QY 77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEUGSDPTKGTVCFCYGHLDVQ 136  
Db 115 -----DTRHKFN-----LLASTGHG--AGGLLAGHTDTV 142  
QY 137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIE 196  
Db 143 PFDDG-RWTRDPFTLTTEHDNKLGLGTADMKG-----FFA-----FILD 180  
QY 197 GMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 256  
Db 181 ALRD-----VDVTLKKPLYILATADEET-SMAGARYFAETTRLR 219  
QY 257 DQDFHSGTGGILHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTE 304  
Db 220 PD-----CAIIGEPTSLQPIRAHKGHMSNAIRIQG-----QSGHSSDPARGVNAIELMH 268  
QY 305 EEINTYKAIHLDLLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTV 364  
Db 269 DAIGRIMQLR-DLLK-----ERYHFEA-----FTVPYPTNLGAIHG----- 304  
QY 365 IPGRVIGKFSIRLVP---HMNVSAVEKQVTRHLEDVFSKRNS--SNKMVVSMTLG-LHP 417  
Db 305 -----GDASNRICACCELMHDIRPLPGMTLNDLNGLLGEALAPVSRWPGRLLTVSELHP 358  
QY 418 WIANIDDTQYLAAKRAIRTVFGTPEPDMIRDGSTIPIAKMFQEIIVHKSIVLILPLGAVDDGE 477  
Db 359 PIPGYECPDPDKLVQVVEKLLGQAQTDVWNYCTEAP----FQTLCTPLVLGP-GSINQA- 412















QY 441 EPDMIRDGSTIPIA-----KMFQE-----IVHKSVVLIPLGAVDDGE 477  
Db 395 EANIVDDG--VPIAYNETHRRRLSEETYVVFVDTTGLSAVYNTIIELAAVKVDGE 448

RESULT 213  
ADJ79463  
ID ADJ79463 standard; protein; 1433 AA.  
XX  
AC ADJ79463;  
XX

20-MAY-2004 (first entry)  
XX  
DE G. stearothermophilus alpha-large subunit.  
XX  
KW DNA polymerase; DNA sequencing; DNA amplification.  
XX  
OS Geobacillus stearothermophilus.  
XX  
PN US2004043414-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 25-SEP-2003; 2003US-00670844.  
XX  
PR 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX

(ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX

O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
PI  
XX  
DR WPI; 2004-225698/21.  
DR N-PSDB; ADJ79462.  
XX

Novel isolated DNA molecule from Bacillus stearothermophilus, encoding  
PT tau subunit of DNA polymerase III-type enzyme, useful in amplification  
PT and sequencing reactions.  
XX  
PS Disclosure; SEQ ID NO 184; 245pp; English.  
XX

The invention relates to an isolated DNA molecule from Bacillus  
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The  
CC subunits are useful for producing DNA polymerases for use in DNA  
CC sequencing and DNA amplification methods. The present sequence is used in  
XX the exemplification of the present invention.  
SQ Sequence 1433 AA;

Query Match 4.5%; Score 118.5; DB 8; Length 1433;  
Best Local Similarity 18.3%; Pred. No. 0.67;  
Matches 98; Conservative 86; Mismatches 179; Indels 173; Gaps 23;

QY 17 LLLLEGMFESSPPPPALLEKVFQYIDLHQDEFVQTLKEW-VAIESDSVQVPFRF---- 71  
Db 11 LILLEQLKMTSDEWMPHFREAIRKVVIDKEE-----KSWHFFQFDNVLPVHVYKTFAD 65

QY 72 --QELFRMVAADTLQRLGARVASVDMGFPQQLPDGQSLPIPPPVILAEIGSDPTKGTVCF 129  
Db 66 RLQTAFRHIAAVRHTMEVEAPRVTEADVQAYW-----PLCLAEL----- 104

QY 130 YGHLDVQPADRGDWLTDPYVLTEVDGKLYCGRGTNDKGPVLAWINAVSAFRALEQDLPV 189  
Db 105 -----QEGMSPLVDWLSRQT-----PELKG 124

QY 190 NIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDLNLSQRKPAITYCTRGNYSF 249  
Db 125 N-KLLVVARHEAEALAI-----KRRFAKKIADVYASFGFPLQLDVSVEPSKQEMEQQF 176

QY 250 MVEVKCRDQDFHSGTFGGILHE-----PMAD--LVALLGSLVDSSGHI 290  
Db 177 LAQKQEQEDEERALAVLTLAREEKAASAPSGPLVIGYPIRDEEPPVRRLETIVEEERRV 236

QY 291 LVPG-IYDEVVPLTEEEINTYKA---IHLDEEYRNSRVEKFLFDTKKEILMHLWRYP 345  
Db 237 VVQGYVFD-----AEVSELKSGRRTLTMKITDYTNSILVKMFSRDKEDAEML----- 283

QY 346 SLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR-----LVPHMNVSAV-----EKQVT 391  
Db 284 ----SGV-----KKGMMVKVRGVSQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRVE 334

QY 392 RHLEDVFSKRN---SSNKMVVSMTLGLHPWIANIDDT-----QYLAAGR-AIRTVFGT 440  
Db 335 LHLTPMSQMDAVTSVTKLIEQAKKGWHPAIAVTDHAVVQSFPEAYSAAKKHGMKVIYGL 394

QY 441 EPDMIRDGSTIPIA-----KMFQE-----IVHKSVVLIPLGAVDDGE 477  
Db 395 EANIVDDG--VPIAYNETHRRRLSEETYVVFVDTTGLSAVYNTIIELAAVKVDGE 448

RESULT 214  
ADJ84903  
ID ADJ84903 standard; protein; 1433 AA.  
XX  
AC ADJ84903;  
XX

03-JUN-2004 (first entry)  
DT  
XX  
DE B. stearthermophilus DNA polymerase III alpha-large subunit.  
XX  
KW DNA polymerase III; DNA pol III; thermophilic bacteria;  
KW polymerase chain reaction; PCR; thermostable polymerase; DNA sequencing;  
KW dnaX; hoiA; holB; dnaA; dnaN; dnaQ; dnaE; ssb.  
XX

Geobacillus stearothermophilus.  
OS  
XX  
PN US2004048309-A1.  
XX

11-MAR-2004.  
PD  
XX  
PF 26-SEP-2003; 2003US-00673098.  
XX

08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX

(ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX

O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
PI  
XX  
DR WPI; 2004-238491/22.  
DR N-PSDB; ADJ84902.  
XX

Novel isolated Thermotoga delta primer subunit of DNA polymerase III-type  
PT enzyme, useful for amplifying and sequencing DNA molecule by polymerase  
PT chain reaction.  
XX  
PS Disclosure; SEQ ID NO 184; 235pp; English.  
XX  
CC The invention relates to an isolated Thermotoga delta' (prime) subunit of



Db	284	-----SGV-----KKGWVKVRSVQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRV	334
Qy	392	RHLEDVFSKRN---SSNMVVSMTLGLHPWIANIDDT-----QYLAAGR-AIRTVFGT	440
Db	335	LHLTPMSQMDAVTSVTKLIEQAKKKGHPAIAVTDHAVVQSFPEAYSAAKHGMKVIYGL	394
Qy	441	EPDMIRDGSTIPIA-----KMFQE-----IVHKSVVLIPLGAVDDGE	477
Db	395	EANIVDDG--VPIAYNETHRRLSEETYVVFVDTTGLSAVYNTIIELAAVKVDGE	448
RESULT 216			
ID	ADM66358	standard; protein; 1433 AA.	
XX	AC	ADM66358;	
XX	DT	15-JUL-2004 (first entry)	
XX	DE	G. stearothermophilus alpha-large subunit.	
XX	XX	DNA polymerase; DNA sequencing; DNA amplification.	
OS	XX	Geobacillus stearothermophilus.	
PN	US2004081995-A1.		
XX	PD	29-APR-2004.	
XX	PF	26-SEP-2003; 2003US-00673127.	
XX	PR	08-APR-1997; 97US-0043202P.	
PR	08-APR-1998; 98US-00057416.		
PR	18-AUG-2000; 2000US-00642218.		
PR	21-NOV-2000; 2000US-00716964.		
XX	PA	(ODON/) O'DONNELL M E.	
PA	(YUZH/) YUZHAKOV A.		
PA	(YURI/) YURIEVA O.		
PA	(JERU/) JERUZALMI D.		
PA	(BRUC/) BRUCK I.		
PA	(KURI/) KURIYAN J.		
XX	PI	O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;	
PI	Kuriyan J;		
XX	DR	WPI; 2004-340140/31.	
DR	N-PSDB; ADM66357.		
XX	PT	Novel isolated Bacillus beta subunit of DNA polymerase III-type enzyme, useful for amplifying and sequencing DNA molecule by polymerase chain reaction.	
XX	PS	Disclosure; SEQ ID NO 184; 245pp; English.	
XX	CC	The invention relates to an isolated DNA molecule from Bacillus stearothermophilus encoding a delta subunit of a DNA polymerase I. The subunits are useful for producing DNA polymerases for use in DNA sequencing and DNA amplification methods. The present sequence is used in the exemplification of the present invention.	
XX	SQ	Sequence 1433 AA;	
Query Match			
Best Local Similarity 4.5%; Score 118.5; DB 8; Length 1433;			
Matches 98; Conservative 86; Mismatches 179; Indels 173; Gaps 23;			
Qy	17	LLLLRGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEW-VAIESDSVQPVPRFR----	71
Db	11	LILLEQLKMTSDWMPHFREAAIRKVIDKEE-----KSWHFYQFDNVLPVHVYKTFAD	65
Qy	72	--QELFRMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPTKGTVCF	129

Db	66	RLQTAFRHIAAVRHTMEVEAPRVTEADVQAYW-----PLCIAEL-----	104
Qy	130	YGHLDVQPADRGDWLTDPYVLTEDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPV	189
Db	105	-----QEGMSPLVDWLSRQT-----PELKG	124
Qy	190	NIKFIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLMWISQRKPAITYGTRGNSYF	249
Db	125	N-KLLVVARHEAEALAI-----KRRFAKKIADVASFPPPLQLDVSVEPSKQEME	176
Qy	250	MVEVKCRDQDFHSGTFGGILHE-----PMAD--LVALLGSLVDSSGHI	290
Db	177	LAQKQDEDEERALAVLTDLAREEKAASAPPSGPLVIGYPIDDEEPPVRRLETIVEEERV	236
Qy	291	LVPG-IYDEVVPLTEEEINTYKA----IHLDL EEYRNSRVEKFLFDTK EEILMHLWRYP	345
Db	237	VVQGYVFD-----AEVSELKSGRTLTMKITDYTNSILVKMFSRDKEDAE	283
Qy	346	SLSIHGIEGAFDEPGTKTIVIPGRVIGKFSIR----LVPHMNVSAV-----EKQVT	391
Db	284	----SGV-----KKGWVKVRSVQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRV	334
Qy	392	RHLEDVFSKRN---SSNMVVSMTLGLHPWIANIDDT-----QYLAAGR-AIRTVFGT	440
Db	335	LHLTPMSQMDAVTSVTKLIEQAKKKGHPAIAVTDHAVVQSFPEAYSAAKHGMKVIYGL	394
Qy	441	EPDMIRDGSTIPIA-----KMFQE-----IVHKSVVLIPLGAVDDGE	477
Db	395	EANIVDDG--VPIAYNETHRRLSEETYVVFVDTTGLSAVYNTIIELAAVKVDGE	448
RESULT 217			
ID	ADO04411	standard; protein; 1433 AA.	
XX	AC	ADO04411;	
XX	DT	26-AUG-2004 (first entry)	
DE	XX	B. stearthermophilus DNA polymerase III alpha subunit.	
XX	KW	DNA polymerase III; Single-stranded DNA binding protein; ssb;	
KW	XX	chromosomal replicase; enzyme; secondary structure element; replication.	
OS	XX	Geobacillus stearothermophilus.	
PN	US2004106137-A1.		
XX	PD	03-JUN-2004.	
XX	PF	25-SEP-2003; 2003US-00670817.	
XX	PR	08-APR-1997; 97US-0043202P.	
PR	08-APR-1998; 98US-00057416.		
PR	18-AUG-2000; 2000US-00642218.		
PR	21-NOV-2000; 2000US-00716964.		
XX	PA	(ODON/) O'DONNELL M E.	
PA	(YUZH/) YUZHAKOV A.		
PA	(YURI/) YURIEVA O.		
PA	(JERU/) JERUZALMI D.		
PA	(BRUC/) BRUCK I.		
PA	(KURI/) KURIYAN J.		
XX	PI	O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;	
PI	Kuriyan J;		
XX	DR	WPI; 2004-419457/39.	
DR	N-PSDB; ADO04410.		
XX	PT	Novel isolated DNA derived from Bacillus stearothermophilus, encoding single-strand DNA binding protein, useful in removing secondary structure element from single-stranded DNA during DNA replication.	
PT			



XX Disclosure; SEQ ID NO 184; 245pp; English.

XX The invention relates to an isolated DNA molecule from Bacillus sp.

CC encoding a single-strand DNA binding protein (ssb) appearing as ADO04402

CC encoding the protein appearing as ADO04403, and DNAs hybridising to

CC complementary sequence of ADO04402 under hybridisation conditions. Also

CC included are an expression system comprising an expression vector into

CC which the ssb gene is inserted and a host cell comprising a heterologous

CC ssb gene. The following are disclosed as new, a kit (comprising a

CC container that contains either a deoxynucleoside triphosphate or a

CC dideoxynucleoside triphosphate, and a container containing DNA polymerase

CC III-type complex), methods and products (for identifying, isolating and

CC cloning DNA molecules encoding subunits encoded by genes of DNA

CC polymerase III-type enzyme from thermophilic bacteria), preparing DNA

CC sequencing using the DNA polymerase III enzymes, recombinant alpha, beta,

CC epsilon, tau, gamma, delta and delta' DNA polymerase III subunits, genes

CC encoding bacterial chromosomal replicases, and producing a recombinant

CC thermostable DNA polymerase III enzyme from a thermophilic bacterium. The

CC ssb protein and gene, derived from Bacillus stearothermophilus, are

CC useful in producing a recombinant thermostable single-strand binding

CC protein useful in removing secondary structure element from ssDNA during

CC replication. The present sequence is a bacterial DNA polymerase III

CC subunit (or fragment).

XX Sequence 1433 AA;

Query Match 4.5%; Score 118.5; DB 8; Length 1433;

Best Local Similarity 18.3%; Pred. No. 0.67;

Matches 98; Conservative 86; Mismatches 179; Indels 173; Gaps 23;

QY 17 LLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEW-VAIESDSVQVPRFR---- 71

DB 11 LILLEQLKMTSDEWMPHFREAAIRKVIDKEE-----KSWHEFYFQDNVLPVHVYKTFAD 65

QY 72 --QELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEELGSDPTKGTVCF 129

DB 66 RLQTAFRHIAAVRHTMEVAPRVTEADVQAYW-----PLCLAEEL----- 104

QY 130 YGHLDVQPADRGDGLTDPVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDPLPV 189

DB 105 -----QEGMSPLVDWLSRQT-----PELKG 124

QY 190 NIKFIIEGMEEGAGSVALBELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYF 249

DB 125 N-KLLVVARHEAEALAI-----KRRFAKKIADVVASFGFPPLQLDVSVEPSKQEMEQQF 176

QY 250 MVEVKCRDQDFHSGTFGGILHE-----PMAD--LVALLGSLVDSSGHI 290

DB 177 LAQKQEQEDEERALAVLTLAREEKAASAPPSGPLVIGYPIDREEPVRRLLETIVEEERRV 236

QY 291 LVPG-IYDEVVPLTEEEINTYKA-----IHLDEEYRNSRVEKFLFDTKKEELMHLWRYP 345

DB 237 VVQGYVFD-----AEVSELKSGRLLTMKITDVTNSILVKMFESRDKEAELM----- 283

QY 346 SLSIHGIEGAFDEPGTKTVPGRVIGKFSIR-----LVPHMNVSAV-----EKQVT 391

DB 284 ----SGV-----KKGMMVVKVSGSVQNDTFVRDLVLIANDLNEIAANERQDTAPEGEKRV 334

QY 392 RHLEDVFSKRN---SSNMVVSMTLGLHPWIANIDDT-----QYLAAGR-AIRTVFGT 440

DB 335 LHLHTPMSQMDAVTSVTKLIEQAKKGWHPAIAVTDHAVVQSFPEAYSAAKKGKMKVIYGL 394

QY 441 EPDMIRGDSTIPIA-----KMFQE-----IVHKSVLPIPLGAVDDGE 477

DB 395 EANIVDDG--VPIAVNETHRRLSEETVYVDFVTGLSAVNTIIELAAYKVKDGE 448

RESULT 218

ADP82488

ID ADP82488 standard; protein; 1433 AA.

XX

AC ADP82488;

XX 26-AUG-2004 (first entry)

DE B. stearothermophilus DNA polymerase III PolC subunit.

XX single-strand binding protein; SSB; DNA-protein complex;

KW DNA polymerase III-type enzyme complex; thermostable DNA polymerase III;

KW secondary structure element; replication; polC; DNA polymerase III;

XX PolC subunit.

OS Geobacillus stearothermophilus.

XX US2004110210-A1.

PD 10-JUN-2004.

XX 26-SEP-2003; 2003US-00673119.

XX 08-APR-1997; 97US-0043202P.

PR 08-APR-1998; 98US-00057416.

PR 18-AUG-2000; 2000US-00642218.

PR 21-NOV-2000; 2000US-00716964.

XX (ODON/) O'DONNELL M E.

PA (YUZH/) YUZHAKOV A.

PA (YURI/) YURIEVA O.

PA (JERU/) JERUZALMI D.

PA (BRUC/) BRUCK I.

PA (KURI/) KURIYAN J.

XX O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I, Kuriyan J;

PI WPI; 2004-440355/41.

DR N-PSDB; ADP82487.

XX Novel isolated Bacillus stearothermophilus single-strand binding protein, useful in removing secondary structure element from single-stranded DNA during DNA replication.

PS Disclosure; SEQ ID NO 184; 245pp; English.

XX The invention describes an isolated Bacillus sp. single-strand binding protein (I), comprising a fully defined sequence (S1) of 164 amino acids as given in specification or encoded by a nucleic acid molecule hybridising to the complement of a fully defined sequence (S2) of 492 base pairs as given in specification. Also described are: a DNA-protein complex (II) comprising a DNA molecule containing a single-stranded region and (I) that is bound to the single-stranded region of the DNA molecule; a kit comprising a container that contains either a deoxynucleoside triphosphate or a dideoxynucleoside triphosphate, and a container that contains a DNA polymerase III-type enzyme complex, and isolating and cloning DNA molecules encoding subunits encoded by genes of DNA polymerase III-type enzyme; kits for amplification and sequencing of DNA molecules; DNA polymerase III enzyme subunits; preparing DNA polymerase III enzyme; DNA molecules obtained by amplifying and sequencing using the DNA polymerase III enzymes; producing and isolating a recombinant thermostable DNA polymerase III enzyme or its subunit from thermophilic bacterium; DNA (III) encoding (I); an expression system comprising an expression vector into which (III) is inserted; and a host cell comprising a heterologous (III). (I) is useful in removing a secondary structure element from single-stranded DNA (ssDNA), particularly during replication. (I) binds to single stranded regions of DNA strands during DNA replication and prevents the rewinding of the DNA strands. This is the amino acid sequence of B. stearothermophilus DNA polymerase III PolC subunit.

XX Sequence 1433 AA;

Query Match 4.5%; Score 118.5; DB 8; Length 1433;

Best Local Similarity 18.3%; Pred. No. 0.67;









Db 117 VSIQYLEAVRRLKVEGHRFRPRTHMTFVPDEEVGGHQMELFVORPEFHALRAGFALDEG 176  
Qy 210 VEKEDRFFSGVDYIVISDNLWISQRKP 237  
Db 177 IANPTDAF-----TVFYSERSP 193

RESULT 223  
ABU30098  
ID ABU30098 standard; protein; 329 AA.  
AC ABU30098;  
XX  
DT 19-JUN-2003 (first entry)  
DE Protein encoded by Prokaryotic essential gene #15625.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Enterococcus faecium.

XX WO200277183-A2.  
PN  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA33968.

XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 58022; 1766pp; English.

XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 329 AA;

Query Match 4.4%; Score 116; DB 6; Length 329;  
Best Local Similarity 20.9%; Pred. No. 0.12;  
Matches 77; Conservative 50; Mismatches 110; Indels 132; Gaps 19;

Qy 22 RGMFSSPSPPP-----ALLEKVQYIDLHQDE-----FVQTLKEWVA 58  
Db 31 KAVILKPSEGPDLLRAKLEEAVASFD-NQDEVFLVLDLWGGTPFNQSNLTFFEEHKDKW-A 88  
Qy 59 IESDSVQPV-----PRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPP 112  
Db 89 IVSGLNLPMLIEAVASRFSMESAEIAAHIIETAKDGVKVKPEELEPAEAPKAAVEDAQP 148  
Qy 113 VILAEIGSDPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTVDGK-LYGRGATDNKGPVL 171  
Db 149 -----KGALP-EGTVV-----GDGKI--KYVLARVDSRLHLHGQVAT----- 181  
Qy 172 AWINAVS-----AFRALEQDLFPVNIKFIIEGMEEAAGSVALEELVEKEKD 215  
Db 182 AWTKAVQPNRIIVVSDAVSKDDLRLRLIEQAAPGVK-----ANVIPISKMIETVAKD 233  
Qy 216 RFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMAD 275  
Db 234 PRFGNTKALLFEN-----SKVLSMGQEDVEAFEKLEQKGVKFDVRKVPNDSR-----D 260  
Qy 276 LVAL-LGSLVDSSGHILVPGIYDEVVPLTTEEINTY-----KAHLDLEEVNRRSRVEKF 329  
Db 261 IKELNVGSMHAHSVGVV-----SKVLSMGQEDVEAFEKLEQKGVKFDVRKVPNDSR----- 312  
Qy 330 LFDTKEEIL 338  
Db 313 --DNMDDIL 319

RESULT 224  
ADC96959  
ID ADC96959 standard; protein; 334 AA.

XX ADC96959;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE E. faecium protein sequence SEQ ID 6586.  
XX  
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.  
XX  
OS Enterococcus faecium.  
XX  
PN US6583275-B1.  
XX  
PD 24-JUN-2003.  
XX  
PF 30-JUN-1998; 98US-00107532.  
XX  
PR 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-799836/75.  
DR N-PSDB; ADC93305.  
XX

PT New isolated nucleic acid derived from Enterococcus faecium encoding an  
PT Enterococcus faecium polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.

XX  
PS Example 1; SEQ ID NO 6586; 243pp; English.

XX  
CC The invention relates to an isolated nucleic acid derived from  
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for prevention or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.

XX  
SQ Sequence 334 AA;

Query Match 4.4%; Score 116; DB 7; Length 334;  
Best Local Similarity 20.9%; Pred. No. 0.12;  
Matches 77; Conservative 50; Mismatches 110; Indels 132; Gaps 19;

Qy 22 RGMFSSPSPPP-----ALLEKVFQYIDLHQDE-----FVQTLKEWVA 58  
Db 36 KAVILKPSGPDLLRAKLEAVASFD-NQDEVFLVLDLWGTFPNQSNTLFEEHKDKW-A 93  
Qy 59 IESDSVQPV-----PRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPP 112  
Db 94 IVSGLNLPMLIEAYASRFSMESAEHIAAHIETAKDGVKVKPEELEPAEAPKAAVEDAQP 153  
Qy 113 VILAELGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEYDGK-LYGRGATDNKGPVL 171  
Db 154 -----KGALP-EGTV-----GDGKI--KYVLARVDSRLHGVAT----- 186  
Qy 172 AWINAVS-----AFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKD 215  
Db 187 AWTKAVQPNRIIVSDAVSKDDLKRLKLIQAAAPGVK-----ANVIPISKMIQVAKD 238  
Qy 216 RFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMAD 275  
Db 239 PRFGNTKALLLFEN-----PEDVLTAVEGGV-----D 265  
Qy 276 LVAL-LGSLVDSGGHILVPGIYDEVVPLTEEEINTY-----KAHLDLLEEYRNSSRVEKF 329  
Db 266 IKELNVGSMASHSVGKVV-----SKVLSMGQEDVEAFEKLEQKGVKFDVRKVPNDSR---- 317  
Qy 330 LFDTKEEIL 338  
Db 318 --DNMDDIL 324

RESULT 225  
ABU41842  
ID ABU41842 standard; protein; 636 AA.  
XX  
AC ABU41842;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #27369.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX

OS Pseudomonas syringae.

XX  
PN WO200277183-A2.

XX  
PD 03-OCT-2002.

XX  
PF 21-MAR-2002; 2002WO-US009107.

XX  
PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX  
PA (ELIT-) ELITRA PHARM INC.

XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX  
DR WPI; 2003-029926/02.

DR  
N-PSDB; ACA45712.

XX  
CC New antisense nucleic acids, useful for identifying proteins or screening  
CC for homologous nucleic acids required for cellular proliferation to  
CC isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 69766; 1766pp; English.

XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 636 AA;

Query Match 4.4%; Score 114.5; DB 6; Length 636;  
Best Local Similarity 25.1%; Pred. No. 0.45;  
Matches 43; Conservative 31; Mismatches 70; Indels 27; Gaps 7;

Qy 51 QTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTL-QRLGARVASVDMGPQQLP-DGQSL 108

Db 163 ETLELVAIPTVRVDGVAQHENEPEFIKIAEKIKSLAERFDLKFRNIDNRVYEVSLDGS-- 220

Qy 109 PIPPVILAELGSDPTKGTVCFYGHLDVQPAD-----RGDGLWLTDPYVLTEVDGKLYGRGA 163

Db 221 -----GDE-----VVGIIHVHADVVPTPENWVLPDGTGLDPFKVTLIGDRMYGRGT 266







Claim 6; Fig 1; 30pp; English.

The present sequence represents Mycoplasma arginini arginine deiminase. The present invention describes: (1) a compound comprising arginine deiminase (AD) covalently bonded via linking group to polyethylene glycol (PEG), and having a molecular weight 12-40 kDa; and (2) a composition as above, but where the linking group is selected from a malimide group, an amide group, an imide group, a carbamate group, an ester group, an epoxy group, a carboxyl group, a hydroxyl group, a carbohydrate, a tyrosine group, a cysteine group and/or a histidine group. AD can be used in the treatment of tumours, e.g. melanomas, hepatomas and sarcomas, and to inhibit metastasis. The modified AD has an enhanced circulating half life

Sequence 409 AA;

	The invention discloses a compound comprising arginine deiminase (ADI) covalently bonded by a linking group to polyethylene glycol (PEG) having a total weight average molecular weight of about 1000-50000. Also disclosed is a method for enhancing the circulating half life or the tumoricidal activity of arginine deiminase by modifying the arginine deiminase by covalently bonding the arginine deiminase by a linking group to PEG. Normal cells can synthesise arginine from citrulline in a 2 step process catalysed by argininosuccinate synthase and argininosuccinate lyase. In contrast, many cancerous cells do not express argininosuccinate synthase and are, therefore, auxotrophic for arginine. Arginine deiminase catalyses the conversion of arginine to citrulline and can be used to eliminate arginine from the cancerous cells. The compound is useful for treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or for treating and inhibiting metastases in a patient. When compared to native arginine deiminase the compound retains most of its enzymatic activity, is far less antigenic, has a greatly extended circulating half-life, and is much more efficacious in the treatment of tumours. The sequence presented is the Mycoplasma arginini arginine deiminase gene, ADIPROT
CC	
XX	
SQ	Sequence 410 AA;
	Query Match            4.3%;   Score 113;   DB 5;   Length 410;
	Best Local Similarity   23.4%;   Pred. No. 0.31;
	Matches   44;   Conservative   36;   Mismatches   70;   Indels   38;   Gaps   8;
QY	328 KFLFDTKKEILMHLWRY-PSLSIHGIEGADEPGTKTVPGRVIGKFSIRLVPHMVSAV 386 :        ::                                                          :
Dd	188 RFVFSNHPKLINTPWYDPSLXL-SIEG-----GDVFYNNDTLVGVSERTD 234 :        ::                                                          :
QY	387 EKQVTRHLEDVFSKXNSSNKWVSMT-----LGLHPWIANDDTQYLAAKRAIRTVF- 438 :        ::
Dd	235 LQTVTLLAKNIIVANKECEFKRIVAINPVKTNLMLHLDTWLTMLDKDKFLYSPIA-NDVFK 293 :        ::
QY	439 -----GTEDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNY 489 
Dd	294 FWDYDLVNGGAEPQPVENG--LPLEGLLQSIINKPVLIIPIA----GEGASQMEIERETH 347 
QY	490 IEGTKLFA 497 :
Dd	348 FDGTNYLA 355

[illegible]















Db 65 LPDDSPVAPPQQRELPSVPOEQTIRIYIVRGLELQPD--NNGLCDPYIKITLGKKV 122

Qy 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI-----KFIIEGMEEAGSVALEELVE 211

Db 123 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVYDYDTFRD--EKVG-----ETIID 176

Qy 212 KEKDRFFS-----GV--DYIVISDNLWISQKPA-----IT 240

Db 177 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQPILSEDGSRIR 235

Qy 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300

Db 236 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 259

Qy 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLS-----IHGIE 353

Db 260 ---EERL---ALHI-----LRTQGLVPEHVETRTLHSTFQPNISQGLQMWVDVFP 304

Qy 354 GAFDEPGTKTIVPGRVIGKFSIRLV--PHMNVSAVEKQVT--RHLEDVFSK----RNSSNK 406

Db 305 KSLGPPGPPFNITPRKAKKYILRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEENK 364

RESULT 241

AAB58325

ID AAB58325 standard; protein; 616 AA.

XX AAB58325;

AC AAB58325;

XX 14-MAR-2001 (first entry)

XX Lung cancer associated polypeptide sequence SEQ ID 663.

DE Human; lung cancer associated protein; neuroprotective; cytostatic;

XX cardioactive; immunomodulatory; muscular active; vulnerary;

KW gastrointestinal; nephrotropic; antiinfective; gynecological;

KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;

KW proliferative disorder; wound healing; infectious disease.

XX

OS Homo sapiens.

XX

PN WO200055180-A2.

XX

PD 21-SEP-2000.

XX

PF 08-MAR-2000; 2000WO-US005918.

XX

PR 12-MAR-1999; 99US-0124270P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

XX

PI Ruben SM;

XX

DR WPI; 2000-587514/55.

DR N-PSDB; AAF18201.

XX

PT Lung cancer associated gene sequences, referred to as lung cancer

PT antigens, useful for treatment, prevention, and diagnosis of disorders

PT such as lung cancer.

XX

PS Claim 11; Page 1163-1165; 1425pp; English.

XX

CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer

CC associated proteins represented in AAB58106 - AAB58548. Lung cancer

CC associated proteins and polynucleotide sequences, their agonists, and

CC antagonists may have neuroprotective; cytostatic; cardioactive;

CC immunomodulatory; muscular active general; vulnerary; gastrointestinal

CC general; nephrotropic; antiinfective; gynecological; or antibacterial

CC activity. The invention also includes antibodies specific for the protein

CC or polynucleotide sequences. The lung cancer associated polynucleotide

CC sequences may be used for detection of lung cancer, chromosome

CC identification, as chromosome markers, and for numerous other diagnostic

CC or research purposes. The proteins may be used to treat disorders such as

CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,

CC cardiovascular, renal, and proliferative disorders. The proteins may also

CC be used in the treatment of wounds and infectious diseases.

CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are

CC used in the course of the invention for the identification and

CC characterisation of the polynucleotide and protein sequences

XX

SQ Sequence 616 AA;

Query Match 4.3%; Score 111.5; DB 3; Length 616;

Best Local Similarity 21.9%; Pred. No. 0.81;

Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;

Qy 102 LPDQGSLLPIPPVILAEEL-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPYVLTEVDGKL 158

Db 84 LPDDPSVPAPPQQRELPSVPOEQTIRIYIVRGLELQPD--NNGLCDPYIKITLGKKV 141

Qy 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI-----KFIIEGMEEAGSVALEELVE 211

Db 142 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVYDYDTFRD--EKVG-----ETIID 195

Qy 212 KEKDRFFS-----GV--DYIVISDNLWISQKPA-----IT 240

Db 196 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQPILSEDGSRIR 254

Qy 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300

Db 255 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 278

Qy 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLS-----IHGIE 353

Db 279 ---EERL---ALHI-----LRTQGLVPEHVETRTLHSTFQPNISQGLQMWVDVFP 323

Qy 354 GAFDEPGTKTIVPGRVIGKFSIRLV--PHMNVSAVEKQVT--RHLEDVFSK----RNSSNK 406

Db 324 KSLGPPGPPFNITPRKAKKYILRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEENK 383

RESULT 242

AAM93651

ID AAM93651 standard; protein; 630 AA.

XX AAM93651;

AC AAM93651;

XX 06-NOV-2001 (first entry)

DT Human polypeptide, SEQ ID NO: 3516.

XX

DE Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

OS

XX EP1130094-A2.

PN

XX 05-SEP-2001.

PD

XX 07-JUL-2000; 2000EP-00114089.

PF

XX 08-JUL-1999; 99JP-00194486.

PR

XX 11-JAN-2000; 2000JP-00118774.

PR

XX 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

DR N-PSDB; AAK94586.

DR

XX 830 Primers useful for synthesizing full length cDNA clones and their use



PT in genetic manipulation.

XX Claim 8; SEQ ID NO 3516; 1380pp + Sequence Listing; English.

PS The invention relates to primers for synthesizing full length cDNA

XX clones. 830 cDNA molecules encoding a human protein have been isolated

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full

CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special

CC methods. The present sequence is a polypeptide encoded by a full length

CC human cDNA of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in CD-ROM

CC format directly from EPO

XX

SQ Sequence 630 AA;

Query Match 4.3%; Score 111.5; DB 4; Length 630;

Best Local Similarity 21.9%; Pred. No. 0.84;

Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;

QY 102 LPDQSLPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPYVLTEVDGKL 158

DB 98 LPDDPSVPAPPRQFRELPSVQECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKVV 155

QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIEGMEEGAGSVALEELVE 211

DB 156 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVDYDTFTRD--EKVG---ETIID 209

QY 212 KEKDRFFS-----GV--DYIVISDNLWISQKPA-----IT 240

DB 210 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQILSEDGSRIR 268

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVV 300

DB 269 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 292

QY 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSSL-----IHGIE 353

DB 293 ---EERL-----ALHI-----LRTQGLVPEHVETRTLHSTFQPNISQGLQMWVDVFP 337

QY 354 GAFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT-RHLEDVFSK----RNSSNK 406

DB 338 KSLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSIITGEEMSDIYVKGWIPGNEENK 397

RESULT 243

ADL31483

ID ADL31483 standard; protein; 630 AA.

XX

AC ADL31483;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human protein encoded by a full length cDNA clone SeqID 3516.

XX

KW human; medicine; signal transduction; glycoprotein; transcription;

XX oligo-capping method.

XX

OS Homo sapiens.

XX

PN EP1396543-A2.

XX

PD 10-MAR-2004.

XX

PF 07-JUL-2000; 2003EP-00025638.

XX

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-0018774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PA Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

PI WPI; 2004-204755/20.

XX N-PSDB; ADL31482.

DR

XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full

PT length human cDNAs.

PT

XX Example 1; SEQ ID NO 3516; 1340pp; English.

PS

XX This invention relates to a novel primers useful for synthesising full

CC length cDNA molecules that encode human proteins. Specifically, it refers

CC to secretory or membrane proteins that are potential therapeutic agents/

CC target molecules in the field of medicine, and in particular genes

CC encoding proteins that are associated with signal transduction,

CC glycoproteins and transcription. The present invention describes a method

CC for efficiently cloning a full length human cDNA from both the 5' and 3'

CC ends using the oligo-capping method. This polypeptide sequence is a full

CC length human protein of the invention.

XX

SQ Sequence 630 AA;

Query Match 4.3%; Score 111.5; DB 8; Length 630;

Best Local Similarity 21.9%; Pred. No. 0.84;

Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;

QY 102 LPDQSLPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPYVLTEVDGKL 158

DB 98 LPDDPSVPAPPRQFRELPSVQECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKVV 155

QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIEGMEEGAGSVALEELVE 211

DB 156 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVDYDTFTRD--EKVG---ETIID 209

QY 212 KEKDRFFS-----GV--DYIVISDNLWISQKPA-----IT 240

DB 210 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQILSEDGSRIR 268

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVV 300

DB 269 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 292

QY 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSSL-----IHGIE 353

DB 293 ---EERL-----ALHI-----LRTQGLVPEHVETRTLHSTFQPNISQGLQMWVDVFP 337

QY 354 GAFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT-RHLEDVFSK----RNSSNK 406

DB 338 KSLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSIITGEEMSDIYVKGWIPGNEENK 397

RESULT 244

ABB89615

ID ABB89615 standard; protein; 770 AA.

XX

AC ABB89615;

XX

DT 24-MAY-2002 (first entry)

XX

DE Human polypeptide SEQ ID NO 1991.

XX

KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

XX vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;

XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;

XX neurological disease; infection; human; secreted protein.

OS

XX Homo sapiens.

XX



Db 127 KLPEDDEPPAPPPAPAGASPLAEPAPPS-----TPAAPKRRGSGSVDETFLALPA 177  
QY 146 -TDPYV-----LTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRALEQD 186  
Db 178 ASEPVIPSSAEBKIMDLKEQPGNTVSSGQEDFPVLFETAASLSPLSTVS-FK--EHG 234  
QY 187 LPVNIKFI--IEG-MEEAGSVALEELVEKEKORF-----FSGVDYIVISDNLWISQRK 236  
Db 235 YLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRRESAEFSVLEY-----SEMG 285  
QY 237 PAITYGTRGNSYFMV-----EVKCRDQDFHSGTFFGGILHEPMDLVALLGSLVDSSGHIL 291  
Db 286 SSFNGSPKGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPQ-ESPATLTKVVKEDG-VM 343  
QY 292 VP---GIYDE---VWPLTEE-----EI-NTY-----K 311  
Db 344 SPEKTMDFNEMKMSVWAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAANMESKVDKK 403  
QY 312 AIHLDLEEV---NSSRVEKFLFDYKEEILMHLWR-----YPSLS 348  
Db 404 CFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFTSATESTAAINFVLE 463  
QY 349 IHGIEGAFDEPCTK----TVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 404  
Db 464 DHTSENKTDEKIEERKAQIITEKTSKPSNPFVLVAIHDSEADYVTTDNL SKV-----T 517  
QY 405 NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHK 464  
Db 518 EAVVATMPEGLTPDLVQEAACESLNEATGTKIAYETKVDLVQTSBAI-----QESIYPT 571  
QY 465 VVLIP 469  
Db 572 AOLCP 576

RESULT 246  
AAM39304  
ID AAM39304 standard; protein; 1447 AA.  
XX  
AC AAM39304;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2449.  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
DR N-PSDB; AAI58460.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
as central nervous system injuries.  
XX  
PS Example 4; SEQ ID NO 2449; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 1447 AA;  
Query Match 4.3%; Score 111.5; DB 4; Length 1447;  
Best Local Similarity 21.8%; Pred. No. 3;  
Matches 88; Conservative 57; Mismatches 137; Indels 121; Gaps 23;  
QY 102 LPDQSLPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDWLTDYPVLTVEVDGKL 158  
Db 945 LPDDPSVPAPPRQFRELPSVPQECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKKV 1002  
QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEODLPVNI----KFIEGMEEGAGSVALEELVE 211  
Db 1003 IEDRDHVIPNTLNPVFGMYBELSCYLPQEKDKISVDYDFTTRD--EKVG---ETIID 1056  
QY 212 KEKDRFFS-----GV--DYIVISDNLWISQRKA-----IT 240  
Db 1057 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQPILSEDSRII 1115  
QY 241 YGTGNSYFMVEVKCRDQDFHSGTFFGGILHEPMA---DLVALLGSLVDSSGHILVPGIYD 297  
Db 1116 YG--GRDYSLDEFEANK-----ILHQHLGAPEERLAL-----HIL----- 1148  
QY 298 EVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDYKEEILMHLWRYPSLSIHGIE---- 353  
Db 1149 RTQGLVPEHVET-RTLHSTFQPNISRYLRIIWNTKDVL-----DEKSITGEEMSDI 1201  
QY 354 -----GAFDEPGTKTVIPGRVI---GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 404  
Db 1202 YVKGWIPGNEENKQKTDVYRSILDGEGNFNWRFPFDYLPAEQLC-----IVAKKE-- 1253  
QY 405 NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRD 447  
Db 1254 -----HFW--SIDQTEFRIPRPLIIQIWDNDKFSILD 1283  
RESULT 247  
AAM39303  
ID AAM39303 standard; protein; 1466 AA.  
XX  
AC AAM39303;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2448.  
XX



KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI58459.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 4; SEQ ID NO 2448; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 1466 AA;

Query Match 4.3%; Score 111.5; DB 4; Length 1466;  
Best Local Similarity 21.8%; Pred. No. 3.1;  
Matches 88; Conservative 57; Mismatches 137; Indels 121; Gaps 23;  
QY 102 LPDQOSLPPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDGLTDPYVLTEVDGKL 158  
Db 964 LPDDPSVPAPPRQFRELPSVPQECTVRIYVRGLELQPD--NNGLCDPYIKITLGKKV 1021  
QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI-----KFIIEGMEAGSVALEELVE 211  
Db 1022 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVDYDTFTRD--EKVG---ETIID 1075  
QY 212 KEKDRFFS-----GV--DYIVISDNLWISQRKPA-----IT 240  
Db 1076 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLQNVARFKGFPQILSDGSRII 1134

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA---DLVALLGSLVDSSGHILVPGIYD 297  
Db 1135 YG--GRDYSLDEFANK-----ILHQHLAGAPEERLAL-----HIL----- 1167  
QY 298 EVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLDTKBEILMHLWRYPSSLHIGIE---- 353  
Db 1168 RTQGLVPEHVET-RTLHSTFQPNISRYLRVIWNTKDVIL-----DEKSITGEEMSDI 1220  
QY 354 -----GAFDEPGTKTVIPGRVI---GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSS 404  
Db 1221 YVKGWIPGNEENKQKTDVYRSLDGEGNFNWRFVFPFDYLPAEQLC-----IVAKKE-- 1272  
QY 405 NKMWVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRD 447  
Db 1273 -----HFW--SIDQTEFRIPRLLIIQIWNNDKFSLDD 1302  
RESULT 248  
ABJ37072  
ID ABJ37072 standard; protein; 1798 AA.  
XX  
AC ABJ37072;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE Human breast cancer / ovarian cancer related protein #48.  
XX  
KW Human; cytostatic; breast cancer; ovarian cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2003000012-A2.  
XX  
PD 03-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-US019773.  
XX  
PR 21-JUN-2001; 2001US-0300159P.  
PR 27-JUN-2001; 2001US-0301351P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Veiby OP;  
XX  
DR WPI; 2003-267848/26.  
DR N-PSDB; ABT31941.  
XX  
PT Determining the presence of breast cancer in an individual, involves  
PT using specific polynucleotide markers.  
XX  
PS Disclosure; Page 211-214; 233pp; English.  
XX  
CC The invention comprises a method for assessing whether a patient is  
CC afflicted with breast cancer or ovarian cancer. The method involves the  
CC use of specific DNA markers. The method of the invention is useful in the  
CC detection and treatment of ovarian and breast cancer. Amino acid  
CC sequences ABJ37025 - ABJ37080 represent human breast/ovarian cancer-  
CC related proteins  
XX  
SQ Sequence 1798 AA;  
Query Match 4.3%; Score 111.5; DB 6; Length 1798;  
Best Local Similarity 21.9%; Pred. No. 4.3;  
Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;  
QY 102 LPDQOSLPPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDGLTDPYVLTEVDGKL 158  
Db 1266 LPDDPSVPAPPRQFRELPSVPQECTVRIYVRGLELQPD--NNGLCDPYIKITLGKKV 1323  
QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIIEGMEAGSVALEELVE 211  
Db 1324 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVDYDTFTRD--EKVG---ETIID 1377







Db 1724 ---EERL-----ALHI-----LRTQGLVPEHVETRLHSTFQPNISQGLQMWVDVFP 1768

Qy 354 GAFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT-RHLEDVFSK-----RNSSNK 406

Db 1769 KSLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEENK 1828

RESULT 252

ABM85357

ID ABM85357 standard; protein; 2061 AA.

XX

AC ABM85357;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human protein sequence hCP49320.

XX

KW Cytostatic; carcinoma; lymphoma; cancer; human.

XX

OS Homo sapiens.

XX

PN WO2003073826-A2.

XX

PD 12-SEP-2003.

XX

PF 28-FEB-2003; 2003WO-US006235.

XX

PR 01-MAR-2002; 2002US-00087192.

XX

PA (SAGR-) SAGRES DISCOVERY.

XX

PI Morris DW;

XX

WPI; 2003-328604/31.

DR

XX

PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma

PT comprises a nucleotide sequence.

XX

PS Claim 5; SEQ ID NO 486; Opp; English.

XX

CC The present invention relates to novel DNA and protein sequences which

CC are associated with carcinomas. The sequences are useful for: (i) for

CC screening drug candidates; (ii) for screening of bioactive agent capable

CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of

CC a bioactive agent capable of modulating the activity of CAP; (iv) for

CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing

CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating

CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;

CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for

CC determining Carcinoma Associated (CA) gene copy number. In addition, the

CC CA genes are useful as DNA vaccines and the CAP are useful as markers of

CC carcinoma including lymphoma. The present sequence is one such CAP. Note:

CC This patent is an equivalent to basic patent US2002182586A1, for which no

CC sequence data was published

XX

SQ Sequence 2061 AA;

Query Match 4.3%; Score 111.5; DB 7; Length 2061;

Best Local Similarity 21.9%; Pred. No. 5.3;

Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;

Qy 102 LPDQSLPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPYVLTEVDGKL 158

Db 1529 LPDDPSVPAPPRQFRELPSVPQECTVRIYVRGLELQPD--NNGLCDPFIKITLGKV 1586

Qy 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI----KFIIEGMEEAGSVALEELVE 211

Db 1587 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVDYDTFTRD--EKVG----ETIID 1640

Qy 212 KEKDRFFS-----GV--DYIVISDNLWISQKPA-----IT 240

Db 1641 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPILSEDGSRIR 1699

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300

Db 1700 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 1723

QY 301 PLTEEEINTYKATHLDLSEYRNSSRVEKFLFDTKKEILMHLWRYPSLS-----IHGIE 353

Db 1724 ---EERL-----ALHI-----LRTQGLVPEHVETRLHSTFQPNISQGLQMWVDVFP 1768

QY 354 GAFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT-RHLEDVFSK-----RNSSNK 406

Db 1769 KSLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEENK 1828

RESULT 253

ADR37739

ID ADR37739 standard; protein; 2061 AA.

XX

AC ADR37739;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human fer-1-like 3 myoferlin protein linked to Ebola pathogenesis Seq232.

XX

KW human; gene trap method; HIV; influenza A; Ebola virus; virucidal;

KW anti-HIV; antibacterial; pathogenesis; viral infection.

OS Homo sapiens.

XX

PN WO2004070002-A2.

XX

PD 19-AUG-2004.

XX

PF 18-NOV-2003; 2003WO-US037143.

XX

PR 18-NOV-2002; 2002US-0427464P.

PR 25-JUN-2003; 2003US-0482604P.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Hodge TW, Morey NJ, Rubin D, Shaw MW, Sanchez A;

XX

WPI; 2004-625495/60.

DR N-PSDB; ADR37738.

XX

PT Decreasing infection of cell by virus, HIV, influenza A or Ebola,

PT comprises interfering with activity or expression of host proteins or

PT activity of host nucleic acids such as Rab9, AXL receptor tyrosine

PT kinase, and Beta-chimerin.

XX

PS Claim 40; SEQ ID NO 232; 396pp; English.

XX

CC This invention relates to novel host cell nucleic acid molecules and the

CC encoded proteins thereof that are involved in viral infection or are

CC associated with the life cycle of a virus. Specifically, it refers to

CC using a gene trap method to identify DNA molecules such as ab9, AXL

CC receptor tyrosine kinase, beta-chimerin and mammalian selenium binding

CC protein that interact and participate in viral infections including HIV,

CC influenza A and Ebola virus. The present invention describes methods to

CC interfere with or disrupt these interactions in order to confer a

CC resistance or inhibition to the infection and effect a prophylactic or

CC therapeutic outcome. In particular, the method comprises disrupting these

CC interactions by contacting the target mRNA with antisense RNA, ribozyme

CC or siRNA molecules, accordingly pharmaceutical compositions derived

CC thereof exhibit virucidal, anti-HIV and antibacterial activities. In

CC addition, it can be used to decrease infection from bacteria and viruses

CC including Campylobacter jejuni, Vibrio cholerae SV40, Legionella

CC pneumophila, Aeromonas hydrophila, Helicobacter pylori, Measles, Herpes

CC Simplex Virus or the Epstein-Barr virus. This polypeptide sequence is

CC encoded by a target human host gene associated with the pathogenesis of

CC an Ebola infection, given in an exemplification of the invention.

XX

SQ Sequence 2061 AA;

```
Query Match      4.3%; Score 111.5; DB 8; Length 2061;
Best Local Similarity 21.9%; Pred. No. 5.3;
Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;

QY 102 LPDQSLPIPPVILAEI--GSDPTKGTVCFY--GHLDVQPADRGDGLTDPYVLTEVDGKL 158
Db 1529 LPDDPSVPAPPRQFRELPSVPOECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKKV 1586

QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI-----KFIIEGMEEAGSVALEELVE 211
Db 1587 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVYDFTTRD--EKVG-----ETIID 1640

QY 212 KEKDRFFS-----GV--DYIVISDNLWISQRKPA-----IT 240
Db 1641 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQPILSEDGSRIR 1699

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEWV 300
Db 1700 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 1723

QY 301 PLTEEEINTYKAHLDLBEYRNSSRVEKFLDFTKEILMHLWRYP SLS-----IHGIE 353
Db 1724 ---EERL---ALHI-----LRTQGLVPEHVETRLHSTFQPNISQGLQMWVDVFP 1768

QY 354 GAFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT--RHLEDVFSK-----RNSSNK 406
Db 1769 KSLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSI TGEEMSDIYVKGWIPGNEENK 1828

RESULT 254
ABM81166
ID ABM81166 standard; protein; 2061 AA.
XX
AC ABM81166;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO12813, SEQ:3014.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN39091.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 3014; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
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CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 2061 AA;

Query Match      4.3%; Score 111.5; DB 8; Length 2061;
Best Local Similarity 21.9%; Pred. No. 5.3;
Matches 79; Conservative 49; Mismatches 117; Indels 115; Gaps 21;

QY 102 LPDQSLPIPPVILAEI--GSDPTKGTVCFY--GHLDVQPADRGDGLTDPYVLTEVDGKL 158
Db 1529 LPDDPSVPAPPRQFRELPSVPOECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKKV 1586

QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI-----KFIIEGMEEAGSVALEELVE 211
Db 1587 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVYDFTTRD--EKVG-----ETIID 1640

QY 212 KEKDRFFS-----GV--DYIVISDNLWISQRKPA-----IT 240
Db 1641 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQPILSEDGSRIR 1699

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEWV 300
Db 1700 YG--GRDYSLDEFEANK-----ILHQ-----HLGAP----- 1723

QY 301 PLTEEEINTYKAHLDLBEYRNSSRVEKFLDFTKEILMHLWRYP SLS-----IHGIE 353
Db 1724 ---EERL---ALHI-----LRTQGLVPEHVETRLHSTFQPNISQGLQMWVDVFP 1768

QY 354 GAFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT--RHLEDVFSK-----RNSSNK 406
Db 1769 KSLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSI TGEEMSDIYVKGWIPGNEENK 1828

RESULT 255
AAB79819
ID AAB79819 standard; protein; 422 AA.
XX
AC AAB79819;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:372.
XX
KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;
KW fine chemical production; microorganism; organic acid; nucleoside;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100843-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB0000923.
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RESULT 259
AAU10540
ID AAU10540 standard; protein; 1478 AA.
XX
AC AAU10540;
XX
DT 14-FEB-2002 (first entry)
XX
DE Rat CIRL-2 variant BC (YSG2) polypeptide.
XX
KW YSG; YSG2; schizophrenia; chronic animal model; LCGU; netrin receptor;
KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
KW calcium-independent alpha-latrotoxin receptor; CIRL; trKE; synapsin 1A;
KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic;
KW tumour necrosis factor alpha; TNF-alpha; rat; CIRL-2 variant BC.
XX
OS Rattus sp.
XX
PN WO200175440-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-GB001486.
XX
PR 31-MAR-2000; 2000GB-00007880.
PR 26-MAY-2000; 2000GB-00012768.
XX
PA (WELF-) WELFIDE CORP.
XX
PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
XX
DR WPI; 2002-010813/01.
DR N-PSDB; AAS16840.
XX
PT Novel chronic animal model of schizophrenia, useful for identifying anti-
PT psychotic drugs and genes that are associated with schizophrenia.
XX
PS Disclosure; Fig 6d; 79pp; English.
XX
CC The invention relates to YSG polynucleotide fragments for use in
CC diagnosing and/or developing treatments for schizophrenia using chronic
CC animal models. The polynucleotides and their encoded polypeptides are
CC used for identification of compounds which modulate the expression of YSG
CC molecules, leading to the manufacture of schizophrenia medicaments. The
CC sequences can also be used for testing candidate compounds for any effect
CC on the polypeptides. Anti-schizophrenic effects of a compound can be
CC determined by measuring local cerebral glucose utilisation (LCGU) or
CC comparing its expression level with that of a control group. The
CC sequences are useful in the identification of genes associated with
CC schizophrenic states and in the development of an antibody. The sequences
CC of the invention include phosphodiesterase 1-alpha, calcium-independent
CC alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain
CC receptor 1 (trKE), netrin receptor (UNC5H1), synapsins 1A and AB and
CC tumour necrosis factor (TNF) alpha. This sequence represents rat calcium-
CC independent alpha-latrotoxin receptor 2 (CIRL-2) variant BC (YSG2)
XX polypeptide
SQ Sequence 1478 AA;

Query Match      4.2%; Score 110.5; DB 5; Length 1478;
Best Local Similarity 22.2%; Pred. No. 3.9;
Matches 109; Conservative 58; Mismatches 153; Indels 171; Gaps 26

QY 73 ELFR-MMAVAADTLQRIGARVASVDMGPPQLPDGQSLP-----IPPV-----IL 115
Db |||: : : | | | : | | | : | | | : | | |
QY 116 AELGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKG P VLA--- 172
Db 474 EALEMKGIKWPQTQRMVMVERPCPKTRG-TASYLC-----MASTGTWNPKGPDLSNCT 526

```



CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1478 AA;

Query Match 4.2%; Score 110.5; DB 7; Length 1478;  
Best Local Similarity 22.2%; Pred. No. 3.9;  
Matches 109; Conservative 58; Mismatches 153; Indels 171; Gaps 26;

QY 73 ELFR-MMAVAADTLQRLGARVASVDMGPQQLPDGQSLP-----IPPV-----IL 115  
DB 416 ELFKTTVSTTSSTSOR--GPVSVTVAGPQEGSRGKTPPPAVSTTKIPPVTNIFPLPERFC 473  
QY 116 AELGSDPTKGTVCYFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLA--- 172  
DB 474 EALEMKGIKWPTQGRGMVVERPCPKGTRG-TASYLC-----NASTGTWNPKGPDLSNCT 526  
QY 173 --WINAVSAFRALEQDLPVNIKFIIEGMEBAGSVALEELVEKEKDRFFSG-----VD 222  
DB 527 SHVWNQLAQ-----KIRSGENAAASLA-NELAKHTKGTVPAGDVSSSVRLME 571  
QY 223 YIVISDNLWISQKPAITYGTRGNSYFMV---EVKCRDQDFHSGTFGGILHEPMADLVAL 279  
DB 572 QLVDILDAQLOELKPS-EKDSAGRSYNKLQKREKTCR-----AY 609  
QY 280 LGS�VDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNS--RVEKFLFDTKEE 336  
DB 610 LKAIVDTVDNLL-----RAETLDCWKHMSSEQAHTATMLLDITLE- 649  
QY 337 ILMHLWRYPSLSIHGEGAFD-----EPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQV 390  
DB 650 -----EGAFVLADNLLP-TRVSMP-----TDNIVLEAVLSTEGQV 685  
QY 391 ---TRHL--EDVFS-----KRNSSN---KMVVSMTLGLHPWIANIDDTQYLAAKRA 433  
DB 686 QDPTFHLGFKGAFSSIQLSANTVKQNSRNLAKVVFIIYRSLGPFPLSTENATVKLGA--- 742  
QY 434 IRTVFGTEPDMIRDGSI-----PIAKMFOEIVHKSVVLIPLGAVDDGEHSQNEKI 484  
DB 743 -----DLLGRNSTIAVNSHVLVSINKESSRVVLTDPVLFSPHIDSDNYF-NANC 792  
QY 485 NRWNYIEGTKL 495  
DB 793 SFWNYSERTMM 803

RESULT 261  
ADE55162  
ID ADE55162 standard; protein; 1488 AA.  
XX  
AC ADE55162;  
XX

DT 29-JAN-2004 (first entry)  
XX Rat Protein AF063102, SEQ ID NO 967.  
DE  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX Rattus norvegicus.  
OS  
XX WO2003016475-A2.  
PN  
XX 27-FEB-2003.  
PD  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
PA  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI  
XX WPI; 2003-268312/26.  
DR GENBANK; AF063102.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
PT  
XX Claim 1; Page; 1017pp; English.  
PS  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1488 AA;

Query Match 4.2%; Score 110.5; DB 7; Length 1488;  
Best Local Similarity 22.2%; Pred. No. 3.9;  
Matches 109; Conservative 58; Mismatches 153; Indels 171; Gaps 26;

QY 73 ELFR-MMAVAADTLQRLGARVASVDMGPQQLPDGQSLP-----IPPV-----IL 115  
DB 416 ELFKTTVSTTSSTSOR--GPVSVTVAGPQEGSRGKTPPPAVSTTKIPPVTNIFPLPERFC 473  
QY 116 AELGSDPTKGTVCYFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLA--- 172  
DB 474 EALEMKGIKWPTQGRGMVVERPCPKGTRG-TASYLC-----NASTGTWNPKGPDLSNCT 526



XX DE Rat Protein AF063102, SEQ ID NO 975.  
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX OS Rattus norvegicus.  
XX PN WO2003016475-A2.  
XX PD 27-FEB-2003.  
XX PF 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
XX PR 01-NOV-2001; 2001US-0346382P.  
XX PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GEHO ) GEN HOSPITAL CORP.  
XX PA (FARB ) BAYER AG.  
XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX FI WPI; 2003-268312/26.  
XX DR GENBANK; AF063102.  
XX PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX PS Claim 1; Page; 1017pp; English.  
XX CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 1488 AA;

Query Match 4.2%; Score 110.5; DB 7; Length 1488;  
Best Local Similarity 22.2%; Pred. No. 3.9;  
Matches 109; Conservative 58; Mismatches 153; Indels 171; Gaps 26;  
QY 73 ELFR-NMAVAADTLQRLGARVASVDMGPQLPDGQSLP-----IPPV-----IL 115  
Db 416 ELEKTTVSTTSSTQSR--GPVSSIVAGPQEGSRGTPKPPPAVSTTKIPPVTNIFPLPERFC 473  
QY 116 AELGSDPFKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLA--- 172  
Db 474 EALEMKGIKWPQTORGMVMVERPCPKTRG-TASYLC-----MASTGTWNPKGPDLSNCT 526

QY 173 --WINAVSAFRALEQDLPVNIKFIIIEGMEEGAGSVALEELVEKEKDRFFSG-----VD 222  
Db 527 SHWVNQLAQ-----KIRSGENAAASLA-NELAKHTKGTVFAGDVSSSVRLME 571  
QY 223 YIVISDNLWISQRKPAITYGTRGNSYFMV---EVKCRDQDFHSGTGGILHEPMADLVAL 279  
Db 572 QLVDILDAQLELKPS-EKDSAGRSYNKLQKREKTCR-----AY 609  
QY 280 LGSILVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDEEYRNSS---RVEKFLFDTKEE 336  
Db 610 LKAIVDTVDNLL-----RAETLDCWKHMNSSEQAHTATMLDLTLE- 649  
QY 337 ILMHLWRYPSLSIHGIEGAFD-----EPGKTIVIPGRVIGKFSIRLVPHMNVSAVEKQV 390  
Db 650 -----EGAFVLADNLLLEP-TRVSMP-----TDNIVLEVAVLSTEGQV 685  
QY 391 ---TRHL--EDVFS-----KRNSSN---KMVVSMTLGLHPWIANIDDTQYLAAKRA 433  
Db 686 QDFTFHLGFGAFSSIQLSANTVKQNSRNLAKVVFIIYRSLGPFSLSTENATVKLGA--- 742  
QY 434 IRTVFGTEPDMIRDGSTI-----PIAKMFOEIYVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 743 -----DLIGRNSTIAVNSHVLVSINKESSRVYITDVPVLFSPHIDSDNYF-NANC 792  
QY 485 NRWNYIEGTKL 495  
Db 793 SFWNYCERTMM 803  
RESULT 264  
ADE55166  
ID ADE55166 standard; protein; 1488 AA.  
XX AC ADE55166;  
XX DT 29-JAN-2004 (first entry)  
XX DE Rat Protein AF063102, SEQ ID NO 971.  
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX OS Rattus norvegicus.  
XX PN WO2003016475-A2.  
XX PD 27-FEB-2003.  
XX PF 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
XX PR 01-NOV-2001; 2001US-0346382P.  
XX PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GEHO ) GEN HOSPITAL CORP.  
XX PA (FARB ) BAYER AG.  
XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX DR WPI; 2003-268312/26.  
XX DR GENBANK; AF063102.  
XX PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX PS Claim 1; Page; 1017pp; English.  
XX CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.



CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1488 AA;

Query Match 4.2%; Score 110.5; DB 7; Length 1488;  
Best Local Similarity 22.2%; Pred. No. 3.9;  
Matches 109; Conservative 58; Mismatches 153; Indels 171; Gaps 26;

QY 73 ELFR-MMAVAADTLQRLGARVASVDMGPQQLPDGQSLP-----IPPV-----IL 115  
Db 416 ELFKTTVSTTSQSQR--GPVSVTAVGPQEGSRGTKPPPAVSTTKIPPVTNFPPLPERFC 473  
QY 116 AELGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPVYLTEVDGKLYGRGATDNKGPVLA--- 172  
Db 474 BALEMKGIKWQOTQGMVMVERPCPKGTRG-TASYLC-----MASTGTWNKGPDLNCT 526  
QY 173 --WINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALBELVEKEKDRFFSG-----VD 222  
Db 527 SHWVNQLAQ-----KIRGENAASLA-NELAKHTKGTVFAGDVSSSVRLME 571  
QY 223 YIVISDNLWISQRKPAITYGTRGNSYFMV---EVKCRDQDFHSGTGGILHEPMDLVAL 279  
Db 572 QLVDILDAQLQELKPS-EKDSAGRSYNKLQKREKTCR-----AY 609  
QY 280 LGS�VDSGGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSS---RVEKFLFDTKEE 336  
Db 610 LKAIVDTVDNLL-----RAETLDCWKHMSSEQAHTATMLDITLE- 649  
QY 337 ILMHLWRYPSLSIHGIEGAFD-----EPGKTIVIPGRVIGKFSIRLVPNMVSAVEKQV 390  
Db 650 -----EGAFVLADNLLP-TRVSM-----TDNIVLEVAVLSTEGQV 685  
QY 391 ---TRHL--EDVFS-----KRNSSN---KMVVSMTLGLHPWIANIDDTQYLAAKRA 433  
Db 686 QDFTFHLGFKGAFSSIQLSANTVKQNSRNGLAKVVFIIYRSLGPFLLSTENATVKLGA--- 742  
QY 434 IRTVFGTEPDMIRGDSI-----PIAKMFQEIYVHKSVDLIPLGAVDDGSHSQNEKI 484  
Db 743 -----DLLGRNSTIAVNSHVLVSINKESSRVYLTDPVLFSPHIDSNDYF-NANC 792  
QY 485 NRWNVIEGTKL 495  
Db 793 SFWNYSERTMM 803

RESULT 265  
ADP79614  
ID ADP79614 standard; protein; 409 AA.

XX  
AC ADP79614;  
XX  
DT 04-NOV-2004 (first entry)  
XX

DE Mycoplasma arthritis arginine deaminase variant.  
XX  
KW Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
OS Mycoplasma arthritis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 111 /label= K111E  
FT /note= "wild-type Lys is substituted with with Glu"  
FT Misc-difference 112 /label= K112E  
FT /note= "wild-type Lys is substituted with with Glu"  
XX  
PN WO2004046309-A2.  
XX  
PD 03-JUN-2004.  
XX  
PF 29-SEP-2003; 2003WO-US030770.  
XX  
PR 18-NOV-2002; 2002US-0427497P.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
DR WPI; 2004-431965/40.  
XX  
XX Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
PS Claim 18; SEQ ID NO 8; 89pp; English.  
XX  
CC The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma arthritis arginine deaminase variant.  
XX  
SQ Sequence 409 AA;

Query Match 4.2%; Score 110; DB 8; Length 409;  
Best Local Similarity 22.6%; Pred. No. 0.59;  
Matches 44; Conservative 38; Mismatches 75; Indels 38; Gaps 8;

QY 321 RNSSRVEKFLFDTKKEILMHLWRY-PSLSIHGIEGAFDEPGTKTIVIPGRVIGKFSIRLVP 379  
Db 181 RRETLSRFRVFRNHPKLVNTPWYDPAKML-SIEG-----GDVFYNNDTLVV 227  
QY 380 HMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMT-----LGLHPWIANIDDTQYLAAGR 432  
Db 228 GVSERTDLDVTLLAKNLVANKECFKRIVAINVPKWTNLMHLDIWLMDKNKFLYSPI 287  
QY 433 AIRTVF-----GTEPDMIRGDSIPIAKMFQEIYVHKSVDLIPLGAVDDGSHSQNE 482  
Db 288 A-NDVFKFWDYDLVNGGAEPQPVENG--LPLEKLLQSIINKKPVLPIA---GEGASQM 340  
QY 483 KINRWNYIEGTKLFA 497  
Db 341 EIERETHFDGNTYIA 355



Db 288 A-NDVFKFWDYDLVNGGAEPQPVEG--LPLEKLLQSIINKKPVLIPIA-----GEGASQM 340

QY 483 KINRWNYIEGTKLFA 497

Db 341 EIERETHFDGTNYIA 355

RESULT 268

ID ADP79615 standard; protein; 409 AA.

XX ADP79615;

DT 04-NOV-2004 (first entry)

DE Mycoplasma arthritidis arginine deaminase variant.

XX Arginine deaminase; cytostatic; virucide; viral replication;

KW nitric oxide synthesis; tumour; liver function; enzyme; variant.

XX Mycoplasma arthritidis.

XX Key Location/Qualifiers

FH Misc-difference 111

FT /label= KillIE

FT /note= "wild-type Lys is substituted with with Glu"

XX WO2004046309-A2.

PN 03-JUN-2004.

PD 29-SEP-2003; 2003WO-US030770.

XX 18-NOV-2002; 2002US-0427497P.

PR (PHOE-) PHOENIX PHARMACOLOGICS INC.

XX Clark MA;

PI WPI; 2004-431965/40.

DR Inhibiting replication of viruses in individual, involves administering

XX composition comprising arginine deiminase bonded to polyethylene glycol,

PT to individual.

XX Claim 18; SEQ ID NO 9; 89pp; English.

PS The invention relates to inhibiting the replication of one or more

XX viruses in an individual and involves administering to the individual a

CC composition comprising an arginine deaminase bonded to polyethylene

CC glycol. The method is useful for inhibiting replication of one or more

CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,

CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,

CC M. hominis, M. arthritidis and its combination. It is useful for treating

CC an individual who is suspected of having been exposed to one or more

CC viruses, for modulating nitric oxide levels in an individual, or for

CC selectively inhibiting viral replication in an individual. The method is

CC also useful for treating a tumour and inhibiting replication of one ore

CC more viruses in an individual. The tumour is melanoma, sarcoma, or

CC hepatoma. The tumour is hepatocellular carcinoma. The method is also

CC useful for improving liver function in an individual. The present

CC sequence represents a Mycoplasma arthritidis arginine deaminase variant.

XX SQ Sequence 409 AA;

Query Match 4.2%; Score 110; DB 8; Length 409;

Best Local Similarity 22.6%; Pred. No. 0.59;

Matches 44; Conservative 38; Mismatches 75; Indels 38; Gaps 8;

QY 321 RNSSRVEKFLFDTKEEILMHLWRY-PSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP 379

Db 181 RRETLSRFRVFRNHPKLVNTPWYDPAAMKL-SIEG-----GDVFYNNDTLVV 227

QY 380 HMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMT-----LGLHPWIANIDDTQYLAAKR 432

Db 228 GVSERTDLDTVTLAKNLVANKECEFKRIVAINVPKWTNLMHLDIWLTMLDKNKFLYSPI 287

QY 433 AIRTVE-----GTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGSHSQNE 482

Db 288 A-NDVFKFWDYDLVNGGAEPQPVEG--LPLEKLLQSIINKKPVLIPIA-----GEGASQM 340

QY 483 KINRWNYIEGTKLFA 497

Db 341 EIERETHFDGTNYIA 355

RESULT 269

ABU48779

ID ABU48779 standard; protein; 650 AA.

XX ABU48779;

AC 19-JUN-2003 (first entry)

DT Protein encoded by Prokaryotic essential gene #34306.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Ureaplasma urealyticum.

OS WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA52649.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 76703; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent











CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.  
XX  
SQ Sequence 1845 AA;

Query Match 4.2%; Score 110; DB 8; Length 1845;  
Best Local Similarity 17.7%; Pred. No. 6.1;  
Matches 86; Conservative 64; Mismatches 126; Indels 210; Gaps 20;  
QY 87 RLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYGHLDVQPADRGDGLT 146  
Db 1246 KLGSRQAQVNLTVDKP-----DPPAGTPC---ASDIRSSSLTSLWY- 1284  
QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-----QDL----- 187  
Db 1285 -----GSSYDGGSAVQSYIEIWDANKTGWELATCRSTSFNVQDLLPDHEYKFRV 1335  
QY 188 -PVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246  
Db 1336 RAINVYGTSEPSQSELTTVGEKPEEPKDE-----VEVSDD---DEKEPEVDYRT--- 1382  
QY 247 SYFMVEVKCRDQDFH-----SGTFGGI----- 268  
Db 1383 --VTINTEQKVSDFYDIEERLGSKGFGQVRLVEKTRKVKWAGKFFKAYSACEKENIRQE 1440  
QY 269 -----LHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 1441 ISIMNCLHHPKLVQCVDAFEKANIMVLEIV---SGGELFERIIDEFELTERECIKYM 1497  
QY 307 -----INTYKAHLDLE-----EYRNSSRVE-----KFLFDTKE 335  
Db 1498 ROISEGVEYIHKQGIHVHLDLKPENIMCVNKTGTRIKLIDFGLARRLENAGSLKVLFGTPE 1557  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVE----- 387  
Db 1558 FVAPEVINYEPI-----GYATDMWSIGVICIYLVSGLSPPFMGDNDN 1598  
QY 388 -----KQVTRHLEDVFS---KRNSSNKMVMSMTLGLHPWIANIDDTQ 426  
Db 1599 ETLANVTSATWDFDEAFDEISDDAKDFISNLLKDKMKRDLCTQCL-QHPWL--MKDTK 1655  
QY 427 YLAAGR 432  
Db 1656 NMEAKK 1661

RESULT 274  
ADQ39533  
ID ADQ39533 standard; protein; 1845 AA.  
XX  
AC ADQ39533;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1196.  
XX  
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
KW cardiant; gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004058052-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-US040978.  
XX  
PR 20-DEC-2002; 2002US-0434778P.  
PR 10-MAR-2003; 2003US-0453135P.  
PR 30-APR-2003; 2003US-0466412P.  
PR 23-SEP-2003; 2003US-0504955P.  
XX  
PA (APPL-) APPLERA CORP.

XX  
PI  
XX  
DR WPI; 2004-533949/51.  
DR N-PSDB; ADQ38705.  
XX  
PT Identifying an individual who has an altered risk for developing  
PT myocardial infarction by detecting a single nucleotide polymorphism in  
PT the individual's nucleic acids.  
XX  
PS Claim 10; SEQ ID NO 1196; 145pp; English.  
XX  
CC The invention relates to a novel method for identifying an individual who  
CC has an altered risk for developing myocardial infarction. The method  
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
CC the nucleotide sequences given in the specification in the individual's  
CC nucleic acids, where the presence of the SNP is correlated with an  
CC altered risk for myocardial infarction in the individual. The invention  
CC further comprises: an isolated nucleic acid molecule comprising at least  
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
CC the specification or its complement and encoding any one of the amino  
CC acid sequences given in the specification; an isolated polypeptide  
CC comprising an amino acid sequence given in the specification; an antibody  
CC that specifically binds to the polypeptide or its antigen-binding  
CC fragment; an amplified polynucleotide containing an SNP given in the  
CC specification and which is between about 16 and 1000 nucleotides in  
CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
CC method for identifying an agent useful in treating or preventing  
CC myocardial infarction. The novel detection method has cardiant activity.  
CC The nucleic acids of the invention may be used in gene therapy. The  
CC method is useful in identifying an individual who has an increased or  
CC decreased risk for developing myocardial infarction and for preparing a  
CC composition for treating or preventing myocardial infarction. This  
CC sequence represents the protein of a human myocardial infarction-  
CC associated gene containing one or more SNP's of the invention. Note: This  
CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.  
XX  
SQ Sequence 1845 AA;

Query Match 4.2%; Score 110; DB 8; Length 1845;  
Best Local Similarity 17.7%; Pred. No. 6.1;  
Matches 86; Conservative 64; Mismatches 126; Indels 210; Gaps 20;  
QY 87 RLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYGHLDVQPADRGDGLT 146  
Db 1246 KLGSRQAQVNLTVDKP-----DPPAGTPC---ASDIRSSSLTSLWY- 1284  
QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-----QDL----- 187  
Db 1285 -----GSSYDGGSAVQSYIEIWDANKTGWELATCRSTSFNVQDLLPDHEYKFRV 1335  
QY 188 -PVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246  
Db 1336 RAINVYGTSEPSQSELTTVGEKPEEPKDE-----VEVSDD---DEKEPEVDYRT--- 1382  
QY 247 SYFMVEVKCRDQDFH-----SGTFGGI----- 268  
Db 1383 --VTINTEQKVSDFYDIEERLGSKGFGQVRLVEKTRKVKWAGKFFKAYSACEKENIRQE 1440  
QY 269 -----LHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 1441 ISIMNCLHHPKLVQCVDAFEKANIMVLEIV---SGGELFERIIDEFELTERECIKYM 1497  
QY 307 -----INTYKAHLDLE-----EYRNSSRVE-----KFLFDTKE 335  
Db 1498 ROISEGVEYIHKQGIHVHLDLKPENIMCVNKTGTRIKLIDFGLARRLENAGSLKVLFGTPE 1557  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVE----- 387  
Db 1558 FVAPEVINYEPI-----GYATDMWSIGVICIYLVSGLSPPFMGDNDN 1598

QY 388 -----KQVTRHLEDVES---KRNSSNKQMVVSMTLGLHPWIANIDDTQ 426  
Db 1599 ETLANVTSATWDFDDEAFDEISDDAKDFISNLLKKDMKNRLDCTQCL-QHPWL--MKDTK 1655  
QY 427 YLAAGR 432  
Db 1656 NMEAKK 1661

RESULT 275  
ADN03875  
ID ADN03875 standard; protein; 1914 AA.  
AC ADN03875;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Antipsoriatic protein sequence #133.  
XX  
KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004028479-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-US030907.  
XX  
PR 25-SEP-2002; 2002US-0414006P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
PI Wu TD;  
XX  
DR WPI; 2004-305105/28.  
DR N-PSDB; ADN03874.  
XX  
PT New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX  
PS Claim 9; SEQ ID NO 269; 3069pp; English.  
PS  
XX The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polypeptides of the invention..  
XX  
SQ Sequence 1914 AA;

Query Match 4.2%; Score 110; DB 8; Length 1914;  
Best local Similarity 17.7%; Pred. No. 6.5;  
Matches 86; Conservative 64; Mismatches 126; Indels 210; Gaps 20;

QY 87 RLGARVASVDMGPPQLPDGQSLPIPPVILAEILGSDPTKGTVCYGHLDVQPADRGDGLT 146  
Db 1315 KLGSRQAQVNLTVVDKP-----DPPAGTPC---ASDIRSSSLTLSWY- 1353

QY 147 DPVVLTEVDGKLYGEGATDNKGPVLAWINAVSAFRALE-----QDL----- 187  
Db 1354 -----GSSYDGGSAVQSYSIEIWDSSANKTWKELATCRSTSFNVQDLLPDHEYKFRV 1404

QY 188 -PWNKFIIEGMEEACGVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGN 246  
Db 1405 RAINVYGTSEPSQSELTTVGKEPPEPKDE-----VEVSDD---DEKEPEVDYRT--- 1451

QY 247 SYFMVEVKCRDQDFH-----SGTFGGI----- 268  
Db 1452 --VTINTEQKVSDFYDIEERLGSKGFGQVRLVEKTRKWAGKFFKAYSACEKENIRQE 1509

QY 269 -----LHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 1510 ISIMNCLHHPKLVQCVDFAFEKANIVMVLIV---SGGELFERIIDDEDFELTERECIKYM 1566  
QY 307 -----INTYKAHLDLE-----EYRNSSRVE-----KFLFDTKE 335  
Db 1567 RQISEGVEYIHKQIVVHLDLKPENIMCVNKTGTRIKLIDFGLARRLENAGSLKVLFGTPE 1626  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLPHMNVSAVE----- 387  
Db 1627 FVAPEVINYEPI-----GYATDMWSIGVICYILVSGLSPFMGNDN 1667  
QY 388 -----KQVTRHLEDVES---KRNSSNKQMVVSMTLGLHPWIANIDDTQ 426  
Db 1668 ETLANVTSATWDFDDEAFDEISDDAKDFISNLLKKDMKNRLDCTQCL-QHPWL--MKDTK 1724  
QY 427 YLAAGR 432  
Db 1725 NMEAKK 1730

RESULT 276  
ADQ39522  
ID ADQ39522 standard; protein; 1914 AA.  
XX  
AC ADQ39522;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1185.  
XX  
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
KW cardiant; gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004058052-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-US040978.  
XX  
PR 20-DEC-2002; 2002US-0434778P.  
PR 10-MAR-2003; 2003US-0453135P.  
PR 30-APR-2003; 2003US-0466412P.  
PR 23-SEP-2003; 2003US-0504955P.  
XX  
PA (APPL-) APPLERA CORP.  
XX  
PI Cargill M, Devlin JJ, Iakubova O;  
XX  
DR WPI; 2004-533949/51.  
DR N-PSDB; ADQ38694.

Identifying an individual who has an altered risk for developing  
myocardial infarction by detecting a single nucleotide polymorphism in  
the individual's nucleic acids.

Claim 10; SEQ ID NO 1185; 145pp; English.

The invention relates to a novel method for identifying an individual who  
has an altered risk for developing myocardial infarction. The method  
comprises detecting a single nucleotide polymorphism (SNP) in any one of  
the nucleotide sequences given in the specification in the individual's  
nucleic acids, where the presence of the SNP is correlated with an  
altered risk for myocardial infarction in the individual. The invention  
further comprises: an isolated nucleic acid molecule comprising at least  
8 contiguous nucleotides where one of the nucleotides is an SNP given in  
the specification or its complement and encoding any one of the amino  
acid sequences given in the specification; an isolated polypeptide  
comprising an amino acid sequence given in the specification; an antibody  
that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the  
CC specification and which is between about 16 and 1000 nucleotides in  
CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
CC method for identifying an agent useful in treating or preventing  
CC myocardial infarction. The novel detection method has cardiant activity.  
CC The nucleic acids of the invention may be used in gene therapy. The  
CC method is useful in identifying an individual who has an increased or  
CC decreased risk for developing myocardial infarction and for preparing a  
CC composition for treating or preventing myocardial infarction. This  
CC sequence represents the protein of a human myocardial infarction-  
CC associated gene containing one or more SNP's of the invention. Note: This  
CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 1914 AA;

Query Match 4.2%; Score 110; DB 8; Length 1914;  
Best Local Similarity 17.7%; Pred. No. 6.5;  
Matches 86; Conservative 64; Mismatches 126; Indels 210; Gaps 20;

QY 87 RLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFGLHDVQPADRGDGLT 146  
Db 1315 KLGSRQAQVNLTVVDPK-----DPPAGTPC---ASDIRSSSLTLSWY- 1353  
QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-----QDL----- 187  
Db 1354 -----GSSYDGGSAVQSYSIEIWDANKTWKELATCRSTSFNVQDLLPDHEYKFRV 1404  
QY 188 -PWNKFIIEGMEERAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246  
Db 1405 RAINVYGTSEPSQSELTTVGEKPEEPKDE-----VEVSDD---DEKEPEVDYRT--- 1451  
QY 247 SYFMVEVKCRDQDFH-----SGTFGGI----- 268  
Db 1452 --VTINTEQKVSDFYDIEERLGSKGFGQVFRLVEKTRKWAGKFFKAYSACEKENIRQE 1509  
QY 269 -----LHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 1510 ISIMNCLHHPKLVQCVDAAFEKANKANIMVMLEIV---SGGELFERIIDDFELTERECIKYM 1566  
QY 307 -----INTYKAIHLDLE-----EYRNSSRVE-----KFLFDTKE 335  
Db 1567 ROISEGVEYIHKQIGIVHLDLKPENIMCVNKTGTRIKLIDFGLARRLENAGSLKVLFGTPE 1626  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVE----- 387  
Db 1627 FVAPEVINYEPI-----GYATDMWSIGVICIYILVSGLSPFMGDNDN 1667  
QY 388 -----KQVTRHLEDVFS---KRNSSNKMVVSMTLGLHPWIANIDDTQ 426  
Db 1668 ETLANVTSATWDFDDEAFDEISDDAKDFISNLLKKDMKNRLDCTQCL-QHPWL--MKDTK 1724  
QY 427 YLAAGR 432  
Db 1725 NMEAKK 1730

RESULT 277

AAU84351  
ID AAU84351 standard; protein; 1953 AA.

XX AC AAU84351;

XX DT 08-MAY-2002 (first entry)

DE Protein MYLK differentially expressed in breast cancer tissue.

XX Human; diagnosis of breast cancer; endometrial cancer; breast tumour;  
KW MAI; mitotic activity index; cytostatic.

XX OS Homo sapiens.

XX

PN WO200210436-A2.

XX 07-FEB-2002.

XX 27-JUL-2001; 2001WO-US0233642.

XX 28-JUL-2000; 2000US-0222093P.

XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX (BAAK/) BAAK J.

XX Baak J, Mutter GL;

XX WPI; 2002-180084/23.

XX N-PSDB; ABK35571.

PT Diagnosing breast cancer comprises determining expression of nucleic acid  
PT molecules or expression products that are differentially expressed in  
PT normal and malignant tissue.

PS Claim 37; Page 195-201; 219pp; English.

XX The present invention relates to a method for diagnosing breast cancer in  
CC a subject suspected of having endometrial cancer. The method comprises  
CC determining the expression of a set of human genes or expression products  
CC in an endometrial sample suspected of being cancerous. The human genes of  
CC the invention are differentially expressed in breast tumours  
CC characterised as high or low MAI (mitotic activity index). These sets of  
CC genes can be used to discriminate between high and low MAI breast  
CC tumours. The invention also provides DNA and protein microarrays for  
CC analysing the expression of the human genes and their protein products.  
CC The methods and arrays are useful for the diagnosis and prognosis of  
CC endometrial cancer, selecting and monitoring treatment regimes, and  
CC identification of compounds useful for the treatment of endometrial  
CC cancer. AAU84311-AAU84361 represent the human proteins of the invention  
CC that are differentially expressed in breast cancer tissue

XX SQ Sequence 1953 AA;

Query Match 4.2%; Score 110; DB 5; Length 1953;  
Best Local Similarity 17.7%; Pred. No. 6.7;  
Matches 86; Conservative 64; Mismatches 126; Indels 210; Gaps 20;

QY 87 RLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFGLHDVQPADRGDGLT 146  
Db 1354 KLGSRQAQVNLTVVDPK-----DPPAGTPC---ASDIRSSSLTLSWY- 1392  
QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-----QDL----- 187  
Db 1393 -----GSSYDGGSAVQSYSIEIWDANKTWKELATCRSTSFNVQDLLPDHEYKFRV 1443  
QY 188 -PWNKFIIEGMEERAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246  
Db 1444 RAINVYGTSEPSQSELTTVGEKPEEPKDE-----VEVSDD---DEKEPEVDYRT--- 1490  
QY 247 SYFMVEVKCRDQDFH-----SGTFGGI----- 268  
Db 1491 --VTINTEQKVSDFYDIEERLGSKGFGQVFRLVEKTRKWAGKFFKAYSACEKENIRQE 1548  
QY 269 -----LHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE----- 306  
Db 1549 ISIMNCLHHPKLVQCVDAAFEKANKANIMVMLEIV---SGGELFERIIDDFELTERECIKYM 1605  
QY 307 -----INTYKAIHLDLE-----EYRNSSRVE-----KFLFDTKE 335  
Db 1606 ROISEGVEYIHKQIGIVHLDLKPENIMCVNKTGTRIKLIDFGLARRLENAGSLKVLFGTPE 1665  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVE----- 387  
Db 1666 FVAPEVINYEPI-----GYATDMWSIGVICIYILVSGLSPFMGDNDN 1706  
QY 388 -----KQVTRHLEDVFS---KRNSSNKMVVSMTLGLHPWIANIDDTQ 426





CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 290 AA;

Query Match 4.2%; Score 109; DB 7; Length 290;  
Best Local Similarity 21.1%; Pred. No. 0.43;  
Matches 71; Conservative 41; Mismatches 138; Indels 86; Gaps 13;

QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFII---EGMEEAGSVALEELVEKEKD 215  
||| ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : :  
Db 9 GRGAADMKGSLASMIIVAFRFVADHPKHGAIAFLITSDDEGPAHHGTKAVVERLAARGE 68  
||| :  
QY 216 RFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMAD 275  
| :  
Db 69 R----LDWCIVGEPSSLSLGDVVKNGRRGSLGAKLTIR-----GV----- 105  
||| :  
QY 276 LVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAHLDLEEYRNSRVEKFLFDTKE 335  
||| :  
Db 106 -----QGHVAYPHLAKNPIHLAAPALAEAAEHWD-----DGNAF---- 140  
||| :  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVICKFSIRLVPHMNVSAVEKQVTRHLE 395  
:  
Db 141 -----FPPTSQF-VSNLNSGTGATNVIPGELTALFNFRFSTESTVEGLQKRV---E 187  
||| :  
QY 396 DVFSKRNSNKMVSMVLGLHPWIAN---IDDTQVLAAKRAIRTVFGTEPDMIRDGSTI 451  
:  
Db 188 AILDKHGLD--WHVEWALSGLPFLTEPGELLD-----AVAASIRAVTGRETFRPSTSGGTS 240  
||| :  
QY 452 P---IAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
||| :  
Db 241 DGRFIATMGTVQVE-----LGPVNATIHQVNERV 269  
||| :

RESULT 280  
ADB11694  
ID ADB11694 standard; protein; 414 AA.  
XX  
AC ADB11694;  
XX  
DT 20-NOV-2003 (first entry)  
DE Alloiococcus otitis antigenic protein SEQ ID NO:5366.  
XX Alloiococcus otitis; antigenic protein; immunogenic; immunisation;  
KW gene therapy; Gram-positive bacterium; infection.  
XX  
OS Alloiococcus otitis.  
XX  
PN WO2003048304-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 25-NOV-2002; 2002WO-US036123.  
XX  
PR 29-NOV-2001; 2001US-0333777P.  
PR 18-NOV-2002; 2002US-0426742P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
XX  
PI Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;  
XX

DR WPI; 2003-505284/47.  
DR N-PSDB; ADB11697.  
XX  
PT New Alloiococcus otitidis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.  
XX  
PS Claim 33; SEQ ID NO 5366; 1019pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I) of  
CC Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.  
CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its  
CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloiococcus otitidis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloiococcus  
CC otitidis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloiococcus  
CC otitidis. The present sequence represents an Alloiococcus otitidis  
CC antigen protein from the present invention.  
XX  
SQ Sequence 414 AA;

Query Match 4.2%; Score 109; DB 6; Length 414;  
Best Local Similarity 18.8%; Pred. No. 0.75;  
Matches 93; Conservative 80; Mismatches 176; Indels 146; Gaps 22;

QY 44 LHQDEFVQTLKEWVAIESDS--VQVPFRFRQELFRMMAVAADTLQRLGARVASVDMGPQQ 101  
:  
Db 5 IDKDQSIKILQDIIQIKSENGHEEEVAKYFQSLADHDIESKLVQYDDDDRAS----- 56  
:  
QY 102 LPDGQSLPIPPVILAEI--GSDPTKGTVCFYGHLDVQPADRGDGLTDPY-VLTEVDGKL 158  
:  
Db 57 -----LVAEISNGEGPVLGIT---GHLDVVGAGDEDDWEYPPFSAHIDDDNVL 101  
:  
QY 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIEGMEEAGSVALEELVEKEKDRFF 218  
:  
Db 102 WGRGASDMKPGIAAMVINFIIEFKE-SQNFKGLRLLATVGEVGYGYSNQLT---REGYV 157  
:  
QY 219 SGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVA 278  
:  
Db 158 DDLDAILIGPCNV-----GIVYTHMGSLNY 183  
:  
QY 279 LLGSLVDSSGHILVPGI-YDEVVPLTETEEINTYKAHLDLEEYRNSRVEKFLFDTKEEI 337  
| :  
Db 184 TLTSKGEAA-HSSAPQLGVNAVENLTEAVSQISKAVEDKAEFFN-----EEL 230  
:  
QY 338 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIG-----KFSIRLVPHMNVSA 385  
:  
Db 231 -----GKTFHNV-----TIKG---GSQVNSLPEYAEYANARTIPEFDNNG 269  
:  
QY 386 VEKQVTRHLEDVFSKRNSNKMVSMVLGLHP-----WIANIDDT-----QYL 428  
| :  
Db 270 V-MDIVRSVIDDLNKKDGF-DLAVEVTADQPPVNSPKDSKLIQTIREVTKDHERLGFQYL 327  
:  
QY 429 AAKRAIRTVFGT-----EPDMIRDGSTIPI-----AKMFQEIIVHKSVVLIPLGAVDDG 476  
:  
Db 328 L--KQMGQVLGTLVKDQPELKGKVDLEILPIAAGTTDAAQFTQGNSTMDIAVYGPVPQL 385  
: :





XX The present invention relates to novel human ORFX polypeptides and their  
CC coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences  
CC were discovered in human atherogenic cells, in particular in platelets  
CC and human umbilical vein endothelial cells (HUVEC) and are expressed in  
CC many other tissues as well. Atherogenic cells are cells which have the  
CC potential to develop atherosclerotic plaques. The ORFX polypeptides and  
CC nucleic acids are useful for treating or preventing a pathological  
CC condition associated with an ORFX-associated disorder, e.g. cancer,  
CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood  
CC coagulation disorders or inflammatory disorders. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/sequence.html?DocID=20020082206  
XX  
SQ Sequence 95 AA;  
  
Query Match 4.1%; Score 108.5; DB 5; Length 95;  
Best Local Similarity 30.5%; Pred. No. 0.085;  
Matches 29; Conservative 18; Mismatches 35; Indels 13; Gaps 2;  
  
QY 409 VSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDIMRDGSTIPIAKMFQIIVHKSVVLI 468  
Db 5 IALDWGMKP-----LAAAKHALTDEWGDALLIGSGASIPIVADFKTKLGLDITVLI 55  
  
QY 469 PLGAVDDGEHSQNEKINRWNYIEG---TKLFAAF 499  
Db 56 GFGLEDDNIHSPNEKNLKSFKHGIRSWARILAAF 90  
  
RESULT 283  
ADT89537  
ID ADT89537 standard; protein; 1162 AA.  
XX  
AC ADT89537;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Mus musculus Nogo protein.  
XX  
KW Nerve regeneration; gene therapy; vaccine; neuroprotective; neurotropic;  
KW Nogo; mouse.  
KW  
OS Mus musculus.  
XX  
PN US2004191240-A1.  
XX  
PD 30-SEP-2004.  
XX  
PF 31-JUL-2003; 2003US-00633423.  
XX  
PR 28-MAR-2003; 2003JP-00092923.  
PR 30-APR-2003; 2003US-00427741.  
XX  
PA (TOHY/) TOHYAMA M.  
PA (YAMA/) YAMASHITA T.  
XX  
PI Tohyama M, Yamashita T;  
XX  
DR WPI; 2004-698659/68.  
DR N-PSDB; ADT89536.  
XX  
PT Regenerating nerves or modulating nerve regeneration comprises inhibiting  
PT or modulating p75 signal transduction pathway by administering a  
PT transduction agent, e.g. p21 or Rho, or an agent that interacts with the  
PT transduction agent.  
XX  
PS Example 2; SEQ ID NO 10; 209pp; English.  
XX  
CC The present invention relates to a method for regenerating nerves or  
CC modulating nerve regeneration. The method involves inhibiting or  
CC modulating a p75 signal transduction pathway. The invention is useful for  
CC treating, preventing or diagnosing neurological diseases based on nerve

CC regeneration and for identifying agents useful for nerve regeneration.  
CC The invention is also useful in gene therapy and for preparing vaccine.  
CC The present sequence is the Mus musculus Nogo protein. Note: This  
CC sequence is said to encoded by SEQ ID NO 9, however this does not appear  
CC to be the same.  
XX  
SQ Sequence 1162 AA;  
  
Query Match 4.1%; Score 108.5; DB 8; Length 1162;  
Best Local Similarity 20.5%; Pred. No. 4.1;  
Matches 124; Conservative 72; Mismatches 204; Indels 205; Gaps 30;  
  
QY 26 SSPSPPPALLEKVFQYI-----DLHQDEFVQTLKEWVAIE----- 60  
Db 16 SPPRPPPAF---KYQFVTEPEDEDEDEDEDEDEDEDEDELEEVLERKPAAGLSAAPVPPA 72  
  
QY 61 -----SDSVQPVPR-----FRQELF-RMMAVAADTLQRLGARVASVDMGPQ 100  
Db 73 AAPLLDFSSDSVFPAPRGPPLPAAPPTAPERQPSWERSPAASAPSLPPAAAVL-----PS 126  
  
QY 101 QLPDQGSPLPIPPVI-----LAELGSDPTKGTVCYGHLDVQPADRGDGL----- 145  
Db 127 KLPEDDEPPARPAPAGASPLAEPAPPS-----TPAAPKRRGSGSVDETLPALPA 177  
  
QY 146 -TDPYV-----LTEVDGKLYGRGATDNKG-----PVLWINAVSAFRALEQD 186  
Db 178 ASEPVIPSSAEKIMDLKEQPGNTVSSQEDFPFVLFETAASPLSPLSTVS-FK--EHG 234  
  
QY 187 LPVNIKFI--IEG-MEEAGSVALEELVEKEKDRF-----FSGVDYIVISDNLWISQRK 236  
Db 235 YLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEY-----SEMG 285  
  
QY 237 PAITYGTRGNSYFMV-----EVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHIL 291  
Db 286 SSFNGSPKGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPO-ESPATLTKVVKEDG-VM 343  
  
QY 292 VP-----GIYDE-----VVPLTEE-----EI-NTY-----K 311  
Db 344 SPEKTMDFNEMKMSVAVPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANMESKVDKK 403  
  
QY 312 AIHLDLEE-----YRNSSRVEKFLFDTKEEILMHLWR-----YPSLS 348  
Db 404 CFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLE 463  
  
QY 349 IHGIEGAFDEPGTK---TVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSS 404  
Db 464 DHTSENKTDEKKIEERKAQIITEKTSPKTNPFLVAIHDSEADYVTTDNLKSV-----T 517  
  
QY 405 NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDIMRDGSTIPIAKMFQIIVHKS 464  
Db 518 EAVVATMPEGLTPDLVQEAACESELNEATGTKIAYETKVDLVQTSEAI-----QESIYPT 571  
  
QY 465 VVLIP 469  
Db 572 AQLCP 576  
  
RESULT 284  
AAM39305  
ID AAM39305 standard; protein; 1496 AA.  
XX  
AC AAM39305;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2450.  
XX  
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.







XX This invention relates to a novel method for targeting disruption of an  
CC arbitrary gene in a genome of an organism which comprises providing the  
CC whole sequential data of the genome of such organism, selecting at least  
CC 1 arbitrary region in the sequence, providing a vector that contains a  
CC sequence homologous with the selected region and a marker gene,  
CC transformation, and homologous recombination. The genome is preferably  
CC the genome of a hyperthermostable archaeobacterium, particularly  
CC Thermococcus kodakaraensis KOD1. The method is for targeting the  
CC disruption of a gene in the genome of an organism, which is applicable in  
CC studying gene structure and functions as well as enzyme activities of  
CC encoded proteins and useful in medicine, forensic science, food or drug  
CC inspection, molecular biology and immunology. With this method, the  
CC disruption of a gene at an arbitrary position in a genome can be achieved  
CC efficiently and reliably. The present sequence is that of a protein  
CC encoded by the genome of Thermococcus kodakaraensis which was derived  
CC using the method of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 546 AA;

Query Match 4.1%; Score 107; DB 8; Length 546;  
Best Local Similarity 20.9%; Pred. No. 1.8;  
Matches 71; Conservative 56; Mismatches 100; Indels 112; Gaps 17;

QY 10 ASLIAVLLLLLGERGMFSPSPALLEKVF-QYIDLHQD-----EFVQTLKEWVA 58  
Db 95 ANVLQIKMISEGKMSRPR-----LQRVLPRIELARDKDERVALKAIEVINTLLESGD 149

QY 59 IESDSVQVPVPRFRQELFR-----MMAVAADTLQRLGARVASVD-----MGPOQLP 103  
Db 150 LSEEDYERVMETLQDVLKSGVPILGEYAAEGLKLGANVVAIAYKLINWLFSLIGSSKKR 209

QY 104 DGQSLPIPPVILAEELGSDPTKGV---CFYGHLDV--QPADRGDGLTDPYVLTVEYDGKL 158  
Db 210 DVQSAAI--TALTEIASKTTSNINRVFDGITDLLSHP-----DPYV---VERAL 255

QY 159 YG-----RGATDNKGPVLAWINAVSAFRALEQDLPVNI--KFIIEGMEEAGSVALE 207  
Db 256 YSIDRLLTREKELSTRNK-----LKAVSKIKELRGDVKLGLLASQVMEKLEKATNIA-E 308

QY 208 ELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGG 267  
Db 309 ETIESE-----GVTKALEVSQYSIDDVE-----K 332

QY 268 ILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306  
Db 333 LLDAGKADIVAEMAK-----LDPVAMEKVLMSLESE 363

RESULT 288  
ABB97379  
ID ABB97379 standard; protein; 552 AA.  
XX  
AC ABB97379;  
XX  
DT 27-JUN-2002 (first entry)  
XX  
DE Novel human protein SEQ ID NO: 647.  
XX  
KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;  
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
KW neuroprotective; antiparkinsonian; protein therapy; EST;  
XX expressed sequence tag.  
OS Homo sapiens.  
XX  
PN WO200222660-A2.  
XX  
PD 21-MAR-2002.  
XX

PF 10-SEP-2001; 2001WO-US026015.  
XX  
PR 11-SEP-2000; 2000US-00659671.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX  
DR WPI; 2002-292408/33.  
DR N-PSDB; ABN32565.  
XX  
PT An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis.  
XX  
PS Example 2; SEQ ID NO 647; 509pp; English.  
XX  
CC The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke  
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.  
CC rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention  
XX  
SQ Sequence 552 AA;

Query Match 4.1%; Score 107; DB 5; Length 552;  
Best Local Similarity 20.2%; Pred. No. 1.8;  
Matches 85; Conservative 62; Mismatches 169; Indels 104; Gaps 19;

QY 103 PDGQ-SLPIPPVILAE-----GSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEV 154  
Db 6 PGRPGLPQPPPLLLLLLPLLVTAEPKPKAGVYATAYWMPAEK----TVQVKNVMDK 61

QY 155 DGKLYGRGATDNKGPVLAW-----INAVSAFRALEQDLPVNIKFIIEG----- 197  
Db 62 NGDAY--GFYNNSVKTTGWGILEIRAGYGSQTLNSNEIMFVAGFLEGYLTAPHMNDHYTN 119

QY 198 -----MEEAGSVALEELVEKEKDRFFSGVDYIVIS--DNLWISQRKPA 238  
Db 120 LYPQLITKPSIMDKVQDFMEKQDKWTRKNIKEYKTDSEFRHTGYVMAQIDGLYVGAKKRA 179

QY 239 ITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSS-----GH 289  
Db 180 ILEGTKPMTLFQIQ-----FLNSVGDLL-----DLIPSLPTKNGSLKVKFKRWDMGH 226

QY 290 I-----LVPGIYDEVVPLTEEEINTYKAI-----HLD---LEEYRNSRVEKFLPDTKEE 336  
Db 227 CSALIKVLPGF--ENILFAHSSWYTYAAMLRIYKHWDFNIIDKDTSSRLS---FSSYPG 281

QY 337 ILMHLWRYPSLS-----IHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVT 391  
Db 282 FLESDDDFYILSSGLLILLQTTNSVFNKTLKQVIPETLLSWQVRVANMADSG----- 335

QY 392 RHLEDVFSKRNSNKMVSMVMTLGLHPWIAN--ID-DTQYLAAKRAIRTVFGTEPDMIRDG 448  
Db 336 KRWADIFSKYNSGTNNQYMMVLDLKKVKLNSLCKGTLIVEIQIPTVEYSEQTDVLRKG 395

RESULT 289  
ABB49299  
ID ABB49299 standard; protein; 321 AA.  
XX  
AC ABB49299;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Listeria monocytogenes protein #2003.  
XX







DE Hyperthermophile Methanopyrus kandleri protein #531.  
XX  
KW hyperthermophile; protein stability enhancement;  
KW protein activity enhancement.  
XX  
OS Methanopyrus kandleri.  
XX  
PN WO2003076575-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 04-MAR-2003; 2003WO-US006664.  
XX  
PR 04-MAR-2002; 2002US-0361742P.  
PR 14-MAY-2002; 2002US-0380423P.  
PR 16-SEP-2002; 2002US-0410974P.  
XX  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
XX  
PI Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;  
XX  
DR WPI; 2003-748383/70.  
DR N-PSDB; ADM27081.  
XX

PT New isolated nucleic acids encoding any of about 1700 Methanopyrus  
PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
PT as diagnostic agents.  
XX  
PS Claim 31; SEQ ID NO 531; 1023pp; English.  
XX  
CC The invention comprises the amino acid sequence of proteins from the  
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the  
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
CC proteins of the invention are useful for enhancing the stability and/or  
CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
CC a variety of diagnostic and analytical methods. The present amino acid  
CC sequence represents a Methanopyrus kandleri protein of the invention.  
XX  
SQ Sequence 565 AA;

Query Match 4.1%; Score 106.5; DB 7; Length 565;  
Best Local Similarity 23.0%; Pred. No. 2.1;  
Matches 81; Conservative 44; Mismatches 108; Indels 119; Gaps 19;  
QY 88 LGARVASVDMGPQQLPDGQSLPIPPV-----ILAELG---SDPTKGTVC 128  
Db 232 LGAPVA'TLMGKGAFEDHPHPLALGMAGMHGTKAANYALTECDVLLAVGCRFSDRTTGDPS 291  
QY 129 FYG-----HLDVQPAD-----RGDGLTDPYVLTEVDGKLYGRGATDNKGPVL 171  
Db 292 GFAPEAKIIHIDIDPAEIGKNIPVDVPIVGDAKLVLRLDLIKELKRRKYLR---ERK--- 344  
QY 172 AWINAVSAFRALEQDLFPVNIKFIEGMEEAGSVALEELV---EKEKDRFSGVDYIVIS 227  
Db 345 RWGERIEELKA-EVEMPP-----ESTESDQRISPRELVRVLHEALKDR-----DYILTT 392  
QY 228 D----NLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHS----GTFGGILHEPMADLVAL 279  
Db 393 DVGQNQMMAR-----YFPVEEPRR---FISSGGLGTMG-----FGLPAA 429  
QY 280 LGS�VDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLE-----EYRN-- 322  
Db 430 LGAKVAAPKTVAVVGDGGFLMTAQELAT--AVDNDIEVKVFVMDNRLLGMVAAQWRLF 487

QY 323 -SSRVEKFLFDTKKEIIMHLWRY-----PSLSIHGIEGAFDEPGTKTV 364  
Db 488 YDERLSESKLDEKTDIVKLTESYGAAGITVEEPSLESAAVEAFETPGTVVV 539  
RESULT 293  
AAM41091  
ID AAM41091 standard; protein; 1464 AA.

XX AAM41091;  
XX 22-OCT-2001 (first entry)  
XX Human polypeptide SEQ ID NO 6022.  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
(HYSE-) HYSEQ INC.  
PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI60247.  
XX

Novel nucleic acids and polypeptides, useful for treating disorders such  
as central nervous system injuries.

Example 2; SEQ ID NO 6022; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
encoded polypeptides (AAM38642-AAM42213) with nootropic,  
immunosuppressant and cytostatic activity. The polynucleotides are useful  
in gene therapy. A composition containing a polypeptide or polynucleotide  
of the invention may be used to treat diseases of the peripheral nervous  
system, such as peripheral nervous injuries, peripheral neuropathy and  
localised neuropathies and central nervous system diseases, such as  
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
utilisation of the activities such as: Immune system suppression,  
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
assays for receptor activity, arthritis and inflammation, leukaemias and  
C.N.S disorders. Note: The sequence data for this patent did not form  
part of the printed specification

Sequence 1464 AA;

Query Match 4.1%; Score 106.5; DB 4; Length 1464;  
Best Local Similarity 21.3%; Pred. No. 9;  
Matches 89; Conservative 58; Mismatches 151; Indels 119; Gaps 23;  
QY 102 LPDQSQSLPIPPVILAEEL-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPYVLTEVDGKL 158  
Db 958 LPDDPSVPAPPRQFRELPSVPQECTRIYIVRGLELQPD--NNGLCDPIYIKITLGKKV 1015  
QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI-----KFIIEGMEERAGSVALEELVE 211

Db	1016	IEDRDHYIPNTLNPVFGRMVYELSCYLPQEKDLKISVDYDTFTRD--EKVG-----ETIID	1069
QY	212	KEK---DRFFS--GV--DYIVISDNLWISQRKPA-----ITV	241
Db	1070	LENPFLSRFGSHCGIPEEYCVGVNTWRDSLPTQLLQNVAREKGFPPQILSEDSGSRIRY	1129
QY	242	GTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA---DLVALLGSLVDSSGHILVPGIYDE	298
Db	1130	G--GRDYSLDEFEANK-----ILHQHLGAPEERLAL-----HIL-----R	1162
QY	299	VVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIE-----	353
Db	1163	TQGLVPEHVET-RTLHSTFQPNISRYLRVLIWNTKDVIL-----DEKSITGEEMSDIY	1215
QY	354	-----GAFDEPGTKTVIPGRVI---GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSN	405
Db	1216	VKGWIPGNEENKQKTDVHYRSLDGEGNFNRVFFPDYLPAEQLC-----IVAKKE---	1266
QY	406	KMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVEGTEPDMIRDGSTIPIAKMFQEIYVH	462
Db	1267	-----HFW--SIDQTEFRIPRRLIIQIWDNDKFSLDYLGFPRTLTCRHTIH	1311
RESULT 294			
AAM41089			
ID	AAM41089	standard; protein; 1464 AA.	
XX			
AC	AAM41089;		
XX			
DT	22-OCT-2001	(first entry)	
DE	Human polypeptide SEQ ID NO 6020.		
XX			
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;		
XX	leukaemia.		
OS	Homo sapiens.		
XX			
PN	WO200153312-A1.		
XX			
PD	26-JUL-2001.		
XX			
PF	26-DEC-2000; 2000WO-US034263.		
XX			
PR	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00552317.		
PR	20-JUN-2000; 2000US-00598042.		
PR	19-JUL-2000; 2000US-00620312.		
PR	03-AUG-2000; 2000US-00653450.		
PR	14-SEP-2000; 2000US-00662191.		
PR	19-OCT-2000; 2000US-00693036.		
PR	29-NOV-2000; 2000US-00727344.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;		
PI	Zhou P, Goodrich R, Drmanac RT;		
XX			
DR	WPI; 2001-442253/47.		
DR	N-PSDB; AAI60245.		
XX			
PT	Novel nucleic acids and polypeptides, useful for treating disorders such		
PT	as central nervous system injuries.		
XX			
PS	Example 2; SEQ ID NO 6020; 10078pp; English.		
XX			

CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the			
CC	encoded polypeptides (AAM38642-AAM42213) with nootropic,			
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful			
CC	in gene therapy. A composition containing a polypeptide or polynucleotide			
CC	of the invention may be used to treat diseases of the peripheral nervous			
CC	system, such as peripheral nervous injuries, peripheral neuropathy and			
CC	localised neuropathies and central nervous system diseases, such as			
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic			
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the			
CC	utilisation of the activities such as: Immune system suppression,			
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic			
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,			
CC	assays for receptor activity, arthritis and inflammation, leukaemias and			
CC	C.N.S disorders. Note: The sequence data for this patent did not form			
CC	part of the printed specification			
XX				
SQ	Sequence 1464 AA;			
Query Match 4.1%; Score 106.5; DB 4; Length 1464;				
Best Local Similarity 21.3%; Pred. No. 9;				
Matches 89; Conservative 58; Mismatches 151; Indels 119; Gaps 23;				
QY	102	LPDQSLPIPPVILAEI-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPPYVLTEVDGKL	158	
Db	958	LPDDPSVPAPPRQFRELPSVPQECTRIYIVRGLELQPD--NGLCDPYIKITLGKKV	1015	
QY	159	Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIIEGMEEGSVALBELVE	211	
Db	1016	IEDRDHYIPNTLNPVFGRMVYELSCYLPQEKDLKISVDYDTFTRD--EKVG-----ETIID	1069	
QY	212	KEK---DRFFS--GV--DYIVISDNLWISQRKPA-----ITY	241	
Db	1070	LENPFLSRFGSHCGIPEEYCVGVNTWRDSLPTQLLQNVAREKGFPPQILSEDSGSRIRY	1129	
QY	242	GTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA---DLVALLGSLVDSSGHILVPGIYDE	298	
Db	1130	G--GRDYSLDEFEANK-----ILHQHLGAPEERLAL-----HIL-----R	1162	
QY	299	VVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIE-----	353	
Db	1163	TQGLVPEHVET-RTLHSTFQPNISRYLRVLIWNTKDVIL-----DEKSITGEEMSDIY	1215	
QY	354	-----GAFDEPGTKTVIPGRVI---GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSN	405	
Db	1216	VKGWIPGNEENKQKTDVHYRSLDGEGNFNRVFFPDYLPAEQLC-----IVAKKE---	1266	
QY	406	KMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVEGTEPDMIRDGSTIPIAKMFQEIYVH	462	
Db	1267	-----HFW--SIDQTEFRIPRRLIIQIWDNDKFSLDYLGFPRTLTCRHTIH	1311	
RESULT 295				
AAM41090				
ID	AAM41090	standard; protein; 1464 AA.		
XX				
AC	AAM41090;			
XX				
DT	22-OCT-2001	(first entry)		
XX				
DE	Human polypeptide SEQ ID NO 6021.			
XX				
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;			
KW	peripheral nervous system; neuropathy; central nervous system; CNS;			
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;			
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;			
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;			
XX	leukaemia.			
OS	Homo sapiens.			
XX				
PN	WO200153312-A1.			
XX				
PD	26-JUL-2001.			





Db 6 PFKLLEKAKDY-----QADNTRFLRDMVAIPSESCDEKRVVHRIKEE-----ME 50  
QY 87 RLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCFCYCHLDVQPADRGDWLT 146  
Db 51 KVGFDKVEID-----PMGN-----VLGYIGHGPR--LVAMDAHIDTVGIGNIKNWDF 95  
QY 147 DPVVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVAL 206  
Db 96 DRYEGMETDELIGRGTSDOEGMASVMVYAGKIIKDL-----GLEDEYTLIV 142  
QY 207 EELVEKEKDRFFSGV--DYIVISDNL---WISQRKPA---ITYGRGNSYFMVEVK---C 255  
Db 143 TGTVQEEED---CDGLCWQYIIEQSGIRPEFVWSTEPTDCQVYRQGRMEIRIDVQGVSC 199  
QY 256 RDQDFHSG-----TFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV---PLTEEEI 307  
Db 200 HGSAPERGDNAIFKMGPIIGE-LQELSORLG-----YDEFLGKGTLTIVSEI 244

RESULT 297

ABG09034

ID ABG09034 standard; protein; 583 AA.

XX AC ABG09034;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #9025.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS73221.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity.  
XX PS Claim 20; SEQ ID NO 39393; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain  
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX CC and in recombinant production of (II). The polynucleotides are also used  
XX CC in diagnostics as expressed sequence tags for identifying expressed  
XX CC genes. (I) is useful in gene therapy techniques to restore normal  
XX CC activity of (II) or to treat disease states involving (II). (II) is  
XX CC useful for generating antibodies against it, detecting or quantitating a  
XX CC polypeptide in tissue, as molecular weight markers and as a food  
XX CC supplement. (II) and its binding partners are useful in medical imaging  
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders  
XX CC involving aberrant protein expression or biological activity. The  
XX CC polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 583 AA;

Query Match 4.0%; Score 105.5; DB 4; Length 583;  
Best Local Similarity 21.7%; Pred. No. 2.7;  
Matches 78; Conservative 50; Mismatches 120; Indels 111; Gaps 23;

QY 102 LPDQGSPLPIPPVILAEEL-GSDPTKGTVCFY--GHLDVQPADRGDWLTDPYVLTVDGKL 158  
Db 28 LPDDPSVPAPPRQFRELPSVPQECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKKV 85  
QY 159 Y---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIIEGMEEAGSVALBELVE 211  
Db 86 IEDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVVDYDTFTRD--EKVG---ETIID 139  
QY 212 KEKDRFFS-----GV--DYIVISDNLWISQRKPA-----IT 240  
Db 140 LE-NRFLSRFGSHCGIPEEYCVSGVNTWRDSLRPTQLLQNVARFKGFPQPILSEDSRIR 198  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMA---DLVALLGSLVDSSGHILVPGIYD 297  
Db 199 YG--GRDYSLDEFEANK-----ILHQHLGAPEERLAL-----HIL----- 231  
QY 298 EVVPLTEEEINTYKAJHLDLEEYRNSRVEKFLFTKBEILMHLWR---YPSLSIHGIEG 354  
Db 232 RTQGLVPEHVET-RTLHSTFQPNISQGT-----LQMWGGMFFPK----- 270  
QY 355 AFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT-RHLEDVFSK----RNSSNK 406  
Db 271 SLGPPGPPFNITPRKAKKYLRVVIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEENK 329

RESULT 298

ABG09032

ID ABG09032 standard; protein; 1430 AA.

XX AC ABG09032;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #9023.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS73219.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity.  
XX PS Claim 20; SEQ ID NO 39393; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain  
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX CC and in recombinant production of (II). The polynucleotides are also used  
XX CC in diagnostics as expressed sequence tags for identifying expressed  
XX CC genes. (I) is useful in gene therapy techniques to restore normal  
XX CC activity of (II) or to treat disease states involving (II). (II) is  
XX CC useful for generating antibodies against it, detecting or quantitating a  
XX CC polypeptide in tissue, as molecular weight markers and as a food  
XX CC supplement. (II) and its binding partners are useful in medical imaging  
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders  
XX CC involving aberrant protein expression or biological activity. The  
XX CC polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity













SQ	Sequence 1378 AA;	
	Query Match	4.0%; Score 104.5; DB 4; Length 1378;
	Best Local Similarity	20.0%; Pred. No. 13;
	Matches 109; Conservative	80; Mismatches 189; Indels 167; Gaps 30;
QY	1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKFQYIDLHQDE-----	48
Db	350 LEDKCGKLDPTFASATLLF-----QKDDPADVQ-LFQEVPKQSEEDMVGRLPHLA	400
QY	49 -----FVQTLKEWVAIESDSVQVPVR-----FRQELFRMMAVAADTLQRL	88
Db	401 ADMQPLVRPCTVTTFLATRMSCLSGWSAPAGPTPRSSIEMKFKNMLFPMIVCPAWI----	456
QY	89 GARVASVDMGPPQQLPDGOSLPPIPV---ILAELGSDPTKGTVCFYGHLDVQPADRGDGL	145
Db	457 -PELNSVEHGPDGISFGAACPLSIVEKTLVDAVAKLPAQKTEVFRGVLEQL-----RWF	509
QY	146 TDPYV--LTEVDGKLYGRGATDNKGPVL---AWINAVSAFRALEQDLPVNIKFIEGME	199
Db	510 AGKQKSVASVCGNIITASPIISDLNPVFMASGAKTLVSRGELPEAEVQE-----EGLG	563
QY	200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWIS---QRKPAITYGTRGNSYFMVEVKR	256
Db	564 GEKSHQIGHFLEKQSSK-FSDPAFPVI---WIQGSMENVPLVDGKAG--YFL----CR	612
QY	257 DQDFHSGTGGILHEPMDLVALGSLVDSSGHILVPGIYDEVV-----PLTEE	305
Db	613 --EFTAGT-----ATCMPYLVGHQENCPD--GPHLLPWLQKDPAPGGDTALHRDPLQOG	663
QY	306 EINT-----YKAHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG	360
Db	664 EIQTIREYK--HLSANKLENLEEMDKFL-DT-----YTLPRLNQKEVE-SLNRPI	711
QY	361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQ-----VTRHLEDV-FSKRNSNKMVV	409
Db	712 T-----GAEIUPIINSPLTKKSSGLDGFTAEFYQRYKEELHINRTKDKNHMII	759
QY	410 SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFQEI	462
	Query Match	4.0%; Score 104.5; DB 4; Length 1379;
	Best Local Similarity	20.0%; Pred. No. 13;
	Matches 109; Conservative	80; Mismatches 189; Indels 167; Gaps 30;
QY	1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKFQYIDLHQDE-----	48
Db	350 LEDKCGKLDPTFASATLLF-----QKDDPADVQ-LFQEVPKQSEEDMVGRLPHLA	400
QY	49 -----FVQTLKEWVAIESDSVQVPVR-----FRQELFRMMAVAADTLQRL	88
Db	401 ADMQPLVRPCTVTTFLATRMSCLSGWSAPAGPTPRSSIEMKFKNMLFPMIVCPAWI----	456
QY	89 GARVASVDMGPPQQLPDGOSLPPIPV---ILAELGSDPTKGTVCFYGHLDVQPADRGDGL	145
Db	457 -PELNSVEHGPDGISFGAACPLSIVEKTLVDAVAKLPAQKTEVFRGVLEQL-----RWF	509
QY	146 TDPYV--LTEVDGKLYGRGATDNKGPVL---AWINAVSAFRALEQDLPVNIKFIEGME	199
Db	510 AGKQKSVASVCGNIITASPIISDLNPVFMASGAKTLVSRGELPEAEVQE-----EGLG	563
QY	200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWIS---QRKPAITYGTRGNSYFMVEVKR	256
Db	564 GEKSHQIGHFLEKQSSK-FSDPAFPVI---WIQGSMENVPLVDGKAG--YFL----CR	612
QY	257 DQDFHSGTGGILHEPMDLVALGSLVDSSGHILVPGIYDEVV-----PLTEE	305
Db	613 --EFTAGT-----ATCMPYLVGHQENCPD--GPHLLPWLQKDPAPGGDTALHRDPLQOG	663
QY	306 EINT-----YKAHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG	360
Db	664 EIQTIREYK--HLSANKLENLEEMDKFL-DT-----YTLPRLNQKEVE-SLNRPI	711
QY	361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQ-----VTRHLEDV-FSKRNSNKMVV	409
Db	712 T-----GAEIUPIINSPLTKKSSGLDGFTAEFYQRYKEELHINRTKDKNHMII	759
QY	410 SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFQEI	462
Db	760 S-----IDAEKAFDKI--QQPFMLKTLNKLGDGTLYLKIIRAIYDKPT	800
QY	463 KSVVL 467	
Db	801 ANIIL 805	
	RESULT 304	
ABG10257		
ID	ABG10257 standard; protein; 1379 AA.	
XX		
AC	ABG10257;	
XX		
DT	13-FEB-2002 (first entry).	
XX		
DE	Novel human diagnostic protein #10248.	
XX		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200175067-A2.	
XX		
PD	11-OCT-2001.	
XX		
PF	30-MAR-2001; 2001WO-US0008631.	
XX		
PR	31-MAR-2000; 2000US-00540217.	
PR	23-AUG-2000; 2000US-00649167.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		

PI	Drmanac RT, Liu C, Tang YT;	
XX		
DR	WPI; 2001-639362/73.	
DR	N-PSDB; AAS74444.	
XX		
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
PT	biodiversity.	
XX		
PS	Claim 20; SEQ ID NO 40616; 103pp; English.	
XX		
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
CC	sequences. (I) is useful as hybridisation probes, polymerase chain	
CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,	
CC	and in recombinant production of (II). The polynucleotides are also used	
CC	in diagnostics as expressed sequence tags for identifying expressed	
CC	genes. (I) is useful in gene therapy techniques to restore normal	
CC	activity of (II) or to treat disease states involving (II). (II) is	
CC	useful for generating antibodies against it, detecting or quantitating a	
CC	polypeptide in tissue, as molecular weight markers and as a food	
CC	supplement. (II) and its binding partners are useful in medical imaging	
CC	of sites expressing (II). (I) and (II) are useful for treating disorders	
CC	involving aberrant protein expression or biological activities. The	
CC	polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic	
CC	amino acid sequences of the invention. Note: The sequence data for this	
CC	patent did not appear in the printed specification, but was obtained in	
CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 1379 AA;	

	Query Match	4.0%; Score 104.5; DB 4; Length 1379;
	Best Local Similarity	20.0%; Pred. No. 13;
	Matches 109; Conservative	80; Mismatches 189; Indels 167; Gaps 30;
QY	1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKFQYIDLHQDE-----	48
Db	350 LEDKCGKLDPTFASATLLF-----QKDDPADVQ-LFQEVPKQSEEDMVGRLPHLA	400
QY	49 -----FVQTLKEWVAIESDSVQVPVR-----FRQELFRMMAVAADTLQRL	88
Db	401 ADMQPLVRPCTVTTFLATRMSCLSGWSAPAGPTPRSSIEMKFKNMLFPMIVCPAWI----	456
QY	89 GARVASVDMGPPQQLPDGOSLPPIPV---ILAELGSDPTKGTVCFYGHLDVQPADRGDGL	145
Db	457 -PELNSVEHGPDGISFGAACPLSIVEKTLVDAVAKLPAQKTEVFRGVLEQL-----RWF	509
QY	146 TDPYV--LTEVDGKLYGRGATDNKGPVL---AWINAVSAFRALEQDLPVNIKFIEGME	199
Db	510 AGKQKSVASVCGNIITASPIISDLNPVFMASGAKTLVSRGELPEAEVQE-----EGLG	563
QY	200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWIS---QRKPAITYGTRGNSYFMVEVKR	256
Db	564 GEKSHQIGHFLEKQSSK-FSDPAFPVI---WIQGSMENVPLVDGKAG--YFL----CR	612
QY	257 DQDFHSGTGGILHEPMDLVALGSLVDSSGHILVPGIYDEVV-----PLTEE	305
Db	613 --EFTAGT-----ATCMPYLVGHQENCPD--GPHLLPWLQKDPAPGGDTALHRDPLQOG	663
QY	306 EINT-----YKAHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG	360
Db	664 EIQTIREYK--HLSANKLENLEEMDKFL-DT-----YTLPRLNQKEVE-SLNRPI	711
QY	361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQ-----VTRHLEDV-FSKRNSNKMVV	409
Db	712 T-----GAEIUPIINSPLTKKSSGLDGFTAEFYQRYKEELHINRTKDKNHMII	759
QY	410 SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFQEI	462





PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 37108; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activities. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1788 AA;

Query Match 4.0%; Score 104.5; DB 4; Length 1788;  
Best Local Similarity 20.0%; Pred. No. 19;  
Matches 109; Conservative 80; Mismatches 189; Indels 167; Gaps 30;  
QY 1 MDPKGLGRMAASLLAVLLLLLGERGMFSSPPPALLEKVFQYIDLHQDE----- 48  
Db 350 LEDKCGKLDPTFASATLLF-----QKDPADVQ-LFQEVKQSEEDMVGRLPHLA 400  
QY 49 -----FVQTLKEWVAIESDSVQPVPR-----FRQELFRMMAVAADTLQRL 88  
Db 401 ADMQPLVRPCTVTTFLATRMSCLSGWSPAGPFRSSIEMKFKNMLFPMIVCPAWI---- 456  
QY 89 GARVASVDMGPPQQLPDQSLPIPPV---ILAEIGSDPTKGTVCYFCHLDVQPADRGDWL 145  
Db 457 -PELNSVEHGPDGISFGAACPLSIVEKTLVDVAKLPAQKTEVFRGVLEQL-----RWF 509  
QY 146 TDPYV--LTEVDGKLYGRGATDNKGPVL-----AWINAVSAFRALEQDLPVNIKFIIEGME 199  
Db 510 AGQVKSVASVGGNIITASPIDLNPFVMASGAKTLVSRGELPEAEVQE-----EGLG 563  
QY 200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWIS---QRKPAITYGTRGNSYFMVEVKCR 256  
Db 564 GEKSHQIGHFLEXQSSK-FSDPAFPVI---WIQGSMENVPGLVDGKAG--YFL-----CR 612  
QY 257 DQDFHSGTGGILHEPMAADLVALLGSLVDSSGHILVPGIYDEVV-----PLTEE 305  
Db 613 --EFTAGT-----ATCMPYLVGHQENCPD--GPHLLPWLQKDPAEPPGGDTALHRDPLQQG 663  
QY 306 EINT-----YKATHLDLEEYRNSRRVEKFLFTKEEILMHLWRYPSPLSIHGIEGAFDEPG 360  
Db 664 EIQTITREYK--HLSANKLENLEEMDKFL-DT-----YTLPRLNQKEVE-SLNRPI 711  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQ-----VTRHLEDV-FSKRNSSNKMVV 409  
Db 712 T-----GAEIVPIINSLPTKSSGLDGFTAEFYQRYKEELHINRTKDKNHMII 759  
QY 410 SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFQEI VH 462  
Db 760 S-----IDAEKAFDKI--QQPFMLKTLNKLIGDGTYLKIIRAIYDKPT 800  
QY 463 KSVVL 467  
: : : |

Db 801 ANIIL 805  
RESULT 307  
ADJ69296  
ID ADJ69296 standard; protein; 2048 AA.  
XX  
AC ADJ69296;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human heat mitochondrial protein as a therapeutic target SeqD1102.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
OS Homo sapiens.  
XX  
PN WO2003087768-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 04-APR-2003; 2003WO-US010870.  
XX  
PR 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX  
DR WPI; 2003-845369/78.  
XX  
PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX  
PS Claim 1; SEQ ID NO 1102; 180pp; English.  
XX  
CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 2048 AA;

Query Match 4.0%; Score 104.5; DB 7; Length 2048;  
Best Local Similarity 21.7%; Pred. No. 23;  
Matches 78; Conservative 49; Mismatches 118; Indels 115; Gaps 21;  
QY 102 LPDQGSLEPPPVILAEEL-GSDPTKGTVCFY--GHLDVQPADRGDWLTPPYVLTEVDGKL 158  
Db 1516 LPDDPSVPAPPQRGRGLPDSVPQECTVRIYIVRGLELQPD--NNGLCDPYIKITLGKV 1573

Qy	159	Y	---GRGATDNKGPVLAWINAVSAFRALEQDLPVNI---	KFIIEGMEEAGSVALEELVE	211
Db	1574	I	EDRDHYIPNTLNPVFGRMVELSCYLPQEKDLKISVYDYDTFRD--	EKVG---ETIID	1627
Qy	212	K	KDRFFS-----GV--DYIVISDNLWISQKKPA-----	IT	240
Db	1628	L	E-NRFLSRFGSHCGIPEEYCVSGVNTWRDQLRPTQLLQNVARFKGFPQILSE	DGSRIR	1686
Qy	241	Y	GTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV		300
Db	1687	Y	G--GRDYSLDFEANK-----ILHQ-----	HLGAP-----	1710
Qy	301	P	LTEEEINTYKAHILDLEEYRNSRVEKFLFTKBEILMHLWRYPSLS-----	IHGIE	353
Db	1711	--E	ERL-----ALHI-----LRTQGLVPEHVETRTLHSTFQPNISQKLMWVDVFP		1755
Qy	354	G	AFDEPGTKTVIPGRVIGKFSIRLV--PHMNVSAVEKQVT-RHLEDVFSK----	RNSSNK	406
Db	1756	K	SLGPPGPPFNITPRKAKKYLRVLIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEENK		1815
RESULT 308					
ABG14767					
ID	ABG14767 standard; protein; 2563 AA.				
XX	ABG14767;				
AC					
XX					
DT	18-FEB-2002 (first entry)				
XX					
DE	Novel human diagnostic protein #14758.				
XX					
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;				
KW	food supplement; medical imaging; diagnostic; genetic disorder.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200175067-A2.				
XX					
PD	11-OCT-2001.				
XX					
PF	30-MAR-2001; 2001WO-US008631.				
XX					
PR	31-MAR-2000; 2000US-00540217.				
PR	23-AUG-2000; 2000US-00649167.				
XX					
PA	(HYSE-) HVSEQ INC.				
XX					
PI	Drmanac RT, Liu C, Tang YT;				
XX					
DR	WPI; 2001-639362/73.				
DR	N-PSDB; AAS78954.				

CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 CC  
 XX Sequence 2563 AA;

Query Match	4.0%;	Score 104.5;	DB 4;	Length 2563;
Best Local Similarity	20.0%;	Pred. No. 33;		
Matches 109;	Conservative 80;	Mismatches 189;	Indels 167;	Gaps 30;

  

QY	1	MDPKLGRMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHQDE-----	48
Db	350	LEDKCGKLDPTFASATLLF-----QKDPADVQ-LFQEVKQSEEDMVGRLPHLA	400
QY	49	-----FVQTLKEWVAIESDSVQVPR-----FRQELFRMMAVAADTLQRL	88
Db	401	ADMQPLVRPCTVTTFLATRMSCLSGWSPPAGPTPRSSIEKMKMLFPMIVCPAWI----	456
QY	89	GARVASVDMGQQLPDGQSLPIPPV---ILABELSDPTKGTVCFYGHLDVQPADRGDWL	145
Db	457	-PELNSVEHGPDGISFGAACPLSIVEKTLVDVAKLPAQKTEVFRGVLEQL-----RWF	509
QY	146	TDPYV--LTEVDGKLYGRGATDNKGPVL----AWINAVSAFRALEQDLFVNKFIIEGME	199
Db	510	AGQVKSVASVGGNIITASPIDLNPVFMASGAKLTLVSRGELPEAEVQE-----EGLG	563
QY	200	EAGSVALEELVEKEKDRFFSGVDYIIVISDNLWIS---QRKPAITYGTRGNSYFMVEVKCR	256
Db	564	GEKSHQIGHFLEKQSSK-FSDPAFPVI---WIOGSMENVPLVDGKAG--YFL-----CR	612
QY	257	DQDFHSGTFGGILHEPMDLVALLGSLVDSSGHILVPGIYDEW-----PLTEE	305
Db	613	--EFTAGT-----ATCMPYLVGHQENCPS--GPHLLPWLQKDPAPGGDTALHRDPLQOG	663
QY	306	EINT-----YKATHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360
Db	664	EIQTTIREYK--HLSANKLENLEEMDKFL-DT-----YTLPRLNQKEVE-SLNRPI	711
QY	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQ-----VTRHLEDV-FSKRNSNKMVV	409
Db	712	T-----GAEIVPIINSLPTKSSGLDGTAEFYQRYKEELHINRTKDKNHMII	759
QY	410	SMTGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFOEIVH	462
Db	760	S-----IDA EKAFDKI--QQPFMLKTLNKLIGIDGTYLKIIRAIYDKPT	800
QY	463	KSVVL 467	
Db	801	ANIIL 805	

  

RESULT 309  
 ABB62643  
 ID ABB62643 standard; protein; 340 AA.  
 XX  
 AC ABB62643;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 14721.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX pharmaceutical.  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX



```
PD 27-SEP-2001.
XX
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06746.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 14721; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 340 AA;

Query Match 4.0%; Score 104; DB 4; Length 340;
Best Local Similarity 22.9%; Pred. No. 1.6;
Matches 61; Conservative 42; Mismatches 103; Indels 60; Gaps 14;

QY 104 DGQSLPI-----PPVILAE LGS DPTKGTVC FYGHLDVQPADRGDWLTDPYVL-T 152
Db 42 DSLNLPVEVFPVAVKSPVVIKWE GSKLPSTILSSHMDVVPV-FPEWTHPEFSADI 100
QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRA--LEQDLPVNIKFIIEGMEHAGSV-ALEEL 209
Db 101 DEEGRIFARGAQDKMSVGTQYLGAI RLLRADGFQPKRTLYVTFVPD--EEIGGIHGMAAF 158
QY 210 VE----KEKDRFF-----SGVDYIVISDNL-WISQRKPAITYGTRGNSYFMVEVKC 255
Db 159 VETDFYKQMNVGFSLDDEGGTSASDVHHLFYAERIRWILKLKVA---GTAGHGSLLL---- 211
QY 256 RDQDFHSGTFGGILHEPMADLVAL LGS LVD-----SSGHI-----LVPGIYDEVV 300
Db 212 -----PDTAGVKLN YVNLKLT EFR ESQIRLKNDKSLSIGDVTTVNLTLQLSGGVQSNV 265
QY 301 -PLTEEEINTYKAHLDLEEYRNSR 325
Db 266 PPLFEAIFDIRLAITLDLVAFEREIR 291

RESULT 310
AAU41311
ID AAU41311 standard; protein; 458 AA.
XX
AC AAU41311;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #2207.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
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OS Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonmeuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59514.
DR
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 2506; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 458 AA;
```

```
Query Match 4.0%; Score 104; DB 4; Length 458;
Best Local Similarity 22.9%; Pred. No. 2.5;
Matches 83; Conservative 51; Mismatches 155; Indels 74; Gaps 20;

QY 43 DLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQL 102
Db 21 DCPQAEVVDICSRMIQIDSONFGPQDA-RGEV-EMCHYVTGLLDEIGVGVTLHESEPGRV 78
QY 103 PDGQSLPIPPVILAE L-----GSDPTKGTVC FYGHLDVQPADRGDWLTDPYVLTEVDGKLY 159
Db 79 -----TLVAEWAPEGTDTSR PALLLHGHS DTVPF EAAD-WTHHFLSGEIH DNCVW 127
QY 160 GRGATDNKGPVLAWINAVSAFRALEQ--DLPVN-IKFIIEGMEEAGSVALEELVEKEKDR 216
Db 128 GRGAIDMKG-FLAMV--LSAIRARQRGEVPSRPIRFIMFADEECSGTLGSLWLGATHPE 184
QY 217 FFGVDYIVISDNLWISQRK-----AITYGTRGNSYFMVEVKCRDQDFHSGTFG-GIL 269
Db 185 AFDGVTE-AISEVGGFSLTTPQGRVYVVIQSAEKLWFRMSA-----TGSTGHGSM 235
QY 270 HEPMADLVAL LGS L--VDSSGHILVPGIYDEVVPLTEEEINTYKA---IHL DLEEYRNS 324
Db 236 RNPDNVAVTRVLDALSRIDS---YQWPD LHH---PVQEEFLNQVAMWGLTIDRDDLESS- 288
```

QY 325 RVEKFLDFTKEEILMHLWRYPSLS-----IHGIEGAFDEPGTK-TVIPGRVIGKFSIR 376  
Db 289 -----LSPIGSLSRMVAACCAHNVTPTVLSAGYKVNVPTRASAEVDAR 332  
QY 377 LVP 379  
Db 333 FIP 335

RESULT 311  
ABM37830  
ID ABM37830 standard; protein; 458 AA.  
AC ABM37830;  
XX 20-OCT-2003 (first entry)  
DT  
XX Propionibacterium acnes predicted ORF-encoded polypeptide #2506.  
DE  
XX  
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
KW immunostimulant; immune response; vaccine.  
XX  
OS Propionibacterium acnes.  
XX  
XX WO2003033515-A1.  
PN  
XX  
PD 24-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032727.  
XX  
PR 15-OCT-2001; 2001US-00978825.  
XX  
XX (CORI-) CORIXA CORP.  
PA  
XX  
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
PI Barth B, Vallieve-Douglass J;  
XX  
DR WPI; 2003-381789/36.  
DR N-PSDB; ACF64443.  
XX

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.  
Example 1; SEQ ID NO 2506; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 458 AA;  
Query Match 4.0%; Score 104; DB 6; Length 458;  
Best Local Similarity 22.9%; Pred. No. 2.5;  
Matches 83; Conservative 51; Mismatches 155; Indels 74; Gaps 20;  
QY 43 DLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPQQL 102  
Db 21 DCPQAEVVDICSRMIQIDSQNFGPQDA-RGEV-EMCHYVTGLLDEIGVGTLHSEFGRV 78  
QY 103 PDGQSLPIPPVILAE---GSDPTKGTVCFCYGHLDVQPADRGDGLTDPYVLTVEVDGKLY 159  
Db 79 -----TLVAEWAPEGTDTSRPALLLHGHSDTVFFEAAD-WTHHPLSCEIHDNCVW 127  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQ--DLPVN-IKPIIEGMEEAGSVALEELVEKEKDR 216  
Db 128 GRGAIDMKG-FLAMV--LSAIRARQRRGEVPSRPPIRFIMFADEECSTGLGSTWLGATHPE 184  
QY 217 FFGVDYIVISDNLWISQKRP-----AITYGTRGNSYFMVEVKCRDQDFHSGTFG-GIL 269  
Db 185 AFDGVTE-AISEVGGFSLTTPQGRVYVIQSAEKGMLWFRMSA-----TGSTGHGSM 235  
QY 270 HEPMADLVALLGSL--VDSSGHILVPGIYDEVVPLTEEEINTYKA---IHLDEEYRNSS 324  
Db 236 RNPDNAVTRVLDALSRIDS---YQWPDLHH---PQOEFLNQVAAMWGLTIDRDDLESS- 288  
QY 325 RVEKFLDFTKEEILMHLWRYPSLS-----IHGIEGAFDEPGTK-TVIPGRVIGKFSIR 376  
Db 289 -----LSPIGSLSRMVAACCAHNVTPTVLSAGYKVNVPTRASAEVDAR 332  
QY 377 LVP 379  
Db 333 FIP 335

RESULT 312  
ABU19192  
ID ABU19192 standard; protein; 1155 AA.  
XX  
AC ABU19192;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #4719.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Borrelia burgdorferi.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA23062.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 471116; 1766pp; English.

PS The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1155 AA;

Query Match 4.0%; Score 104; DB 6; Length 1155;  
Best Local Similarity 20.7%; Pred. No. 11;  
Matches 75; Conservative 55; Mismatches 113; Indels 120; Gaps 19;

QY 174 INAVSAFRALEQDLPVNIKPIIEGMEEA-----GSVALE-----ELVE 211

Db 26 LNSYEKFLQLDK-LKSKKPLLNEGLESVFRNFFPIKSGNGDVALEYERYIENDALNFTE 84

QY 212 KEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHE 271

Db 85 KECKR--KGQSYEAV-----LKVRLNLQFLTTEIRQKDVVMGTI----- 122

QY 272 PMADLVALLGS-LVDSSGHILV-----PGI--YDEVVPLTEEEINTYKAHLDLE---- 318

Db 123 ---PLMTERGTFIINGAERVVVSQIHRSPGVVYKE-KDLYSARIIPYKGSWLEFEIDSK 178

QY 319 ---EYRNSSRVEKFL-----FDTKEEILMHLWRYPSSLISIHGIEGAFDEPGTKTVIP 366

Db 179 KDLYVKIDRKXRIILTLFLRALGFDTRKTIETTFYNIKKIKV-----EDGTRDLP 230

QY 367 GRVIGKFSIRLVPNMVNSAVEKQVTRHLEDVFSKRNSNKMVMSMTLGLHPWIANIDDTQ 426

Db 231 GQYLAK-SINIRENNMYRAGDKITLQDVEDFL--QNGWNEIE-----LVDFDGYN 277

QY 427 YLAAKRAIRT-----VFGTEPDMIRDGSTIPIAKMFQEIHVKSVVLIPLGAVD 474

Db 278 DISGKRFVSSNVILNCKEKEDAFFA-----LKDGS-----KELPKESVWLAVYGSLF 324

QY 475 DGE 477

Db 325 PGE 327

ID ABM00025 standard; protein; 260 AA.

XX AC ABM00025;

XX DT 02-APR-2003 (first entry)

XX DE Allergen Hevb8 SEQ ID NO 16.

XX KW Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity; detergent; personal care composition; cosmetic.

XX OS Unidentified.

XX PN WO200183559-A2.

XX PD 08-NOV-2001.

XX PF 30-APR-2001; 2001WO-DK000293.

XX PR 28-APR-2000; 2000DK-00000707.

XX PR 10-MAY-2000; 2000US-0203345P.

XX PR 28-FEB-2001; 2001DK-00000327.

XX PR 21-MAR-2001; 2001US-0277817P.

XX PA (NOVO ) NOVOZYMES AS.

XX PI Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;

XX WPI; 2001-626552/72.

XX Selecting protein variants having modified immunogenicity, used to produce vaccines, detergents and personal care compositions, involves localizing epitope sequences on the three-dimensional structure of a protein.

XX Claim 55; Page 492; 513pp; English.

XX The invention relates to selecting a protein variant having modified immunogenicity, compared to a parent protein, comprising using the antibody binding sequence to localise epitope sequences on the three dimensional structure of the parent protein and defining an epitope area including amino acids within 5 Angstrom of the epitope amino acids. The method is useful for identifying structural epitopes on the 3-dimensional surface of commercial and environmental allergens. Compositions containing the protein variants are used as vaccines, detergents and personal care compositions, e.g. shampoo, balsam, hair conditioners, hair waving compositions, hair dyeing compositions, hair tonic, hair liquid, hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen, shaving foam, cream soap, skin milk or foundation. The present sequence is that of a polypeptide of the invention

XX SQ Sequence 260 AA;

Query Match 3.9%; Score 103.5; DB 4; Length 260;  
Best Local Similarity 22.9%; Pred. No. 1.2;  
Matches 64; Conservative 36; Mismatches 64; Indels 115; Gaps 17;

QY 144 WLT--DPYVLTVDG-KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKPIIEGMEE 200

Db 2 WQTYVDHLMCDIDGRLTAAGIIGHDGSVWAQSSFPQFKSDE-----VAAVMKDFDE 55

QY 201 AGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP-AITYGTRGNSYFMVEVKCRDQD 259

Db 56 PGSLAPTGL-----HLGGTKYMWI-----QGEPGA VIRKKS----- 88

QY 260 FHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN----- 308

Db 89 -----GGI-----TVKRTGQALIIGIYDE--PLTPGQCNMIVERLGDYLL 126

QY 309 -----TYKAIHL--DLEEYRNSSRVEKFLDFTKEEILMH---LW-----RYPSLSI 349

Db 127 DQGLSWQTYVDDHLMCDIDGRL-----TAAAIIGHDGSVWAQSSFPQFKSDEV 176





RESULT 315  
 ADA89636  
 ID ADA89636 standard; protein; 805 AA.  
 XX  
 AC ADA89636;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Staphylococcus aureus antigenic protein #175.  
 XX  
 KW antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;  
 KW antibacterial; neuroprotective; immunosuppressive; antiinflammatory;  
 KW antitumor; immunostimulant; ophthalmological; pathogenic microbe;  
 KW bacteraemia; septic shock; organ infection; skin infection;  
 KW bacterial basal colonisation; bacterial eye infection; peritonitis; septicaemia;  
 KW tuberculosis; food poisoning; blood infection; gonorrhoea; endocarditis;  
 KW sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;  
 KW necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;  
 KW gastro-enteritis; dysentery; shigellosis; skin disorder.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 PN WO2003011899-A2.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-GB003606.  
 XX  
 PR 02-AUG-2001; 2001GB-00018825.  
 PR 09-JAN-2002; 2002GB-00000349.  
 XX  
 PA (UYSH-) UNIV SHEFFIELD.  
 PA (BIOS-) BIOSYNEXUS INC.  
 XX  
 PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;  
 XX  
 DR WPI; 2003-256434/25.  
 XX  
 DT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,  
 XX useful as a vaccine for immunizing humans against e.g. bacteremia, septic  
 PT shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or  
 PT impetigo.  
 XX  
 PS Claim 4; Page 155-156; 189pp; English.  
 XX  
 CC The present invention describes an antigenic protein or its part, which  
 CC is for use as a vaccine. The antigenic protein is encoded by an isolated  
 CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene  
 CC sequences (designated dnaSA and dna SE, respectively; and which encodes a  
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine  
 CC composition comprising at least one antigenic protein; (2) a method of  
 CC immunising an animal against a disease or condition caused by a  
 CC pathogenic microbe by administering the antigenic protein or the vaccine;  
 CC (3) an antibody or its binding part obtainable by the method above; (4)  
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a  
 CC hybridoma cell line produced by the method of (4); and (6) identifying  
 CC opsonic antigens expressed by a pathogenic microbe. The antigenic  
 CC proteins have antibacterial, neuroprotective, immunosuppressive,  
 CC antiinflammatory, antitumor, immunostimulant and ophthalmological  
 CC activities, and can be used in vaccines. The antigenic proteins or  
 CC vaccines can be used for immunising an animal (specifically a human)  
 CC against a disease or condition caused by a pathogenic microbe, e.g.  
 CC bacteraemia, septic shock, organ infection, skin infection, bacterial  
 CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,  
 CC bacteria-associated food poisoning, blood infections, peritonitis,  
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,  
 CC strep throat, streptococcal-associated toxic shock, necrotising  
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,  
 CC dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning,  
 CC skin disorders, S. epidermidis-associated septicaemia, peritonitis or  
 CC endocarditis. The present sequence represents a S. aureus antigenic  
 CC protein sequence from the present invention.  
 XX

CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ

Query Match 3.9%; Score 103.5; DB 6; Length 932;  
Best Local Similarity 21.8%; Pred. No. 8.5;  
Matches 79; Conservative 50; Mismatches 136; Indels 97; Gaps 16;

QY 144 WLTPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFR---ALEQDLPVNIKFIEGMEE 200  
Db 305 WIEQPLI-----NKNPIENRLNAVEELLNNSLQEDLKSIYDIERI 349  
QY 201 AGSVALEELVEKEKDRF---FSGVDYIVISDNLWISQRPKPAITYGTFGNSYFMVEVKCRD 257  
Db 350 VGKVASKSVNAKELISLKCSIGKVPYI---KEYLSNFK-----SDLFLNMEQCID 396  
QY 258 --QDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHL 315  
Db 397 TLEDIHKLKLDKALDNP-----SLSVKEGNIKEGFNEEVDLSREAKSNGKKWI-A 446  
QY 316 DLEBYRNSRVEKEFLFDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVPGRVIGKFSI 375  
Db 447 SLEQKEKETGIKSL-----KVSYNKVFGYFIE-----ITKANL 480  
QY 376 RLVPH-----MNVSAVEKQVTRHLEDVFSKRNSSNKMVSMTLGLHPWI-----ANIDD 424  
Db 481 NLVPEGRYIRKQTLNAERYITPELKEMEEKILGABEKLIDIEYKLFTEIRDFIEENIDR 540  
QY 425 TQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF--QEIVHKSVVLIPLCAVDDGEHSQNE 482  
Db 541 MQKTA--RIISDI-----DCLCSLATVALENNYIKPNINAKDEILI-----EGRHPVVE 588  
QY 483 KI 484  
Db 589 KV 590

RESULT 317  
AAY49070  
ID AAY49070 standard; protein; 1435 AA.

XX AAY49070;

XX 05-JAN-2000 (first entry)

XX

DE PolC gene product Pol III-L.  
XX  
KW Gram positive bacteria; dnaE; dnaX; dnaB; PolC; dnaN; dnaG; helicase;  
KW alpha subunit; DNA polymerase III holoenzyme; gamma subunit; tau subunit;  
KW clamp loader; glue protein; replication; antibiotic.  
XX  
OS Staphylococcus aureus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1033. .1047  
FT /note= "Encoded by GTA"

PN WO9937661-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 25-JAN-1999; 99WO-US001547.  
XX  
PR 27-JAN-1998; 98US-0074522P.  
PR 22-JUL-1998; 98US-0093727P.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI O'donnell ME, Zhang D, Whipple R;  
XX  
XX WPI; 1999-590685/50.  
DR N-PSDB; AAZ31004.  
XX

PT New isolated dnaE, dnaX and dnaB genes from Gram positive bacteria, used  
PT to develop screening assays for identifying antibiotic compounds.  
XX  
PS Example 6; Page 25-30; 132pp; English.

XX This is the PolC gene product Pol III-1 of Staphylococcus aureus. The  
CC invention relates to a number of isolated DNA molecules from Gram  
CC positive bacterium, corresponding to dnaE (AAZ31001), dnaX (AAZ31002), and  
CC dnaB (AAZ31003). The PolC, dnaN and dnaG genes (AAZ31004-231006) are also  
CC identified. The dnaE gene corresponds to the alpha subunit of the  
CC Escherichia coli, DNA polymerase III holoenzyme, dnaX corresponds to the  
CC gamma and tau subunits, and dnaB corresponds to the helicase. The alpha  
CC subunit is the actual DNA polymerase, the gamma complex forms the clamp  
CC loader and tau is a "glue protein". DnaX encodes both gamma and Tau, Tau  
CC is the product of the full gene, while gamma is the product of the first  
CC two thirds of the gene. The DNA sequences of the invention can be used to  
CC identify agents that inhibit or promote DNA replication by acting on  
CC various parts of the gram positive bacterial DNA polymerase holoenzyme.  
CC The products and methods of the invention can be used for identifying  
CC pharmacological agents or lead compounds for agents active at the level  
CC of a replication protein function, particularly DNA replication. The  
CC agents identified can be used as antibiotics

XX Sequence 1435 AA;

Query Match 3.9%; Score 103.5; DB 2; Length 1435;  
Best Local Similarity 19.9%; Pred. No. 17;  
Matches 66; Conservative 52; Mismatches 122; Indels 91; Gaps 11;

QY 184 EQDLPVNIKFIEGMEEAGSVALBELVE-----KEKDRFSGVDYIVISDNLWISQRP 237  
Db 168 EQNLASLEAHIOEEDQSARLATEKLEKMAEKAKAQDNKQSAVDKCQIGKPIQIENIKP 227  
QY 238 AITYGTFGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYD 297  
Db 228 -----IESIEEEFKVAIEGV-- 243  
QY 298 EVVPLTEEEINTYK-AIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSSLIHGIEGAF 356  
Db 244 -IFDINLKELKSGRHIIVEIKVTDYDLSLVKMFTRKNKD----LEHFKALSV----- 291  
QY 357 DEPGTKTVPGRVIGKFSIR-LVPHMN-----VSAVEKQVTRHLEDVFSKRNSS 404  
Db 292 ---GKWVRAQGRIEEDTFIRDLVMMMSDIEEIKKATKKDKAEKRVEFHLHTAMSQMDGI 348



QY 405 NKWVSMTLGL---HPWIANID-----DTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 349 PNIGAYVKQAADWGHGHPAIAVTDHNVVQAFPDAAHAAAEKHGKIMYGMGLVDDG--VPI 406  
QY 454 AKMFQEIIVHKSUVLIPLGAVDDGEHSQNEKI 484  
Db 407 AYKPDVVLKDATYVVFVETTGLSNQYDKI 437

RESULT 318  
AAB31934  
ID AAB31934 standard; protein; 1435 AA.  
XX  
AC AAB31934;  
DT 15-MAY-2001 (first entry)  
XX

Amino acid sequence of a partial polC polypeptide.

DE dnaE; Gram positive bacteria; polC; dnaE; hola; holB; dnaX; dnaN; ssb;  
XX dnaG; dnaB; antibiotic; replication; cell growth; cell death;  
KW bacterial infection.  
KW

Staphylococcus aureus.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 207 /note= "encoded by AAC"  
FT Misc-difference 208 /note= "encoded by GAA"  
FT Misc-difference 952 /note= "encoded by ACA"  
FT Misc-difference 1035 /note= "encoded by CGT"  
FT Misc-difference 1147 /note= "encoded by GAATTC"  
FT Misc-difference 1148 /note= "encoded by GGT"  
FT Misc-difference 1149 /note= "encoded by ACA"  
FT Misc-difference 1150 /note= "encoded by GGA"  
FT Misc-difference 1151 /note= "encoded by TTC"  
FT Misc-difference 1152 /note= "encoded by GTG"  
FT Misc-difference 1259 /note= "encoded by ATG"  
FT Misc-difference 1408 /note= "encoded by TCT"  
FT

WO200109164-A2.

08-FEB-2001.

28-JUL-2000; 2000WO-US020666.

29-JUL-1999; 99US-0146178P.

(UYRQ ) UNIV ROCKEFELLER.

O'donnell ME, Bruck I, Zhang D, Whipple R;

WPI; 2001-147453/15.

N-PSDB; AAF54734.

XX Isolated DNA molecule from a Gram positive bacterium encoding DNA  
PT replication proteins used to identify compounds which have antibiotic  
PT activity.

PS Disclosure; Page 35-39; 239pp; English.

XX The present sequence represents a partial polC polypeptide. The

CC specification describes DNA molecules from Gram positive bacteria, which  
CC comprise a coding region from a polC, dnaE, hola, holB, dnaX, dnaN, ssb,  
CC dnaG or a dnaB gene. These sequences encode proteins that replicate the  
CC chromosome of Gram positive bacteria. They are used for sequencing and  
CC amplification of DNA and in drug discovery to identify compounds which  
CC have antibiotic activity through interference with replication. They are  
CC used in methods for identifying compounds that are active at the level of  
CC DNA replication and result in arrest of cell growth or cell death of  
CC bacteria to treat bacterial infections in animals  
XX

SQ Sequence 1435 AA;

Query Match 3.9%; Score 103.5; DB 4; Length 1435;  
Best Local Similarity 19.9%; Pred. No. 17;  
Matches 66; Conservative 52; Mismatches 122; Indels 91; Gaps 11;

QY 184 EQDLPVNIKFIIIEGMEEGAGSVALEELVE-----KEKDRFFSGVDYIVISDNLWISQRKP 237  
Db 168 EQNLASLEAHIQEEDQSARLATEKLEKMAEKAKAQDNKQSAVDKQCIQKPIQIENIKP 227  
QY 238 AITYGTRGNSYFNVVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYD 297  
Db 228 -----IESIIIEEFKVAIEGV-- 243  
QY 298 EVVPLTEEEINTYK-AIHLGLEEYRNSSRVKFLFDTKKEILMHLWRYPSLSIHGIEGAF 356  
Db 244 -IFDINLKELKSGRHIVEIKVTDYDTSVLKMFTRKNKDD---LEHFKALSV----- 291  
QY 357 DEPGTKTVIPGRVIGKFSIR-LVPHMN-----VSAVEKQVTRHLEDVFSKRNS 404  
Db 292 ---GKWVRAQGRIEEDTFIRDLVMMMSDIEETKATKKDKAEKRVFHLHTAMSQMDGI 348  
QY 405 NKWVSMTLGL---HPWIANID-----DTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 349 PNIGAYVKQAADWGHGHPAIAVTDHNVVQAFPDAAHAAAEKHGKIMYGMGLVDDG--VPI 406  
QY 454 AKMFQEIIVHKSUVLIPLGAVDDGEHSQNEKI 484  
Db 407 AYKPDVVLKDATYVVFVETTGLSNQYDKI 437

RESULT 319

ABW01647

ID ABW01647 standard; protein; 1435 AA.

AC ABW01647;

DT 12-FEB-2004 (first entry)

DE Staphylococcus aureus Pol III-L protein.

XX Polymerase III enzyme; dnaE; dnaX; dnaB; Gram positive bacteria;  
KW drug discovery; antibiotic activity; enzyme.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT Misc-difference 1033.1048

FT /note= "Encoded by GTACCT"

XX US2003129633-A1.

XX 10-JUL-2003.

XX 28-OCT-2002; 2002US-00282287.

XX 13-FEB-1998; 98US-0074572P.

XX 22-JUL-1998; 98US-0093727P.

XX 22-JAN-1999; 99US-00235245.

XX (ODON/) O'DONNELL M E.

PA (ZHAN/) ZHANG D.

PA (WHIP/) WHIPPLE R.

XX O'donnell ME, Zhang D, Whipple R;  
XX WPI; 2003-829557/77.  
DR N-PSDB; AAD62919.  
XX New DNA replication proteins (i.e. subunits of the Staphylococcus aureus  
PT DNA polymerase III enzyme) and genes, useful in drug discovery to screen  
PT large libraries of chemicals for identification of compounds with  
PT antibiotic activity.  
XX Disclosure; Page 14-17; 69pp; English.  
PS The invention relates to an isolated polypeptide, which comprises at  
XX least one functionally active subunit of a Staphylococcus aureus DNA  
CC polymerase III enzyme. The subunit comprises a 573 residue dnaE amino  
CC acid sequence, a 566 residue dnaX amino acid sequence and/or a 457  
CC residue dnaB amino acid sequence. The proteins and nucleic acids  
CC replicate the chromosome of Gram positive bacteria and are useful in drug  
CC discovery to screen large libraries of chemicals for identification of  
CC compounds with antibiotic activity. The present sequence is S. aureus Pol  
CC III-L protein  
XX Sequence 1435 AA;  
SQ Query Match 3.9%; Score 103.5; DB 7; Length 1435;  
Best Local Similarity 19.9%; Pred. No. 17;  
Matches 66; Conservative 52; Mismatches 122; Indels 91; Gaps 11;  
QY 184 EQDLPVNIKFIEGMEEAGSVALEELVE-----KEKDRFFSGVDYIVISDNLWISQRKP 237  
Db 168 EQNLASLEAHIQEEDQSARLATEKLEKMAEKAKAQDNKQSAVDKQCQIGKPIQIENIKP 227  
QY 238 AITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYD 297  
Db 228 -----IESIIIEEFKVAIEGV-- 243  
QY 298 EVVPLTEEEINTYK-AIHLDEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAF 356  
Db 244 -IFDINLKELKSGRHIVEIKVTDYTDLSLVKMFTRKNKOD-----LEHFKALSV----- 291  
QY 357 DEPGTKTVIPGRVIGKFSIR-LVPHMN-----VSAVEKQVTRHLEDVFSKRNS 404  
Db 292 ---GKWVRAQGRIEEDTFIRDLVMMMSDIEEIKKATKKDKAEKRVFEHLHTAMSQMDGI 348  
QY 405 NKMVVSMTLGL---HPWIANID-----DTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 349 PNIGAYVKQAADWGHGHPAIAVTDHNVVQAFPDAAHAAAEKHGKMIYMGEGMLVDDG--VPI 406  
QY 454 AKMFQEIYVHKSIVLPLGAVDDGGEHSQNEKI 484  
Db 407 AYKPDVVLKDATYVVFVDVETTGLSNQYDKI 437  
RESULT 320  
AAU34070  
ID AAU34070 standard; protein; 1436 AA.  
XX AAU34070;  
AC AAU34070;  
XX 14-FEB-2002 (first entry)  
DT Staphylococcus aureus cellular proliferation protein #346.  
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX Staphylococcus aureus.  
OS WO200170955-A2.  
PN 27-SEP-2001.  
XX  
XX

PF 21-MAR-2001; 2001WO-US009180.  
XX 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX WPI; 2001-611495/70.  
DR N-PSDB; AAS51929.  
XX New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
PT Example 3; SEQ ID NO 5566; 511pp; English.  
XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 1436 AA;  
SQ Query Match 3.9%; Score 103.5; DB 4; Length 1436;  
Best Local Similarity 19.9%; Pred. No. 17;  
Matches 66; Conservative 52; Mismatches 122; Indels 91; Gaps 11;  
QY 184 EQDLPVNIKFIEGMEEAGSVALEELVE-----KEKDRFFSGVDYIVISDNLWISQRKP 237  
Db 168 EQNLASLEAHIQEEDQSARLATEKLEKMAEKAKAQDNKQSAVDKQCQIGKPIQIENIKP 227  
QY 238 AITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYD 297  
Db 228 -----IESIIIEEFKVAIEGV-- 243  
QY 298 EVVPLTEEEINTYK-AIHLDEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAF 356  
Db 244 -IFDINLKELKSGRHIVEIKVTDYTDLSLVKMFTRKNKOD-----LEHFKALSV----- 291  
QY 357 DEPGTKTVIPGRVIGKFSIR-LVPHMN-----VSAVEKQVTRHLEDVFSKRNS 404  
Db 292 ---GKWVRAQGRIEEDTFIRDLVMMMSDIEEIKKATKKDKAEKRVFEHLHTAMSQMDGI 348  
QY 405 NKMVVSMTLGL---HPWIANID-----DTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 349 PNIGAYVKQAADWGHGHPAIAVTDHNVVQAFPDAAHAAAEKHGKMIYMGEGMLVDDG--VPI 406  
QY 454 AKMFQEIYVHKSIVLPLGAVDDGGEHSQNEKI 484  
Db 407 AYKPDVVLKDATYVVFVDVETTGLSNQYDKI 437







XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA32920.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 56974; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 330 AA;  
SQ  
Query Match 3.9%; Score 103; DB 6; Length 330;  
Best Local Similarity 19.1%; Pred. No. 1.9;  
Matches 62; Conservative 50; Mismatches 78; Indels 134; Gaps 17;  
QY 40 QYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQELFRMMAVAADTLQRLGARVASVDM 97  
Db 112 QEIATH---ILETAKDGVKVKPEELQPAEAPK-----AAATEDAQP KGS----- 152  
QY 98 GPQQLPDGQSLPIPPVILAE LGS DPTKGTVC FYGHL DVQPADRGDWLTDPYVLT EVDGK 157  
Db 153 -----LPP-----GTVV-----GDGKI--KFVLARIDSR 174  
QY 158 -LYGRGATDNKGPVLAWINAVSAFR-----ALEQDLPVNIKFIIEGMEE 200  
Db 175 LLHGQVAT-----AWTKATQPNRIIVVSDAVAKDDLKRLK LIEQAAPGVK----- 219  
QY 201 AGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDF 260  
| : : : : || | : : : :  
: |

Db 220 ANVIPISKMIEVAKDPRFGNTKALLLFN-----PEDV 252  
QY 261 HSGTFTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY-----KAIHL 315  
Db 253 LKVVEGGV-EIPEVN-----VGSMAHSVGKVVV-----SKVLSMGQEDVDTFDELKAKGIKF 303  
QY 316 DLEEYRNSSR--VEKFLFDTKKEI 337  
Db 304 DVRKVPNDSKANNMDEILKKAKNEL 327  
RESULT 325  
ADH87067  
ID ADH87067 standard; protein; 385 AA.  
XX ADH87067;  
AC ADH87067;  
XX 22-APR-2004 (first entry)  
XX Enterococcus faecalis polypeptide #1547.  
DE Enterococcus faecalis infection; transcription regulatory element;  
XX Enterococcus faecalis infection; transcription regulatory element;  
KW antibacterial.  
XX Enterococcus faecalis.  
OS Enterococcus faecalis.  
XX US6617156-B1.  
XX 09-SEP-2003.  
PF 13-AUG-1998; 98US-00134000.  
XX 15-AUG-1997; 97US-0055778P.  
PR (DOUC/) DOUCETTE-STAMM L A.  
XX (BUSH/) BUSH D.  
PI Doucette-Stamm LA, Bush D;  
XX WPI; 2003-895394/82.  
DR N-PSDB; ADH83662.  
XX New nucleic acid comprising a sequence encoding an *Enterococcus faecalis*  
PT polypeptide, useful for preparing a composition for diagnosing or  
PT treating *E. faecalis* infection.  
XX Disclosure; SEQ ID NO 4952; 193pp; English.  
PS The invention relates to *Enterococcus faecalis* polynucleotides and  
XX polypeptides. The invention also relates to a recombinant expression  
CC vector comprising a polynucleotide operably linked to a transcription  
CC regulatory element, a cell comprising a recombinant vector, a method for  
CC producing an *E. faecalis* polypeptide, an isolated nucleic acid comprising  
CC a sequence not given in the specification, a recombinant vector  
CC comprising the nucleic acid and a cell comprising the recombinant vector.  
CC The polynucleotides can be used to detect the presence of *E. faecalis* in  
CC a sample. The sequences are useful for preparing a composition for  
CC diagnosing or treating *Enterococcus faecalis* infection. This sequence  
CC represents an *E. faecalis* polypeptide of the invention.  
XX Sequence 385 AA;  
SQ  
Query Match 3.9%; Score 103; DB 7; Length 385;  
Best Local Similarity 19.1%; Pred. No. 2.4;  
Matches 62; Conservative 50; Mismatches 78; Indels 134; Gaps 17;  
QY 40 QYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQELFRMMAVAADTLQRLGARVASVDM 97  
Db 167 QEIATH---ILETAKDGVKVKPEELQPAEAPK-----AAATEDAQP KGS----- 207  
QY 98 GPQQLPDGQSLPIPPVILAE LGS DPTKGTVC FYGHL DVQPADRGDWLTDPYVLT EVDGK 157  
Db 208 -----LPP-----GTVV-----GDGKI--KFVLARIDSR 229





XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 19640; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 887 AA;

Query Match 3.9%; Score 102.5; DB 8; Length 887;  
Best Local Similarity 19.6%; Pred. No. 9.7;  
Matches 86; Conservative 61; Mismatches 152; Indels 139; Gaps 21;

QY 19 LLERGMFSP-----SPPPALLEKVFQYIDLHQ----DEFVQTLKEWVAIESDSVQPV 67  
DB 103 VIEKSVSEEPAPLKWVETPEPTIVKSV---VDAEQMALRAEEARKRSLLIARQAEELKE- 158  
QY 68 PRFRQELFRMVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSD----- 121  
DB 159 ---KQEKRRQQAQAQANVKK-----EPAPAEQESGPATAVTPGVSVTEISSKLPETGA 207  
QY 122 -----PTKGTVCIFYGHLD----VQPADRG-----DGWLTDPYVLTE--VD 155  
DB 208 AATPATSTAPATTSTTAATKGAPQKPVVPEEKGEKKKPTKQDAWKDEPVKRREPKEAR 267  
QY 156 GKLYG---RGATDNKG-----PVL--AWINAVSAFRALEQDLPVNI 191  
DB 268 GDLGGQEWMRKDKHGKYKSDQLQSHAFSVPTPEPVIHEVLIPETISVGALAKMAVKA 327  
QY 192 KFIIEGMEEAGS-VALEELVEKE-----KDRFFSGVDYIVISDNL 230  
DB 328 AEVIKVLKMGSMVTINQMLDQETAMVVVEEMGHIAKIAASDNPESEFLEVD--VSSDEA 385  
QY 231 WISQRKPAIT---YGRGNSYFMVEVKCRDQDFHSGTGGILH-----EPMADLVALL 280  
DB 386 RMEPRAPVVTVMGHVDHGKTSLLDYI--RRTRVAGGEAGGITQHIGAVHVTSGVITFL 443  
QY 281 GSLVDSSGH-----ILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNS 323

DB 444 ----DTPGHEAFTAMRARGAKITDIVLVVAADDGVMPQTIEAIHHAKAANIPIVVAVNK 499  
QY 324 SRVEKFLFD-TKEEILMH 340  
DB 500 MDKPEANFDRIKQELVNH 517  
  
RESULT 328  
AAB48264  
ID AAB48264 standard; protein; 1118 AA.  
XX  
AC AAB48264;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Rice magnesium chelatase subunit (clone rlr2.pk0018.e9[FIS]).  
XX  
KW Magnesium chelatase; transgenic; herbicide; gene marker; plant breeding;  
KW rice.  
XX  
OS Oryza sativa.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 477 /note= "encoded by GG"  
XX  
PN WO200075340-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US015351.  
XX  
PR 04-JUN-1999; 99US-0137461P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Butler KH, Famodu OO, Gutteridge S, Maxwell CA;  
XX  
DR WPI; 2001-091215/10.  
DR N-PSDB; AAC84583.  
XX  
XX Isolated nucleic acid fragments encoding magnesium chelatase subunits,  
PT useful as probes for genetic and physical mapping of genes, as markers  
PT for traits linked to these genes, and in plant breeding.  
XX  
PS Claim 10; Page 80-83; 103pp; English.  
XX  
CC The invention relates to nucleic acid fragments encoding magnesium  
CC chelatase subunits. The nucleic acid fragments may be used to create  
CC transgenic plants in which the new polypeptides are present at higher or  
CC lower levels than normal or in cell types or developmental stages in  
CC which they are not normally found, and for overexpression in bacterial or  
CC yeast hosts to efficiently produce large amounts of the encoded  
CC polypeptides which could then be used for screening different compounds  
CC for potential herbicidal activity. The polynucleotides may also be used  
CC as probes for genetic and physical mapping of the genes that they are part  
CC of, and as markers for traits linked to these genes. Such information is  
CC useful in plant breeding. The polypeptides are used for preparing  
CC antibodies, which are useful for detecting the polypeptides in situ or in  
CC vitro, and as a target to facilitate design and/or identification of  
CC inhibitors of enzymes that may be used as herbicides. Host cells may also  
CC be used directly for screening different compounds for potential  
CC herbicidal activity. The present sequence represents the rice magnesium  
CC chelatase subunit  
XX  
SQ Sequence 1118 AA;

Query Match 3.9%; Score 102.5; DB 4; Length 1118;  
Best Local Similarity 17.9%; Pred. No. 14;  
Matches 89; Conservative 68; Mismatches 112; Indels 229; Gaps 24;  
  
QY 166 NKGVP--LAWINAVSAFRALEQDLVPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSG--- 220

Db 247 DKGNGVGTAAALNVFNFSVLDLKKD-GYNVEGLPDTAEALIEEVIHDKAQNPNLN 305  
QY 221 -----VDYIVISDNLM-----ISQRKPAITYGTR-GNSY----- 248  
Db 306 VAYRMNVREYQSLTSYASLLEENWGKPPGNLNSDGENLLVYGKQYGNVFIGVQPTFFGYEG 365  
QY 249 -----FMVEVKCRDQDFHSGTFGGILHEP-----MADLV---A 278  
Db 366 DPMELLFSKSASPHHGFAAYTFVEKIFQADAVLHFGTHGSLEFMPGKQVGMSDACYPDS 425  
QY 279 LLGSLVDSSGHILVPGIY-----DEWVPLT---EEEINTYKAIHLDL 317  
Db 426 LIGN-----IPNIYYAANNPSEATVAKRRSYANTISYLTTPPAENAGLYKGLK--- 473  
QY 318 EYVRNRRVEKFLDFTKEEILMHLWRYPSPSLSIHGI-----EGAFDERGT 361  
Db 474 QLSRSSLLNQSLKDT-----GRGPQIVSSIIISTAKQCNDLKDVPPLPEEGVELPPNE 525  
QY 362 KTVIPGRVIGK---FSIRLVP---H-----MNVSAVEK----- 388  
Db 526 RDLIVGKVYAKIMEIESRLLPCGLHVI GEPPSAIEAVATLVNIAASLDRPEDEIYSLPNIL 585  
QY 389 --QVTRHLEDV-----FSKRNSSNK-MVVSMT----- 412  
Db 586 AQTVGRIEDVYRGDKGILADVELLRQITEASRGAITTFVERTTNKGQVVDVTNKLST 645  
QY 413 ---LGL-HPWIANIDDTQYLAKR-AIRTVF----- 438  
Db 646 MLGFGISEPWWQHLSTKTFIRADREKLRTLFTFLGECCLKLIVADNELGSLKLALEGSYVE 705  
QY 439 -GTEPDMIRDGSTIPIAK 455  
Db 706 PGPGGDPINPKVLPTGK 723

RESULT 329  
AAB13586  
ID AAB13586 standard; protein; 539 AA.  
XX AAB13586;  
AC AAB13586;  
XX 06-MAR-2001 (first entry)  
DT Streptomyces globisporus C-1027 gene cluster ORF 24.  
DE Enediyne C-1027 biosynthesis gene cluster; apoprotein; chromophore;  
XX aminomutase; cancer.  
KW Streptomyces globisporus.  
XX WO2000040596-A1.  
PD 13-JUL-2000.  
PF 06-JAN-2000; 2000WO-US0000446.  
XX 06-JAN-1999; 99US-0115434P.  
PR 05-JAN-2000; 2000US-00477962.  
XX (REGC ) UNIV CALIFORNIA.  
PA Shen B, Liu W, Christenson SD, Standage S;  
PI WPI; 2000-465947/40.  
XX N-PSDB; AAA63348, AAA63349.  
DR Isolated nucleic acid comprising a nucleic acid encoding any of C-1027  
XX open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), useful for  
PT the production of enediyne C-1027 antitumor antibiotics.  
XX Claim 15; Page 127-129; 160pp; English.  
PS  
XX

CC The present sequence is the protein which is encoded by open reading  
CC frame 24 of the Streptomyces globisporus enediyne C-1027 gene cluster.  
CC Enediyne C-1027 is an antibiotic, consisting of an apoprotein and a non-  
CC peptidic chromophore, which acts by damaging DNA. The sequences within  
CC the gene cluster, and the proteins they encode, can be used in the  
CC treatment of cancer, along with antagonists of the protein. This protein  
CC is an aminomutase  
XX Sequence 539 AA;  
SQ  
Query Match 3.9%; Score 102; DB 3; Length 539;  
Best local similarity 20.7%; Pred. No. 5;  
Matches 111; Conservative 59; Mismatches 171; Indels 194; Gaps 26;  
QY 36 EKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFR-MMVAADTLQR--LGARV 92  
Db 71 EMIYMQVDKSKVELEQT---NLVRSHSAGVGPLFAEDEARAIVAARLNTLAKGHSVRP 126  
QY 93 ASVDMGPQQLPDQCSLPIPPVILAEGLSDPTKGTVCFYGHL-----DVQP--- 137  
Db 127 IILERLAQYLNNEGITPAIP-----EIGSLGASGDLAPLSHVASTILIGEGVLRDGRPVET 181  
QY 138 ---ADRGDWLTDPYVLTEVDGKLYRGATDNKGPVLAWINAVSAF-----RALE 184  
Db 182 AQVLAERG---IEPLELRFKEG-----LALINGTSGMTGLGSLVVGRALE 223  
QY 185 Q-----DLPVNIKFIEGM----- 198  
Db 224 QAQAEIVTALLIEAVRGSTSPFLAEGHDIAHPHEGQIDTAANMRALMRGSGLTVEHADL 283  
QY 199 -----EEAGSVALEELVEKEKDRFFSGVDYIV--ISDNLWISQRKPAITYGTRGNSYF 249  
Db 284 RRELQDKKEAGKVORSEIYQKAYSLRAIPQVVGAVRDTLYHARHKLRTELNSANDNPL 343  
QY 250 MVEVKCRDQDFHSGTFGGILHEPMA---DLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306  
Db 344 FFEKGK---EIFHGANFHG---QPIAFAMDFVTI-----ALTQLGVLAERQ 382  
QY 307 INTYKAIHLDLEEYRNSSRVEKFLDFTKEEILMHLWRYPSPSLSIHGIEGAFDEPGETKTVIP 366  
Db 383 INRVLNRLH-----SYGLPEFLVSGD-----PGLH-SGFAGA-QYPATALVAE 423  
QY 367 GRVIGKFSIRLVPNMVNSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL---GLHPWIAN- 421  
Db 424 NRTIGPASTQSV-----SNGDNQDVSMGLISARNARRVLSNN 462  
QY 422 --IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVD 474  
Db 463 NKILAVEYLAAQAQAV-DISG-----RFDGLSPAATYEAARR--LVPTILGVD 507

RESULT 330  
ADE47738  
ID ADE47738 standard; protein; 1738 AA.  
XX ADE47738;  
AC ADE47738;  
XX 29-JAN-2004 (first entry)  
DT Human NOV32a protein SEQ ID NO:100.  
DE  
XX human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;  
KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;  
KW anti-HIV; antiasthmatic; antibacterial; virucide; neuroprotective;  
KW nootropic; antiparkinsonian; antilipaemic; gene therapy; vaccine.  
XX Homo sapiens.  
OS  
XX WO2003076642-A2.  
PN  
XX 18-SEP-2003.  
PD  
XX 02-AUG-2002; 2002WO-US024459.  
PF







PI Buchrieser C;  
XX WPI; 2003-148459/14.  
XX  
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX  
XX  
PS Claim 2; SEQ ID NO 2439; 1205pp; French.  
XX  
CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
SQ Sequence 337 AA;

Query Match 3.9%; Score 101.5; DB 6; Length 337;  
Best Local Similarity 21.4%; Pred. No. 2.7;  
Matches 69; Conservative 47; Mismatches 121; Indels 85; Gaps 15;

QY 52 TLKEWAIESDSVQVPRFRQELFRMMAVADTLQRLGARVASVDM-----GPQQLPDG 105  
Db 25 SLDTWIEVKQERIQRPEDREEVEK-----AIEELQAKISELDAILAKKPPPELPPG 77  
QY 106 QSLPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLT-EVDGKLYGR--- 161  
Db 78 KPLIKVSGVLEEF-----ETLCVIGYF-----TDRE-----YDPVAFARQEELELYGRLLM 123  
QY 162 ---GATDNKGPVLAWINAVSAFRALEQDLPNIKFIIEGMEEAGSVALE-----ELV 210  
Db 124 SLAGNTSGS-----NASTNVR--KRDVCDPVRGKINGIPFYGWLGTVAKAGDYVELA 174  
QY 211 EXEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHS----- 262  
Db 175 VTEKEGHY--VVYAIAHPGLRIVSMTPRCKQGIHSNAKYQI---RGTWYGSVLVFFVFM 228  
QY 263 --GTFGGILHEPMADLVALLGSLVDSSGHILVPGIY-----DEVVPLTEE----- 305  
Db 229 IGGIFDGKVRREDIDYMKCISSEFLGLMAIVLSPLIYFSCMRKPKPTFRLABEIFTVLGFP 288  
QY 306 ---EINTYKAHLDLEEYRNSS 324  
Db 289 NPTEINLEKFTKKRLKEIKVNS 310

RESULT 333  
ADA33943  
ID ADA33943 standard; protein; 353 AA.  
XX  
AC ADA33943;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Acinetobacter baumannii protein #1104.  
XX  
KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;

KW plant biocontrol agent.  
XX  
OS Acinetobacter baumannii.  
XX  
PN US6562958-B1.  
XX  
PD 13-MAY-2003.  
XX  
PF 04-JUN-1999; 99US-00328352.  
XX  
PR 09-JUN-1998; 98US-0088701P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton G, Bush D;  
XX  
DR WPI; 2003-576092/54.  
DR N-PSDB; ADA29817.  
XX  
PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
PT for diagnosing a bacterial disease, as components of antibacterial  
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
PT plants.  
XX  
PS Example; SEQ ID NO 5230; 328pp; English.  
XX  
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.  
CC The A. baumannii nucleic acids and polypeptides are useful as reagents  
CC for diagnosing a bacterial disease, as components of antibacterial  
CC vaccines, as targets for antibacterial drugs, to detect the presence of  
CC A. baumannii and other Acinetobacter species in a sample, in screening  
CC compounds for the ability to interfere with the A. baumannii life cycle  
CC or to inhibit A. baumannii infection, and as biocontrol agents for  
CC plants. The present sequence represents the amino acid sequence of an A.  
CC baumannii protein.  
XX  
SQ Sequence 353 AA;

Query Match 3.9%; Score 101; DB 6; Length 353;  
Best Local Similarity 20.9%; Pred. No. 3.2;  
Matches 65; Conservative 39; Mismatches 89; Indels 118; Gaps 15;

QY 215 DRF-----FSGVDYIVISDN---LW-----ISQRKPAITYGTRGNSYFMVEVKCRDQDFH 261  
Db 52 DKFSQQVHFHAIDFARSRNIFLLWQLKNLIQIQIQAIVHAQAGKA---AELIARIKPFL 108  
QY 262 SG-----TFGGILHEPMADLV-----ALLGSLVDSSGHILVPGIYDEVVPLTEEEI 307  
Db 109 SGPKFVTVHGTGKKNKSAYLAGDAVIAVSQALTQGIPESKAHVVYNGVYPPQVLTENKE 168  
QY 308 NTYKAHLDLEEYRNSSRVE-----KFLPDTKEELMHLWRYPSLSIHGIEGA 355  
Db 169 KLLQSIQKDFTELDTSKKVVMCIGRLESVKNISLLIESMQQIDANLW----- 215  
QY 356 FDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR-----HLE 395  
Db 216 -----IVGDGSLR-----ASLEKQVSELNMQNRVAFGLGFRDARDLVQLA 255  
QY 396 DVF---SKR-----NSSNKMVVSMTLGLHPW-----IANIDDTQYLAAKRAIRT 436  
Db 256 DIVVLSSDRGFFPLVMVEALQADKAMASTKVNGLVIEWLPEQYLAIEIGTQGLA--KAIE- 312  
QY 437 VFGTEPDMIRD 447  
Db 313 -YALQPEAQND 322  
  
RESULT 334  
AAE35497  
ID AAE35497 standard; protein; 656 AA.  
XX  
AC AAE35497;  
XX

DT	17-JUN-2003	(first entry)	
XX	Streptomyces amphibiosporus lactimidomycin ORF3 protein.		
DE			
XX	Polyketide biosynthesis; dorrigocin; DORR; lactimidomycin; LACT.		
KW	Streptomyces amphibiosporus.		
XX			
OS	WO200288176-A2.		
XX			
PN	07-NOV-2002.		
XX			
PF	26-APR-2002; 2002WO-CA0000591.		
XX			
PR	26-APR-2001; 2001US-0286346P.		
XX			
PA	(ECOP-) ECOPIA BIOSCIENCES INC.		
XX			
PI	Farnet CM, Zazopoulos E, Staffa A, Yang X;		
XX			
DR	WPI; 2003-201222/19.		
DR	N-PSDB; AAD54230, AAD54233.		
XX			
XX	Novel isolated or purified polypeptide involved in biosynthesis of		
PT	polyketide dorrigocin or polyketide lactimidomycin, useful for preparing		
PT	dorrigocin or lactimidomycin.		
XX			
PS	Claim 13; Page 233-235; 312pp; English.		
XX			
CC	The invention relates to novel proteins involved in the biosynthesis of		
CC	polyketide dorrigocin (DORR) or lactimidomycin (LACT) biosynthesis by		
CC	microorganisms. Sequences of the invention allow direct manipulation of		
CC	dorrigocin, lactimidomycin and related chemical structures via chemical		
CC	engineering of the enzymes involved in the biosynthesis of dorrigocin and		
CC	lactimidomycin. They are useful for introducing chemical handles into		
CC	normally inert positions that permit subsequent chemical modifications		
CC	and facilitate the development of polyketides. The genes and proteins of		
CC	the invention can also be used to generate a focused library of analogues		
CC	around a polyketide lead candidate to fine-tune the compound for optimal		
CC	properties. They are useful for generating antibodies specific for the		
CC	polyketide biosynthesis. The present sequence is S. amphibiosporus		
CC	lactimidomycin ORF3 protein		
XX			
SQ	Sequence 656 AA;		
Query Match			
Best Local Similarity 3.9%; Score 101; DB 6; Length 656;			
Matches 94; Conservative 19.3%; Pred. No. 8.4;			
94; Mismatches 69; Indels 174; Gaps 25;			
QY	89	GARVASVD-MGPQQ---LPDQGSLLPIPPVILAEELGSDPTKGTVCYFGLDVPADRGD	143
DB	22	GAMLAQIEHRGPDEAGCFLDDRTAMGTVRLSIIDLASG-----QPVGSPDG	68
QY	144	--WLT---DPYVLTEVDGKLYGRGA-----TDNKGVPVLAWINAVSAFRALEQDLPVNIKF	193
DB	69	RYWLCYNGELNYRELRAELAGRGVSFRTESDTEVLMAWAHWG-----RS	114
QY	194	IIEGMEEAGSVALEELVEKE---KDRFFSGVDYIVISDNLWI--SQRKPAITYGTRGNS	247
DB	115	CLERFNGAFAFALKDVTGTGELHLARDRFGKRPLYVARHGDAWLFASEMKAFLAY--PGFE	172
QY	248	YFMVEVKCRDQDFHSGTGF-----GILHEPMADLVALLG-----SLVDS	286
DB	173	FAF-----DEEHLASTFATWTPLPAQSGYRGVEQLPMGEYLTVRGTETGRWASLDLT	226
QY	287	SGHILVPGIYDEVVPLTEEEINTYKAHLDLE---EYRNSSRVEKFLFDT---KEEILMH	340
DB	227	GGE--PPATEDEAVDL-----VRADLEAAVDLRLRSDVEGVYASGGLDSSILAH	274
QY	341	LMRY-----PSLSIHGIEGAFDEPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTRHL	394
DB	275	LTKERAGLPPTFTFSIQFEDAEFDE-----TAEQEELTKH-	308





Db 411 SGGSTTSIAELLEQLFPR-STHG-----TLIE-----KLSGGE 443

Qy 388 KQVTRHLEDVFSKRN-----SSNKMVSMTL-----GLHPWIANIDDTQYLAAKRA- 433

Db 444 KKRLYLLKLLLEKPNVLLDEPTNDLDIATLTVLENFLOGFAGPVLTVSHDRYFLDKVAT 503

Qy 434 -----IRTVFGTEPDMIRDGS-TIPIAKMFOEIVHKSVVLIPLGAVDDGGEHSQNEK 483

Db 504 KILAFEDGKIRPFFGHYTDYLDKAFETDMANQVQKAEKEKVVKVR-----EDKKRMTYQE 559

Qy 484 INRWNYIEG-----TKLFAAFFLEM 503

Db 560 KOEWASIEGDIETLEKRIAIAIEEM 584

RESULT 337

ABP81435

ID ABP81435 standard; protein; 623 AA.

XX

AC ABP81435;

XX

DT 04-MAR-2003 (first entry)

DE Streptococcus pneumoniae polypeptide SEQ ID NO 352.

XX Streptococcus pneumoniae; infection; otitis media; antibacterial;

KW diagnosis; gene therapy.

XX Streptococcus pneumoniae.

OS

XX WO200283855-A2.

XX

PD 24-OCT-2002.

XX

PF 12-APR-2002; 2002WO-US011524.

XX

PR 16-APR-2001; 2001US-0283948P.

PR 18-APR-2001; 2001US-0284443P.

XX

XX (AMCY ) AMERICAN CYANAMID CO.

XX

PI Zagursky RJ, Masi AW, Green BA, Chakravarti DN, Russell DP;

PI Wooters JL;

XX

DR WPI; 2003-093010/08.

DR N-PSDB; ABZ42283.

XX

PT New Streptococcus pneumoniae polynucleotides, useful for treating or

PT preventing S. pneumoniae infections, or non-systemic diseases, e.g.

PT otitis media, which are induced or exacerbated by S. pneumoniae.

XX

PS Claim 42; Page 579-582; 1091pp; English.

XX

CC The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of

CC a Streptococcus pneumoniae genomic sequence, a fragment or degenerate

CC variant of the polynucleotide or a nucleic acid sequence 95% identical to

CC one of the polynucleotides. The S. pneumoniae polynucleotides and encoded

CC polypeptides (ABP81299-ABP81674) are useful for treating or preventing S.

CC pneumoniae infections or non-systemic diseases, e.g. otitis media, which

CC are induced or exacerbated by S. pneumoniae. These are also useful for

CC detecting S. pneumoniae in a biological sample or diagnosing S.

CC pneumoniae infection in a subject. The polynucleotides have antibacterial

CC activity and are useful in gene therapy

XX

SQ Sequence 623 AA;

Query Match 3.8%; Score 100.5; DB 6; Length 623;

Best Local Similarity 20.2%; Pred. No. 8.6;

Matches 114; Conservative 79; Mismatches 197; Indels 175; Gaps 28;

Qy 35 LEKVFOYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVAS 94

Db 99 LIREYELIMLDYSEDKQARLERVMAEMDSLQ-----AWEIESQVKTVLKGIQDLS 150

Qy 95 VDMGPQQLPDG--QSLPIPPVILAE---LGDPTKGTVCFYGHLDVQPADRGDWLT-- 146

Db 151 TPVG--ELSGGLRRRVQLAQVLLGNHDLALLLDEPT-----NHLDAIAIE-----WLTFLF 197

Qy 147 -----DPYVLTEVDGKLY---GRGATDNKG----- 168

Db 198 LKNSKKTVLFIITHDRYFLDALSTRIFELDRAGLTEYQGNQDYVRLKAEQDERDAALLHK 257

Qy 169 -----PVLAWINAVSAFRALEQDLFVNIKFIIEGMEEGSVALEEL-VEKEKDRFFSGV 221

Db 258 KEQLYKQELAWMRROPQARATKQOARIN-RFHDLKKEVSGSSAETDLTMNFETSRI--GK 314

Qy 222 DYIVISDNLWISQKPAITYGTRGNSYFMVEVKCDQDFHSGTFG--GILHEPMADLVAL 279

Db 315 KVIEFQDVSFAYENKPILQ-----NFNLLVQAKDR-----IGIVGDNGVGKSTLLNLIA- 363

Qy 280 LGS�VDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSRVEKFLFDTKBEI-- 337

Db 364 -GSLEPTAGQVVI---GETVRIA-----YFSQOIEGLDESKRVINYLQEVABEVKT 410

Qy 338 -----LMHLWRVPSLSIHGIEGAFDEPGTKIVIPGRVIGKFSIRLVPNMVNSAVE 387

Db 411 SGGSTTSIAELLEQLFPR-STHG-----TLIE-----KLSGGE 443

Qy 388 KQVTRHLEDVFSKRN-----SSNKMVSMTL-----GLHPWIANIDDTQYLAAKRA- 433

Db 444 KKRLYLLKLLLEKPNVLLDEPTNDLDIATLTVLENFLOGFAGPVLTVSHDRYFLDKVAT 503

Qy 434 -----IRTVFGTEPDMIRDGS-TIPIAKMFOEIVHKSVVLIPLGAVDDGGEHSQNEK 483

Db 504 KILAFEDGKIRPFFGHYTDYLDKAFETDMANQVQKAEKEKVVKVR-----EDKKRMTYQE 559

Qy 484 INRWNYIEG-----TKLFAAFFLEM 503

Db 560 KOEWASIEGDIETLEKRIAIAIEEM 584

RESULT 338

ADS41904

ID ADS41904 standard; protein; 648 AA.

XX

AC ADS41904;

XX

DT 02-DEC-2004 (first entry)

XX

DE Bacterial polypeptide #20334.

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX

PN 18-DEC-2003.

XX

PD 20-FEB-2003; 2003US-00369493.

XX

PR 21-FEB-2002; 2002US-0360039P.

XX

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;





22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(NUVE-) NUVELO INC.	
Emtage P, Dederda DA, Boyle BJ, Wang J, Chen H, Wan C;	
Yamazaki V, Asundi V, Liu C, Tang YT, Drmanac RT;	
WPI; 2003-679633/64.	
New pharmaceutical composition comprising an anti-cell surface antigen consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 or VpreB1 antibody, useful for diagnosing or treating e.g., cancer or autoimmune disorders.	
Disclosure; SEQ ID NO 43; 145pp; English.	
The invention relates to a new pharmaceutical composition comprising an anti-cell surface antigen (CSA), consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 (TLR9) or VpreB1, antibody specific for cells that cause a disease e.g., B-cell lymphoma, where the antibody specifically binds to a polypeptide having an amino acid sequence not given in the specification or its extracellular portion. The pharmaceutical composition is useful for diagnosing or treating cancer, autoimmune disorders, systemic lupus erythematosus, pericarditis lupus, Sjogren's syndrome, Hashimoto thyroiditis or rejection of transplanted tissues or organs. This sequence corresponds to a protein used in the invention. (Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).	
Sequence 826 AA;	
Query Match 3.8%; Score 100.5; DB 7; Length 826;	
Best Local Similarity 18.9%; Pred. No. 13;	
Matches 94; Conservative 77; Mismatches 186; Indels 141; Gaps 25;	
22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(NUVE-) NUVELO INC.	
Emtage P, Dederda DA, Boyle BJ, Wang J, Chen H, Wan C;	
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WPI; 2003-679633/64.	
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Disclosure; SEQ ID NO 43; 145pp; English.	
The invention relates to a new pharmaceutical composition comprising an anti-cell surface antigen (CSA), consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 (TLR9) or VpreB1, antibody specific for cells that cause a disease e.g., B-cell lymphoma, where the antibody specifically binds to a polypeptide having an amino acid sequence not given in the specification or its extracellular portion. The pharmaceutical composition is useful for diagnosing or treating cancer, autoimmune disorders, systemic lupus erythematosus, pericarditis lupus, Sjogren's syndrome, Hashimoto thyroiditis or rejection of transplanted tissues or organs. This sequence corresponds to a protein used in the invention. (Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).	
Sequence 826 AA;	
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Best Local Similarity 18.9%; Pred. No. 13;	
Matches 94; Conservative 77; Mismatches 186; Indels 141; Gaps 25;	
22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(NUVE-) NUVELO INC.	
Emtage P, Dederda DA, Boyle BJ, Wang J, Chen H, Wan C;	
Yamazaki V, Asundi V, Liu C, Tang YT, Drmanac RT;	
WPI; 2003-679633/64.	
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Disclosure; SEQ ID NO 43; 145pp; English.	
The invention relates to a new pharmaceutical composition comprising an anti-cell surface antigen (CSA), consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 (TLR9) or VpreB1, antibody specific for cells that cause a disease e.g., B-cell lymphoma, where the antibody specifically binds to a polypeptide having an amino acid sequence not given in the specification or its extracellular portion. The pharmaceutical composition is useful for diagnosing or treating cancer, autoimmune disorders, systemic lupus erythematosus, pericarditis lupus, Sjogren's syndrome, Hashimoto thyroiditis or rejection of transplanted tissues or organs. This sequence corresponds to a protein used in the invention. (Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).	
Sequence 826 AA;	
Query Match 3.8%; Score 100.5; DB 7; Length 826;	
Best Local Similarity 18.9%; Pred. No. 13;	
Matches 94; Conservative 77; Mismatches 186; Indels 141; Gaps 25;	
22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(NUVE-) NUVELO INC.	
Emtage P, Dederda DA, Boyle BJ, Wang J, Chen H, Wan C;	
Yamazaki V, Asundi V, Liu C, Tang YT, Drmanac RT;	
WPI; 2003-679633/64.	
New pharmaceutical composition comprising an anti-cell surface antigen consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 or VpreB1 antibody, useful for diagnosing or treating e.g., cancer or autoimmune disorders.	
Disclosure; SEQ ID NO 43; 145pp; English.	
The invention relates to a new pharmaceutical composition comprising an anti-cell surface antigen (CSA), consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 (TLR9) or VpreB1, antibody specific for cells that cause a disease e.g., B-cell lymphoma, where the antibody specifically binds to a polypeptide having an amino acid sequence not given in the specification or its extracellular portion. The pharmaceutical composition is useful for diagnosing or treating cancer, autoimmune disorders, systemic lupus erythematosus, pericarditis lupus, Sjogren's syndrome, Hashimoto thyroiditis or rejection of transplanted tissues or organs. This sequence corresponds to a protein used in the invention. (Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).	
Sequence 826 AA;	
Query Match 3.8%; Score 100.5; DB 7; Length 826;	
Best Local Similarity 18.9%; Pred. No. 13;	
Matches 94; Conservative 77; Mismatches 186; Indels 141; Gaps 25;	
22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(NUVE-) NUVELO INC.	
Emtage P, Dederda DA, Boyle BJ, Wang J, Chen H, Wan C;	
Yamazaki V, Asundi V, Liu C, Tang YT, Drmanac RT;	
WPI; 2003-679633/64.	
New pharmaceutical composition comprising an anti-cell surface antigen consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 or VpreB1 antibody, useful for diagnosing or treating e.g., cancer or autoimmune disorders.	
Disclosure; SEQ ID NO 43; 145pp; English.	
The invention relates to a new pharmaceutical composition comprising an anti-cell surface antigen (CSA), consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 (TLR9) or VpreB1, antibody specific for cells that cause a disease e.g., B-cell lymphoma, where the antibody specifically binds to a polypeptide having an amino acid sequence not given in the specification or its extracellular portion. The pharmaceutical composition is useful for diagnosing or treating cancer, autoimmune disorders, systemic lupus erythematosus, pericarditis lupus, Sjogren's syndrome, Hashimoto thyroiditis or rejection of transplanted tissues or organs. This sequence corresponds to a protein used in the invention. (Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).	
Sequence 826 AA;	
Query Match 3.8%; Score 100.5; DB 7; Length 826;	
Best Local Similarity 18.9%; Pred. No. 13;	
Matches 94; Conservative 77; Mismatches 186; Indels 141; Gaps 25;	
22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(NUVE-) NUVELO INC.	
Emtage P, Dederda DA, Boyle BJ, Wang J, Chen H, Wan C;	
Yamazaki V, Asundi V, Liu C, Tang YT, Drmanac RT;	
WPI; 2003-679633/64.	
New pharmaceutical composition comprising an anti-cell surface antigen consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 or VpreB1 antibody, useful for diagnosing or treating e.g., cancer or autoimmune disorders.	
Disclosure; SEQ ID NO 43; 145pp; English.	
The invention relates to a new pharmaceutical composition comprising an anti-cell surface antigen (CSA), consisting of CD84Hyl, alpha2MHY, IgFBP-7Hyl, Toll-like receptor 9 (TLR9) or VpreB1, antibody specific for cells that cause a disease e.g., B-cell lymphoma, where the antibody specifically binds to a polypeptide having an amino acid sequence not given in the specification or its extracellular portion. The pharmaceutical composition is useful for diagnosing or treating cancer, autoimmune disorders, systemic lupus erythematosus, pericarditis lupus, Sjogren's syndrome, Hashimoto thyroiditis or rejection of transplanted tissues or organs. This sequence corresponds to a protein used in the invention. (Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).	
Sequence 826 AA;	
Query Match 3.8%; Score 100.5; DB 7; Length 826;	
Best Local Similarity 18.9%; Pred. No. 13;	
Matches 94; Conservative 77; Mismatches 186; Indels 141; Gaps 25;	
22-NOV-2002; 2002US-00302444.	
19-DEC-2002; 2002US-00327413.	
19-DEC-2002; 2002US-00327491.	
(	



CC	a sensor within an organism, or a specific tissue or specific cells; a	XX	Disclosure; SEQ ID NO 18; 459pp; English.
CC	method of making vault-like particles; and a method of making vault-like	PS	
CC	particles comprising one, or more than one, substance. The method or the	XX	
CC	vault-like particles are useful for delivering substances to an organism,	CC	The invention relates to a novel method of using vaults as carrier
CC	or to a specific tissue or to specific cells, or to an environmental	CC	molecules to deliver one, or more than one, substance to an organism, or
CC	medium. The vault-like particles are also useful for preventing damage by	CC	to a specific tissue or to specific cells, or to an environmental medium.
CC	a substance (e.g., toxin) to an organism, to a specific tissue, to	CC	The method comprises providing vaults, incorporating the substance into
CC	specific cells, or to an environmental medium. This sequence represents a	CC	the vaults, and administering the vaults comprising the substance to the
CC	HIV-Tat (TAT) peptide + rat major vault protein, MVP-TAT of the	CC	organism, to the specific tissue, to the specific cells, or to the
CC	invention.	CC	environmental medium. The invention further comprises: a vault-like
XX		CC	particle, comprising a major vault protein (MVP) or modified MVP, and/or
SQ	Sequence 872 AA;	CC	further comprising a vault poly-ADP ribose polymerase (VPARP) or a
	Query Match 3.8%; Score 100.5; DB 8; Length 872;	CC	portion of a VPARP, comprising at least about 150 consecutive residues of
	Best Local Similarity 20.7%; Pred. No. 15;	CC	VPARP; a method of preventing damage by one, or more than one, substance
	Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;	CC	to an organism, to a specific tissue, to specific cells, or to an
		CC	environmental medium by sequestering the substance within a vault-like
QY	32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPFRFRQ 72	CC	particle; a method of delivering one or more than one substance,
Db	206 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLHRTGEEWLVTVQDTEAHVPDVYE 265	CC	particularly a sensor to an organism, to a specific tissue, to specific
QY	73 ELFRMMAVAADTLQRLGARVASVDMGQQLPDQSLPIPPVILAEIGSD-PTKGTVCIFYG 131	CC	cells, or to an environmental medium; a method of detecting a signal from
Db	266 EVLGVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESFF- 309	CC	a sensor within an organism, or a specific tissue or specific cells; a
QY	132 HLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191	CC	method of making vault-like particles; and a method of making vault-like
Db	310 ---LQGERLERGIQDVYVLSQQGLL-----LKAQLPLEEGESEKVVSH 351	CC	particles comprising one, or more than one, substance. The method or the
QY	192 K----FIIEGMEEGAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243	CC	vault-like particles are useful for delivering substances to an organism,
Db	352 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVYQDVKTGKVRVAV 401	CC	or to a specific tissue or to specific cells, or to an environmental
QY	244 RGN SYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275	CC	medium. The vault-like particles are also useful for preventing damage by
Db	402 IGSTYMLTQDEVLWEKELPSGVEELLNLGHDPLAD 436	CC	a substance (e.g., toxin) to an organism, to a specific tissue, to
		CC	specific cells, or to an environmental medium. This sequence represents a
		CC	Cysteine rich peptide joined to rat major vault protein (CP-MVP) of the
		CC	invention.
		XX	Sequence 873 AA;
		SQ	Query Match 3.8%; Score 100.5; DB 8; Length 873;
			Best Local Similarity 20.7%; Pred. No. 15;
			Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;
QY	32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPFRFRQ 72	QY	32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPFRFRQ 72
Db	218 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLHRTGEEWLVTVQDTEAHVPDVYE 277	Db	218 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLHRTGEEWLVTVQDTEAHVPDVYE 277
QY	73 ELFRMMAVAADTLQRLGARVASVDMGQQLPDQSLPIPPVILAEIGSD-PTKGTVCIFYG 131	QY	73 ELFRMMAVAADTLQRLGARVASVDMGQQLPDQSLPIPPVILAEIGSD-PTKGTVCIFYG 131
Db	278 EVLGVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESFF- 321	Db	278 EVLGVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESFF- 321
QY	132 HLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191	QY	132 HLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191
Db	322 ---LQGERLERGIQDVYVLSQQGLL-----LKAQLPLEEGESEKVVSH 363	Db	322 ---LQGERLERGIQDVYVLSQQGLL-----LKAQLPLEEGESEKVVSH 363
QY	192 K----FIIEGMEEGAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243	QY	192 K----FIIEGMEEGAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243
Db	364 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVYQDVKTGKVRVAV 413	Db	364 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVYQDVKTGKVRVAV 413
QY	244 RGN SYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275	QY	244 RGN SYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275
Db	414 IGSTYMLTQDEVLWEKELPSGVEELLNLGHDPLAD 448	Db	414 IGSTYMLTQDEVLWEKELPSGVEELLNLGHDPLAD 448
		RESULT 344	
		ADS17737	
ID	ADS17737 standard; protein; 877 AA.	ID	ADS17737 standard; protein; 877 AA.
XX		XX	
AC	ADS17737;	AC	ADS17737;
XX		XX	
DT	16-DEC-2004 (first entry)	DT	16-DEC-2004 (first entry)
XX		XX	
DE	Rat major vault protein + antennapedia protein.	DE	Rat major vault protein + antennapedia protein.
XX		XX	
KW	vault; carrier molecule; major vault protein; MVP;	KW	vault; carrier molecule; major vault protein; MVP;
XX		XX	
OS	vault poly-ADP ribose polymerase; VPARP; toxin.	OS	vault poly-ADP ribose polymerase; VPARP; toxin.
XX		XX	
OS	Rattus norvegicus.	OS	Rattus norvegicus.
XX		XX	
OS	Drosophila melanogaster.	OS	Drosophila melanogaster.
XX		XX	







PT comprises incorporating the substance(s) into the vaults and  
XX administering them.

PS Disclosure; SEQ ID NO 28; 459pp; English.

XX  
CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Hist7 joined to rat major vault protein (Hist7-MVP) of the invention.

XX  
SQ Sequence 892 AA;

Query Match 3.8%; Score 100.5; DB 8; Length 892;  
Best Local Similarity 20.7%; Pred. No. 15;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQ 72  
DB 237 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLRHTGEEWLVTVQDTEAHVPDVYE 296  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEIGSD-PTKGTVCFYG 131  
DB 297 EVLGVVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESKFF- 340  
QY 132 HLDVQPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
DB 341 ---LQPGERLERGIQDVYVLSQQGLL-----LKAQLPLEEGESEKVS 382  
QY 192 K----FIIEGMEEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQKPAITYGT 243  
DB 383 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVQDVKTGKVRV 432  
QY 244 RGNYSFYMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
DB 433 IGSTYMLTQDEVLWEKELPSGVEELLNLGHDPLAD 467

RESULT 348  
ADSI17785  
ID ADSI17785 standard; protein; 894 AA.

XX  
AC ADSI17785;  
XX  
DT 16-DEC-2004 (first entry)  
DE Polylysine + rat major vault protein + antennapedia protein.  
XX  
KW vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
XX  
OS Rattus norvegicus.  
OS Drosophila melanogaster.

OS Synthetic.

PN WO2004081533-A2.

XX  
PD 23-SEP-2004.

XX  
PF 10-MAR-2004; 2004WO-US007434.

XX  
PR 10-MAR-2003; 2003US-0453800P.

XX  
PA (REGC ) UNIV CALIFORNIA.

PI Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;

XX  
DR WPI; 2004-690644/67.

DR N-PSDE; ADS17786.

XX  
PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.

PS Disclosure; SEQ ID NO 130; 459pp; English.

XX  
CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Polylysine + rat major vault protein + antennapedia protein of the  
CC invention.

XX  
SQ Sequence 894 AA;

Query Match 3.8%; Score 100.5; DB 8; Length 894;  
Best Local Similarity 20.7%; Pred. No. 15;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQ 72  
DB 223 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLRHTGEEWLVTVQDTEAHVPDVYE 282  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEIGSD-PTKGTVCFYG 131  
DB 283 EVLGVVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESKFF- 326  
QY 132 HLDVQPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
DB 327 ---LQPGERLERGIQDVYVLSQQGLL-----LKAQLPLEEGESEKVS 368  
QY 192 K----FIIEGMEEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQKPAITYGT 243  
DB 369 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVQDVKTGKVRV 418





CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Polylysine + rat major vault protein + human EGF peptide of the  
CC invention.

XX Sequence 934 AA;

Query Match 3.8%; Score 100.5; DB 8; Length 934;  
Best Local Similarity 20.7%; Pred. No. 16;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQPVPRFRQ 72  
Db 223 PAVFEVLDLVDVILTEKTLHLRALQNFRLRGVLRHRTGEWLTVQDTEAHVPDVYE 282  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSD-PTKGTVCFYG 131  
Db 283 EVLGVPPIITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESKFF- 326  
QY 132 HLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 327 ---LQGERLERGIQDVVVLSEQQGLL-----LQALQPLEEGESEKVS 368  
QY 192 K-----FIIEGMEEAGSVALEELVEKEK-----DRFSGVDYIVISDNLWISQRPATYGT 243  
Db 369 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVQDVKTGKVRVAV 418  
QY 244 RGNYSYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
Db 419 IGSTYMLTQDEVLWEKELPSGVEELNLGHDPLAD 453

RESULT 351  
ADS17697

ID ADS17697 standard; protein; 957 AA.  
XX  
AC ADS17697;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE GAL4 peptide joined to rat major vault protein (GAL4-MVP).  
XX  
KW vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
XX  
OS Rattus norvegicus.  
OS Synthetic.  
XX  
FN WO2004081533-A2.  
XX  
PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX  
DR WPI; 2004-690644/67.  
DR N-PSDB; ADS17698.

XX Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.

PS Disclosure; SEQ ID NO 36; 459pp; English.

XX The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC GAL4 peptide joined to rat major vault protein (GAL4-MVP) of the  
CC invention.

XX Sequence 957 AA;

Query Match 3.8%; Score 100.5; DB 8; Length 957;  
Best Local Similarity 20.7%; Pred. No. 17;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQPVPRFRQ 72  
Db 302 PAVFEVLDLVDVILTEKTLHLRALQNFRLRGVLRHRTGEWLTVQDTEAHVPDVYE 361  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSD-PTKGTVCFYG 131  
Db 362 EVLGVPPIITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESKFF- 405  
QY 132 HLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 406 ---LQGERLERGIQDVVVLSEQQGLL-----LQALQPLEEGESEKVS 447  
QY 192 K-----FIIEGMEEAGSVALEELVEKEK-----DRFSGVDYIVISDNLWISQRPATYGT 243  
Db 448 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIVQDVKTGKVRVAV 497  
QY 244 RGNYSYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
Db 498 IGSTYMLTQDEVLWEKELPSGVEELNLGHDPLAD 532

RESULT 352  
ADS17771

ID ADS17771 standard; protein; 968 AA.  
XX  
AC ADS17771;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE GAL4 + rat major vault protein + HIV-Tat peptide.  
XX  
KW vault; carrier molecule; major vault protein; MVP;





XX SQ Sequence 973 AA;  
Query Match 3.8%; Score 100.5; DB 8; Length 973;  
Best Local Similarity 20.7%; Pred. No. 17;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;  
QY 32 PALLEKVQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPFRFRQ 72  
Db 302 PAVFEEVLDLVDVILTEKTLALRALQNFRDLRGVLHRTGEWLTVQDTEAHVPDVYE 361  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSD-PTKGTVCIFYG 131  
Db 362 EVLGVPVPIIT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESFF- 405  
QY 132 HLDVQPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 406 ---LQGERLERGIQDVVYLSEQQGLL-----LQALQPLEEGESEKVS 447  
QY 192 K----FIIEGMEEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243  
Db 448 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIIYQDVKTGKVRVAV 497  
QY 244 RGNYSYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
Db 498 IGSTYMLTQDEVLWEKELPSGVEELNLGHDPLAD 532  
RESULT 354  
ADS17703  
ID ADS17703 standard; protein; 992 AA.  
XX ADS17703;  
XX 16-DEC-2004 (first entry)  
DE RNA binding peptide MS2 joined to rat major vault protein (MS2-MVP).  
XX vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
XX Rattus norvegicus.  
OS Synthetic.  
OS WO2004081533-A2.  
XX 23-SEP-2004.  
XX 10-MAR-2004; 2004WO-US007434.  
XX 10-MAR-2003; 2003US-0453800P.  
XX (REGC ) UNIV CALIFORNIA.  
XX Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX WPI; 2004-690644/67.  
DR N-PSDB; ADS17704.  
XX Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.  
XX Disclosure; SEQ ID NO 42; 459pp; English.  
XX The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like

CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC RNA binding peptide MS2 joined to rat major vault protein (MS2-MVP) of  
CC the invention.  
XX Sequence 992 AA;  
SQ Query Match 3.8%; Score 100.5; DB 8; Length 992;  
Best Local Similarity 20.7%; Pred. No. 18;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;  
QY 32 PALLEKVQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPFRFRQ 72  
Db 337 PAVFEEVLDLVDVILTEKTLALRALQNFRDLRGVLHRTGEWLTVQDTEAHVPDVYE 396  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSD-PTKGTVCIFYG 131  
Db 397 EVLGVPVPIIT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESFF- 440  
QY 132 HLDVQPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 441 ---LQGERLERGIQDVVYLSEQQGLL-----LQALQPLEEGESEKVS 482  
QY 192 K----FIIEGMEEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243  
Db 483 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIIYQDVKTGKVRVAV 532  
QY 244 RGNYSYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
Db 533 IGSTYMLTQDEVLWEKELPSGVEELNLGHDPLAD 567  
RESULT 355  
ADS17781  
ID ADS17781 standard; protein; 1003 AA.  
XX ADS17781;  
XX 16-DEC-2004 (first entry)  
XX MS2 + rat major vault protein + HIV-Tat peptide.  
DE vault; carrier molecule; major vault protein; MVP;  
XX vault poly-ADP ribose polymerase; VPARP; toxin.  
KW Rattus norvegicus.  
OS Human immunodeficiency virus 1.  
OS Synthetic.  
XX WO2004081533-A2.  
XX 23-SEP-2004.  
XX 10-MAR-2004; 2004WO-US007434.  
XX 10-MAR-2003; 2003US-0453800P.  
XX (REGC ) UNIV CALIFORNIA.  
PA

XX PI Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX WPI; 2004-690644/67.  
DR N-PSDB; ADS17782.  
XX  
PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.  
XX  
PS Disclosure; SEQ ID NO 126; 459pp; English.  
XX  
CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC MS2 + rat major vault protein + HIV-Tat peptide of the invention.  
XX  
SQ Sequence 1003 AA;  
  
Query Match 3.8%; Score 100.5; DB 8; Length 1003;  
Best Local Similarity 20.7%; Pred. No. 18;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;  
  
Qy 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFQ 72  
Db 337 PAVFEEVLDLVDVAVILTEKTALHLRALQNFRLDRGLVHRTGTEWLVTVQDTEAHVPDVYE 396  
Qy 73 ELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSD-PTKGTVCIFYG 131  
Db 397 EVLGVVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVRVKGESFF- 440  
Qy 132 HLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 441 ---LQGERLERGIQDVVVLSEQQGLL-----LKAQPLEEGESEEEKVSH 482  
Qy 192 K----FIEGMEEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243  
Db 483 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIYVDVKTGKVRVAV 532  
Qy 244 RGN SYMVEVKCR-DQDFHSGT--FCGILHEPMAD 275  
Db 533 IGSTYMLTQDEVLWEKELPSGVVEELLNLGHDPLAD 567  
  
RESULT 356  
ADS17775  
ID ADS17775 standard; protein; 1008 AA.  
XX  
AC ADS17775;  
XX 16-DEC-2004 (first entry)  
DT

XX MS2 peptide + rat major vault protein + antennapedia protein.  
DE  
XX vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
KW  
XX  
OS Rattus norvegicus.  
OS Drosophila melanogaster.  
OS Synthetic.  
XX  
PN WO2004081533-A2.  
XX  
PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
XX Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
PI  
XX WPI; 2004-690644/67.  
DR N-PSDB; ADS17776.  
DR  
XX  
XX Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.  
XX  
PS Disclosure; SEQ ID NO 114; 459pp; English.  
XX  
CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC MS2 peptide + rat major vault protein + antennapedia protein of the  
CC invention.  
XX  
SQ Sequence 1008 AA;  
  
Query Match 3.8%; Score 100.5; DB 8; Length 1008;  
Best Local Similarity 20.7%; Pred. No. 18;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;  
  
Qy 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFQ 72  
Db 337 PAVFEEVLDLVDVAVILTEKTALHLRALQNFRLDRGLVHRTGTEWLVTVQDTEAHVPDVYE 396  
Qy 73 ELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSD-PTKGTVCIFYG 131  
Db 397 EVLGVVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVRVKGESFF- 440





CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Rat major vault protein + anti-CEA scFv diabody peptide of the invention.  
XX  
SQ Sequence 1040 AA;

Query Match 3.8%; Score 100.5; DB 8; Length 1040;  
Best Local Similarity 20.7%; Pred. No. 19;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;  
QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQ 72  
Db 206 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLHRTGEWLTVQDTEAHVPDVYE 265  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSD-PTKGTVCVYG 131  
Db 266 EVLGVVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESKSF- 309  
QY 132 HLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 310 ---LQGERLERGIQDVYVLSQQGLL-----LKAQPLEEGESEKVS 351  
QY 192 K----FTIEGMEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243  
Db 352 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIYQDVKTGKVRVAV 401  
QY 244 RGN SYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
Db 402 IGSTYMLTQDEVLWEKELPSGVEELLNLGHDPLAD 436

RESULT 359  
ADS17709  
ID ADS17709 standard; protein; 1100 AA.  
XX  
AC ADS17709;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Green fluorescent protein joined to rat major vault protein (GL-MVP).  
XX  
KW vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
OS Rattus norvegicus.  
OS Synthetic.  
XX  
PN WO2004081533-A2.  
XX  
PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.

XX (REGC ) UNIV CALIFORNIA.  
PA Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX  
XX WPI; 2004-690644/67.  
DR N-PSDB; ADS17710.  
DR  
XX  
PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.  
XX  
PS Disclosure; SEQ ID NO 48; 459pp; English.  
XX

CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Green fluorescent protein joined to rat major vault protein (GL-MVP) of  
CC the invention.

XX Sequence 1100 AA;  
SQ  
Query Match 3.8%; Score 100.5; DB 8; Length 1100;  
Best Local Similarity 20.7%; Pred. No. 21;  
Matches 57; Conservative 50; Mismatches 93; Indels 75; Gaps 13;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQ 72  
Db 445 PAVFEEVLDLVDVILTEKTAHLRALQNFRDLRGVLHRTGEWLTVQDTEAHVPDVYE 504  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSD-PTKGTVCVYG 131  
Db 505 EVLGVVPITT-----LGPRHYCVILDPMG-PDGKN-----QLGQKRVVKGESKSF- 548  
QY 132 HLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 549 ---LQGERLERGIQDVYVLSQQGLL-----LKAQPLEEGESEKVS 590  
QY 192 K----FTIEGMEAGSVALEELVEKEK----DRFFSGVDYIVISDNLWISQRKPAITYGT 243  
Db 591 QAGDCWLIRGPLEYVPSAKVEVVEERQAIPLDQ-----NEGIYQDVKTGKVRVAV 640  
QY 244 RGN SYFMVEVKCR-DQDFHSGT--FGGILHEPMAD 275  
Db 641 IGSTYMLTQDEVLWEKELPSGVEELLNLGHDPLAD 675

RESULT 360  
ADS17789  
ID ADS17789 standard; protein; 1127 AA.  
XX









Db 112 EWALRDVRIDLANDITFRR-----WLENLNT-----IKKAGKRAL- 147

QY 208 ELVEKEKDRFFSGVD-----YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQ 258

Db 148 -----RFYGLGDEPSQGEENVFVPFDKSLNRSQRK-AISKALGSEDFFLVH----- 192

QY 259 DFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINT--YKAHILD 316

Db 193 -----GPGF---TGKTRTLVELIRQEVKRGKVKLATAESNVAVDNLVERLSRSGIKIVRIG 245

QY 317 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 376

Db 246 -----HPSRVSKHLHET---TLAYL-----ITQHELYGELREL-----RVIGQ----- 280

QY 377 LVPHMNVSAVEKQVT-----RHLED-----VFSKRNSSNMVSMTLGLHPWI--- 419

Db 281 -----SLAEKRDITYTKPTPKFRRGLSDEEIIKLAERKRGARGLSARLIMEMAEWIKLN 333

QY 420 ----ANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFQEIIVHKS 464

Db 334 RQVQKAFDDARKL-EERIARDII-READVVLTTNSSAALEVVDYDYYDVA-IIDEATQST 390

QY 465 V--VLIPLGAVD----DGEHSQ 480

Db 391 IPSILIPLNKVERFVLADGHKQ 412

RESULT 365

AAB96566

ID AAB96566 standard; protein; 654 AA.

XX AAB96566;

DT 29-OCT-2001 (first entry)

DE Putative P. abyssi superfamily I DNA helicase.

DE Hyperthermophilic archaeon; hyperthermophilic protein.

KW Pyrococcus abyssi.

OS Pyrococcus abyssi.

PN FR2792651-A1.

XX 27-OCT-2000.

XX 21-APR-1999; 99FR-00005034.

XX 21-APR-1999; 99FR-00005034.

XX (CNRS ) CNRS CENT NAT RECH SCI.

PA (IFRE-) IFREMER INST FR RECH EXPL MER.

XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

PI Querellou J, Weissenbach J, Saurin W, Heilig R;

XX WPI; 2001-126236/14.

XX New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry.

XX Claim 7; Page 1295-1297; 1657pp; French.

XX The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG666436

XX Sequence 654 AA;

Query Match 3.8%; Score 99.5; DB 4; Length 654;

Best Local Similarity 20.5%; Pred. No.12;

Matches 103; Conservative 72; Mismatches 162; Indels 165; Gaps 29;

QY 49 FVQTLKEWVAIESDVQVPVPRFRQELFRMMAVAADTLQR----LGARVASVDMGPQQLPD 104

Db 7 FINRLKELVEIERA--EIEAMRLEMRRRLSGIERERLGRAILNLNGKIIGEELGYFLVKY 64

QY 105 GQSLPIPP-----VILAELGSDPTK-----GTVCFYGH-----LDVQPADRGDGLWLT 147

Db 65 GRNREIKTEISVGLVVISK--RDPLKSDLLGTVEKGKRFIVVALETVP----- 112

QY 148 PYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALE 207

Db 113 EWALRDVRIDLANDITFRR-----WLENLNT-----IKKAGKRAL- 148

QY 208 ELVEKEKDRFFSGVD-----YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQ 258

Db 149 -----RFYGLGDEPSQGEENVFVPFDKSLNRSQRK-AISKALGSEDFFLVH----- 193

QY 259 DFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINT--YKAHILD 316

Db 194 ----GPGF---TGKTRTLVELIRQEVKRGKVKLATAESNVAVDNLVERLSRSGIKIVRIG 246

QY 317 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 376

Db 247 -----HPSRVSKHLHET---TLAYL-----ITQHELYGELREL-----RVIGQ----- 281

QY 377 LVPHMNVSAVEKQVT-----RHLED-----VFSKRNSSNMVSMTLGLHPWI--- 419

Db 282 -----SLAEKRDITYTKPTPKFRRGLSDEEIIKLAERKRGARGLSARLIMEMAEWIKLN 334

QY 420 ----ANIDDTQYLAAKRAIRTVFGTEPDMIR-----DGSTIPIAKMFQEIIVHKS 464

Db 335 RQVQKAFDDARKL-EERIARDII-READVVLTTNSSAALEVVDYDYYDVA-IIDEATQST 391

QY 465 V--VLIPLGAVD----DGEHSQ 480

Db 392 IPSILIPLNKVERFVLADGHKQ 413

RESULT 366

ABG14952

ID ABG14952 standard; protein; 807 AA.

XX ABG14952;

AC ABG14952;

XX 18-FEB-2002 (first entry)

DT Novel human diagnostic protein #14943.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PA Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS79139.

XX







Db 112 YDNSA-MENLLKSI-----ESIRRFASQFDL----- 137  
QY 330 LFDTKKEILMHLWRYPSLSIHGI-EG-----AFDEPGTKT-----VIPGRVIGKFS 374  
Db 138 -----LKAGGIAEGDVSVNMAFLKAGTPSPPTGFMNLQPSAEAGFD 180  
QY 375 IRLVPHMNVSAVEKQV-----TRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQY 427  
Db 181 IRVPPSVDAEALERRLVEEWAPARNMSFEF-KQLTKGQFLTAAODSNPWGLENVAVK 239  
QY 428 LAAKRAIR-TVFGTEPMDIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGGEHSQNEKINR 486  
Db 240 EAGRTSKPEIFPASTD-----ARYFRKAGVPAFGFSPISNTPSLLHDHNEYLGK 289  
QY 487 WNYIEGTKLFAA 498  
Db 290 AEYLGKIEVYVS 301

RESULT 368  
AAB48266  
ID AAB48266 standard; protein; 1031 AA.  
XX AAB48266;  
AC  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Wheat magnesium chelatase subunit (clone wdk4c.pk005.f24[FIS]).  
XX  
KW Magnesium chelatase; transgenic; herbicide; gene marker; plant breeding;  
KW wheat.  
XX  
OS Triticum aestivum.  
XX  
PN WO200075340-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US015351.  
XX  
PR 04-JUN-1999; 99US-0137461P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Butler KH, Famodu OO, Gutteridge S, Maxwell CA;  
XX  
DR WPI; 2001-091215/10.  
DR N-PSDB; AAC84585.  
XX

Isolated nucleic acid fragments encoding magnesium chelatase subunits,  
useful as probes for genetic and physical mapping of genes, as markers  
for traits linked to these genes, and in plant breeding.  
XX  
PS Disclosure; Page 86-89; 103pp; English.  
XX  
CC The invention relates to nucleic acid fragments encoding magnesium  
CC chelatase subunits. The nucleic acid fragments may be used to create  
CC transgenic plants in which the new polypeptides are present at higher or  
CC lower levels than normal or in cell types or developmental stages in  
CC which they are not normally found, and for overexpression in bacterial or  
CC yeast hosts to efficiently produce large amounts of the encoded  
CC polypeptides which could then be used for screening different compounds  
CC for potential herbicidal activity. The polynucleotides may also be used  
CC as probes for genetic and physical mapping the genes that they are part  
CC of, and as markers for traits linked to these genes. Such information is  
CC useful in plant breeding. The polypeptides are used for preparing  
CC antibodies, which are useful for detecting the polypeptides in situ or in  
CC vitro, and as a target to facilitate design and/or identification of  
CC inhibitors of enzymes that may be used as herbicides. Host cells may also  
CC be used directly for screening different compounds for potential  
CC herbicidal activity. The present sequence represents a wheat magnesium  
CC chelatase subunit

XX  
SQ Sequence 1031 AA;  
Query Match 3.8%; Score 99; DB 4; Length 1031;  
Best Local Similarity 18.6%; Pred. No. 26;  
Matches 107; Conservative 76; Mismatches 170; Indels 222; Gaps 28;  
QY 10 ASLLAVLLLLLGERG--MFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESVQPV 67  
Db 175 SSIYSVLKDLKKGYNVEGLPETPEELIEV-----IHDKE-----AQFNSPNLNVV 221  
QY 68 PRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTV 127  
Db 222 YRMNVREYQALTPYANMLEENWGK-----PP----- 247  
QY 128 CFYGHLDVQPADRGDWLTDYPVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL 187  
Db 248 ---GHLN---SDGENLL-----VYKQYGN-----IFIGVQPTF-GYEGD- 280  
QY 188 PVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRPATVYTRGNS 247  
Db 281 PMRLLFSKSASPHGFAAYYTFVEK-----IFKADAVLHFGTHGSL 321  
QY 248 YFM--VEVKCRDQDFHSGTGGI-----LHEPMADLVALLGSLVDSSGHILVP-----G 294  
Db 322 EFMPGKQVGMSDACFPDSLIGNIPNIYYAANNPSEATVAKRRSYANTISYLTTPAENAG 381  
QY 295 IYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEG 354  
Db 382 LYKGLKQLS-ELIASYQS---LKDTRGRGNQIVSSIISTAKQ--CNLDKDVLDLDEGEEL 434  
QY 355 AFDEPGTKTVIPGRVIGK---FSIRLVP---H-----MNVSAVEK----- 388  
Db 435 PANE---RDLVVGKVVYKLMIEIESRLPCGLHVICEPTAVEAVATLVNIALDRPEENI 491  
QY 389 -----QVTRHLEDVF-----SKNSSNMKV- 408  
Db 492 FSLPGILAAVTGRTIEDVYRGSKGILADVELLKQITEASRGAVGAFVEKTNKSGQVVD 551  
QY 409 -----VSMTLGL---HPWIANIDDTQYLAAGR-AIRTVFG----- 439  
Db 552 VKSKLSSILGFLGSEPWVEYLSQTKFIRADRDKLRTLFGFLGECCLKLIVADNELGALKTA 611  
QY 440 -----TEP-----DMIRDGSTIPIAKMFQEIYVHKS 465  
Db 612 LEGSYVEPGPGGDPFRNPKVLPTGKNIHALDPQSI 646

RESULT 369  
AAU00983  
ID AAU00983 standard; protein; 1704 AA.  
XX  
AC AAU00983;  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Drosophila melanogaster genome derived nompC polymorphic variant #1.  
XX  
KW Fruitfly; nompC; mechanosensory transduction channel; MSC; sensory cell;  
KW diagnosis; treatment; ion flux; ion concentration; membrane potential;  
KW signal transduction; transcription; mechanical stimulus detection; human;  
KW genotype; forensic; paternity; epidemiology; animal; human disorder;  
KW inhibitor; activator; polymorphic variant; interspecies homologue;  
KW in vivo expression; in vitro expression; modulator; pharmaceutical;  
KW hyperactivation; mechanosensation; hearing loss.  
XX  
OS Drosophila melanogaster.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 6  
FT /note= "Wild-type Leu substituted by Ile"  
XX  
PN WO200118020-A1.

XX 15-MAR-2001.  
PD  
XX  
XX 02-AUG-2000; 2000WO-US021026.  
PF  
XX  
XX 09-SEP-1999; 99US-00392812.  
PR  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX  
PI Zuker CS, Walker RG, Willingham A;  
XX  
XX WPI; 2001-244556/25.  
DR  
XX  
XX New isolated eukaryotic mechanosensory transduction protein useful as  
PT probes for sensory cells in animals and to diagnose and treat human  
PT conditions involving loss of mechanosensory transduction.  
PT  
XX  
PS Disclosure; Page; 93pp; English.  
XX  
CC The sequence represents a polymorphic variant of the Drosophila  
CC melanogaster genome derived mechanosensory transduction channel (MSC)  
CC protein, nompC. The protein and its associated nucleic acids are used as  
CC probes for sensory cells in animals and can be used to diagnose and treat  
CC a number of human conditions involving loss of mechanosensory  
CC transduction activity. MSC proteins can be used in assays to detect  
CC changes in ion flux, ion concentration, membrane potential, signal  
CC transduction, transcription or other biological or biophysical effects of  
CC mechanical stimulus detection. MSC proteins and nucleic acids can be used  
CC to genotype an animal or human for forensic, paternity, epidemiological  
CC or other investigation and for detecting mutations in mechanosensory  
CC transduction protein that eliminate or reduce function of the channel.  
CC Specific regions of MSC proteins and nucleic acids are useful for  
CC assaying inhibitors and activators of mechanosensory transduction  
CC channels, as well as for molecules that interact with the genes and  
CC proteins to form polymorphic variants and interspecies homologues.  
CC Biologically active MSC protein channels are useful for testing these  
CC modulators of mechanosensory transduction channels using in vivo and in  
CC vitro expression. The modulators are useful in the pharmaceutical  
CC industry, for treating a number of human disorders involving loss or  
CC hyperactivation of mechanosensation, e.g. hearing loss. N.B. The present  
CC sequence is not given in the specification but is derived from the  
CC Drosophila melanogaster nompC protein given in Fig 1  
XX  
SQ Sequence 1704 AA;

Query Match 3.8%; Score 99; DB 4; Length 1704;  
Best Local Similarity 19.5%; Pred. No. 57;  
Matches 69; Conservative 41; Mismatches 116; Indels 128; Gaps 15;

Qy 223 YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQ-----DFHS--G 263  
Db 1007 FLFVSKEYW-----PTLVY-----CRNQCFALAPFLACVQILDFLSFHLPFG 1048

Qy 264 TFGGILHEPMADLVALLGSLVDSGHILVPGIYDEVVPLTBEETINTYKAHLDLEEYRNS 323  
Db 1049 PWAIIIGDLIKDLARFLAVLA-----IFVFGFSMHIVALNQSFANFSPE---DLRSFEKK 1100

Qy 324 SRVEKFLFDTKEEILMH---LWRYPSLSIHGIEGAFDEPGTKTVIPG----- 367  
Db 1101 NNRNGYFSDMEQMTCPPDLRRWRKMSI-----VASANSDESTRTPFGGTSTSPHSLLEI 1156

Qy 368 -----RVIGKFSIRLVPHMNVSAREKQVTRHLEDV 397  
Db 1157 PSPCMHVDVFIQSIOTKIKQSIGNSIDITNARLPAGAFSLRRLPTTKFCTIETIDRIESI 1216

Qy 398 FSKRNSN-KWVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKM 456  
Db 1217 TKNDNATDTDYRCSYMVG-----PMTPFLLAFERLFFAVFG-----QTTTLDINPM 1261

Qy 457 -----FQEIVHK-----SVVLIPLGAVDDGEHSQNEKINR-WNYIEGT 493  
Db 1262 RHLRPEWTEVLFKEVFGIYLLVSVVVLINLLIAMMSDITYQIRQMNRNWGLVDRT 1315

RESULT 370  
AAU00985  
ID AAU00985 standard; protein; 1704 AA.  
XX  
AC AAU00985;  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Drosophila melanogaster genome derived nompC polymorphic variant #3.  
XX  
KW Fruitfly; nompC; mechanosensory transduction channel; MSC; sensory cell;  
KW diagnosis; treatment; ion flux; ion concentration; membrane potential;  
KW signal transduction; transcription; mechanical stimulus detection; human;  
KW genotype; forensic; paternity; epidemiology; animal; human disorder;  
KW inhibitor; activator; polymorphic variant; interspecies homologue;  
KW in vivo expression; in vitro expression; modulator; pharmaceutical;  
KW hyperactivation; mechanosensation; hearing loss.  
XX  
OS Drosophila melanogaster.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 22 /note= "Wild-type Arg substituted by Lys"  
FT  
XX WO200118020-A1.  
XX  
PD 15-MAR-2001.  
XX  
XX 02-AUG-2000; 2000WO-US021026.  
XX  
PR 09-SEP-1999; 99US-00392812.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PI Zuker CS, Walker RG, Willingham A;  
XX  
DR WPI; 2001-244556/25.  
XX  
PT New isolated eukaryotic mechanosensory transduction protein useful as  
PT probes for sensory cells in animals and to diagnose and treat human  
PT conditions involving loss of mechanosensory transduction.  
XX  
PS Disclosure; Page; 93pp; English.  
XX  
CC The sequence represents a polymorphic variant of the Drosophila  
CC melanogaster genome derived mechanosensory transduction channel (MSC)  
CC protein, nompC. The protein and its associated nucleic acids are used as  
CC probes for sensory cells in animals and can be used to diagnose and treat  
CC a number of human conditions involving loss of mechanosensory  
CC transduction activity. MSC proteins can be used in assays to detect  
CC changes in ion flux, ion concentration, membrane potential, signal  
CC transduction, transcription or other biological or biophysical effects of  
CC mechanical stimulus detection. MSC proteins and nucleic acids can be used  
CC to genotype an animal or human for forensic, paternity, epidemiological  
CC or other investigation and for detecting mutations in mechanosensory  
CC transduction protein that eliminate or reduce function of the channel.  
CC Specific regions of MSC proteins and nucleic acids are useful for  
CC assaying inhibitors and activators of mechanosensory transduction  
CC channels, as well as for molecules that interact with the genes and  
CC proteins to form polymorphic variants and interspecies homologues.  
CC Biologically active MSC protein channels are useful for testing these  
CC modulators of mechanosensory transduction channels using in vivo and in  
CC vitro expression. The modulators are useful in the pharmaceutical  
CC industry, for treating a number of human disorders involving loss or  
CC hyperactivation of mechanosensation, e.g. hearing loss. N.B. The present  
CC sequence is not given in the specification but is derived from the  
CC Drosophila melanogaster nompC protein given in Fig 1  
XX  
SQ Sequence 1704 AA;

Query Match 3.8%; Score 99; DB 4; Length 1704;  
Best Local Similarity 19.5%; Pred. No. 57;



Matches 69; Conservative 41; Mismatches 116; Indels 128; Gaps 15;

```

QY 223 YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQ-----DFHS--G 263
Db 1007 FLFVSKEYW-----PTLVY-----CRNQCFALAFLLACVQILDFLSFHLFG 1048
QY 264 TFGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLLEYS 323
Db 1049 PWAIIIGDLLKDLARFLAVLA-----IFVFGFSMHIVALNQSFANFSPE---DLRSFEKK 1100
QY 324 SRVEKFLFDTKKEILMH-----LWRYPSSLHIGIEGAFDEPGTKTVIPG----- 367
Db 1101 NRNRGYFSDMEQMTCHPDLRRWRIMSI-----VASANSDESTRTTTPGGTSTSPHSLLEI 1156
QY 368 -----RVIGKFSIRLVPHMNVSAVEKQVTRHLEDV 397
Db 1157 PSPCMHVDVFIQSIOTKIKQISNIDITNARLPGAFSLRRLPTTKFCTIETIEDRIESI 1216
QY 398 FSKRNSSN-KMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTITIAKM 456
Db 1217 TKNDNATDTDYRCSYMLG-----PMTPLAFERLFFAVFG-----QTTLDINPM 1261
QY 457 -----FQEIIVHK-----SVVLIPLGAVDGGEHSQNEKINR-WNYIEGT 493
Db 1262 RHLRPEWTEVLFKFVGGIYLLVSVVVLINLLIAMSDTYQRIQMNRNWGLVDRT 1315

RESULT 371
AAU00984
ID AAU00984 standard; protein; 1704 AA.
XX
AC AAU00984;
XX
XX 04-JUL-2001 (first entry)
DE Drosophila melanogaster genome derived nompC polymorphic variant #2.
XX
KW Fruitfly; nompC; mechanosensory transduction channel; MSC; sensory cell;
KW diagnosis; treatment; ion flux; ion concentration; membrane potential;
KW signal transduction; transcription; mechanical stimulus detection; human;
KW genotype; forensic; paternity; epidemiology; animal; human disorder;
KW inhibitor; activator; polymorphic variant; interspecies homologue;
KW in vivo expression; in vitro expression; modulator; pharmaceutical;
KW hyperactivation; mechanosensation; hearing loss.
XX
OS Drosophila melanogaster.
XX
XX Key Location/Qualifiers
FH Misc-difference 13
FT /note= "Wild-type Gly substituted by Ala"
XX
XX WO200118020-A1.
XX
XX 15-MAR-2001.
XX
XX 02-AUG-2000; 2000WO-US021026.
XX
XX 09-SEP-1999; 99US-00392812.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Zuker CS, Walker RG, Willingham A;
XX
XX WPI; 2001-244556/25.
XX
XX New isolated eukaryotic mechanosensory transduction protein useful as
XX probes for sensory cells in animals and to diagnose and treat human
XX conditions involving loss of mechanosensory transduction.
XX
XX Disclosure; Page; 93pp; English.
XX
XX The sequence represents a polymorphic variant of the Drosophila
XX melanogaster genome derived mechanosensory transduction channel (MSC)
CC

```



Db 134 DIKKRVIAHLLSVD-----LPDPSAIDEEVVVIAE-----DLTPSDTAQ 172  
QY 143 GWLTDPYV---LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGME 199  
Db 173 --LNKKYVKAFTVDVGR-----TSHSAIMARSLEIPAVV----- 205  
QY 200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQD 259  
Db 206 --GTGQITSTVKKDQELVVDGVTGEVIID-----PSDQEIENEEKASEYE 249  
QY 260 FHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKA--IHLDL 317  
Db 250 SMKAENKLDKDEPS---ISKDGVQVELAANIGTPKDLEGVSDNGAEGIGLYRTEFLYMDS 306  
QY 318 EYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEG-----AFDEPGTKTV---IPG 367  
Db 307 PELPS---EEDQFQAYKEVL-----EGVDGKPVVVRTMDIGGDKELPYLDLPD 351  
QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLG----LHPWIANID 423  
Db 352 -----EMNPFGLGYRALRISLDR--DEIF--RTQIRALLRASTYGQLRIMFPMVSNLD 399  
QY 424 DTQYLAAKRAIRTVFGTEPDMIRD-GST-----IPIAKMFOEIVHKSVVLIPL 470  
Db 400 EL-----RAAKAIVQEEKDKLEDQQTISDSLQIGIMIEIPAAAMLADQFAKEVDFFSV 453  
QY 471 GAVDDGEHSQ-----NEKIN 485  
Db 454 GTNDLIQYTMAADRLNERVS 473

RESULT 374  
ADB11784  
ID ADB11784 standard; protein; 580 AA.  
AC ADB11784;  
XX 20-NOV-2003 (first entry)  
DT 20-NOV-2003 (first entry)  
DE Alloiooccus otitis antigenic protein SEQ ID NO:5276.  
XX Alloiooccus otitis.  
KW Alloiooccus otitis; antigenic protein; immunogenic; immunisation;  
KW gene therapy; Gram-positive bacterium; infection.  
XX Alloiooccus otitis.  
OS WO2003048304-A2.  
XX 12-JUN-2003.  
XX 25-NOV-2002; 2002WO-US036123.  
XX 29-NOV-2001; 2001US-0333777P.  
PR 18-NOV-2002; 2002US-0426742P.  
XX (AMHP ) WYETH HOLDINGS CORP.  
PA Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;  
XX WPI; 2003-505284/47.  
XX N-PSDB; ADB11787.

PT New Alloiooccus otitis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.  
XX Claim 33; SEQ ID NO 5276; 1019pp; English.  
XX The present invention describes an isolated polynucleotide (I) of  
CC Alloiooccus otitis genomic DNA, which encodes an antigenic protein.  
CC Alloiooccus otitis is a Gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its

CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloiooccus otitis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloiooccus  
CC otitis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloiooccus  
CC otitis. The present sequence represents an Alloiooccus otitis  
CC antigen protein from the present invention.  
XX  
SQ Sequence 580 AA;

Query Match 3.8%; Score 98.5; DB 6; Length 580;  
Best Local Similarity 19.1%; Pred. No. 12;  
Matches 84; Conservative 70; Mismatches 149; Indels 137; Gaps 21;  
QY 83 DTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGD 142  
Db 141 DIKKRVIAHLLSVD-----LPDPSAIDEEVVVIAE-----DLTPSDTAQ 179  
QY 143 GWLTDPYV---LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGME 199  
Db 180 --LNKKYVKAFTVDVGR-----TSHSAIMARSLEIPAVV----- 212  
QY 200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQD 259  
Db 213 --GTGQITSTVKKDQELVVDGVTGEVIID-----PSDQEIENEEKASEYE 256  
QY 260 FHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKA--IHLDL 317  
Db 257 SMKAENKLDKDEPS---ISKDGVQVELAANIGTPKDLEGVSDNGAEGIGLYRTEFLYMDS 313  
QY 318 EYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEG-----AFDEPGTKTV---IPG 367  
Db 314 PELPS---EEDQFQAYKEVL-----EGVDGKPVVVRTMDIGGDKELPYLDLPD 358  
QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLG----LHPWIANID 423  
Db 359 -----EMNPFGLGYRALRISLDR--DEIF--RTQIRALLRASTYGQLRIMFPMVSNLD 406  
QY 424 DTQYLAAKRAIRTVFGTEPDMIRD-GST-----IPIAKMFOEIVHKSVVLIPL 470  
Db 407 EL-----RAAKAIVQEEKDKLEDQQTISDSLQIGIMIEIPAAAMLADQFAKEVDFFSV 460  
QY 471 GAVDDGEHSQ-----NEKIN 485  
Db 461 GTNDLIQYTMAADRLNERVS 480

RESULT 375  
ADB11782  
ID ADB11782 standard; protein; 603 AA.  
XX  
AC ADB11782;  
XX 20-NOV-2003 (first entry)  
DT 20-NOV-2003 (first entry)  
XX Alloiooccus otitis antigenic protein SEQ ID NO:5278.  
DE Alloiooccus otitis; antigenic protein; immunogenic; immunisation;  
XX Alloiooccus otitis; Gram-positive bacterium; infection.  
KW gene therapy; Gram-positive bacterium; infection.





[illegible][illegible]





```
CC function of BRCA2 in oncogenesis or subcellular localisation of BRCA2
CC protein in normal and cancerous cells. The present sequence represents
CC human BRCA2 (Omi3)
XX
SQ Sequence 3418 AA;

Query Match          3.8%; Score 98.5; DB 2; Length 3418;
Best Local Similarity 18.1%; Pred. No. 1.9e+02;
Matches 101; Conservative 73; Mismatches 167; Indels 217; Gaps 26;

QY 21 ERGMFSSPPPP-----ALLEKVFOYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 75
Db 58 EPNLFKTPQRKPSYNQLASTPIIFKEQGLTLPLYQSPVKELDKFKLDLGRNVNPSRHKSL 117

QY 76 RMMVAADTLQRLGARVASVDMGPPQLPDGQSLPI-----PPVIL--AELGSDPTKGT 126
Db 118 RTVKTMDQ-----ADDVSCPLNLSCLSESPVVLQCTHTVTPQRDKSV 159

QY 127 VCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-- 184
Db 160 VC-----GSLFHTPKFVKGRQTPKHISESLGAEVPDMSWSSSLATPPTLSST 207

QY 185 -----QDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDN 229
Db 208 VLIVRNEEASETVFPHDTTANVKSYSFNHDES-----LKKNDRFIASV---TDSEN 255

QY 230 LWISQRKPAITYG---TRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS 286
Db 256 ---TNQREAAASHGFGKTSGNS-FKVN-SCKD---HIG-----KS 286

QY 287 SGHILVPGIYDEVVPLTEEE-----INT-----YKAIHLDLEEYRN 322
Db 287 MPHVLEDEVYETVVDTSEEDSFSLCFSKCRTKNLQKVRTSKTRKKIFHEANADECEKSKN 346

QY 323 SSRVEKFLF-----DT-----KEEILMHLWRYPSSLIHGIEG 354
Db 347 QVK-EKYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVPSSLACEWSQLTSLGLNG 405

QY 355 AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLG 414
Db 406 A-----QMEKIPLLLHISCDQNISE--KOLLDTENKPKKDFLTSENS 445

QY 415 LHPWIANI-----DDTQY-----LAAKRAIRTVFGTEPDMIRDGST 450
Db 446 L-PRISSLPKSEKPLNEETVWNKRDEEQHLESHTDCILAVKQAI-----SGT 491

QY 451 IPIAKMFQEIHKSVVLI 468
Db 492 SPVASSFQGI-KKSIFRI 508

RESULT 380
AAY04358
ID AAY04358 standard; protein; 3418 AA.
XX
AC AAY04358;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human BRCA2 (omi5) protein.
XX
KW Human; BRCA2; genetic testing; protein therapy; haplotype; detection;
XX gene therapy; breast cancer; ovarian cancer.
OS Homo sapiens.
XX
PN WO9909164-A1.
XX
PD 25-FEB-1999.
XX
PF 14-AUG-1998; 98WO-US016905.
XX
PR 15-AUG-1997; 97US-0055784P.
```

```
PR 07-NOV-1997; 97US-0064926P.
PR 12-NOV-1997; 97US-0065367P.
PR 01-MAY-1998; 98US-00071715.
PR 22-MAY-1998; 98US-00084471.
XX
PA (ONCO-) ONCORMED INC.
XX
PI Murphy PD, White MB, Rabin MB, Olson SJ, Yoshikawa M, Jackson GM;
PI Eskandari T, Schryer B, Park M;
XX
DR WPI; 1999-190163/16.
XX N-PSDB; AAX30259.
PT New coding sequence haplotypes of the human BRCA2 gene - used to develop
PT products for determining susceptibility to, detection and treatment of
PT breast or ovarian cancer.
XX
PS Claim 20; Page 155-162; 226pp; English.
XX
CC The present invention describes genomic DNA which contains a BRCA2 gene
CC where the first 12 nucleotides beginning exon 5 are 5'-TCCTGTTGTTCT-3' as
CC in sequence (I) (see AAX03249), where nucleotides numbers 5782-5790 are
CC GTTGTGTT as in sequence (IV) (see AAX30255), and where the last 20
CC nucleotides encoding exon 15 are 5'-CTGCGTGTCTCATAAACAG-3' as in
CC sequence (II) (see AAX30251) and the first 20 nucleotides beginning exon
CC 16 are 5'-CTGTATACGTATGCGGTTTC-3' as in sequence (III) (see AAX30253).
CC Products and methods from the present invention can be used for
CC identifying mutations in the BRCA2 gene leading to predisposition or
CC higher susceptibility to breast or ovarian cancer. They can also be used
CC for detection and gene therapy for breast and ovarian cancers. They can
CC be used in methods for monitoring disease progression, for determining
CC patients suited for gene and protein replacement progression, or for
CC detecting the presence or quantifying the amount of a tumour growth
CC inhibitor following such therapy. The BRCA2 protein, polypeptides, their
CC functional equivalents, antibodies, and PNs may also be useful in the
CC study of the characteristics of BRCA2 proteins, such as structure and
CC function of BRCA2 in oncogenesis or subcellular localisation of BRCA2
CC protein in normal and cancerous cells. The present sequence represents
CC human BRCA2 (omi5)
XX
SQ Sequence 3418 AA;
```

```
Query Match          3.8%; Score 98.5; DB 2; Length 3418;
Best Local Similarity 18.1%; Pred. No. 1.9e+02;
Matches 101; Conservative 73; Mismatches 167; Indels 217; Gaps 26;

QY 21 ERGMFSSPPPP-----ALLEKVFOYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 75
Db 58 EPNLFKTPQRKPSYNQLASTPIIFKEQGLTLPLYQSPVKELDKFKLDLGRNVNPSRHKSL 117

QY 76 RMMVAADTLQRLGARVASVDMGPPQLPDGQSLPI-----PPVIL--AELGSDPTKGT 126
Db 118 RTVKTMDQ-----ADDVSCPLNLSCLSESPVVLQCTHTVTPQRDKSV 159

QY 127 VCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-- 184
Db 160 VC-----GSLFHTPKFVKGRQTPKHISESLGAEVPDMSWSSSLATPPTLSST 207

QY 185 -----QDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDN 229
Db 208 VLIVRNEEASETVFPHDTTANVKSYSFNHDES-----LKKNDRFIASV---TDSEN 255

QY 230 LWISQRKPAITYG---TRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS 286
Db 256 ---TNQREAAASHGFGKTSGNS-FKVN-SCKD---HIG-----KS 286

QY 287 SGHILVPGIYDEVVPLTEEE-----INT-----YKAIHLDLEEYRN 322
Db 287 MPHVLEDEVYETVVDTSEEDSFSLCFSKCRTKNLQKVRTSKTRKKIFHEANADECEKSKN 346

QY 323 SSRVEKFLF-----DT-----KEEILMHLWRYPSSLIHGIEG 354
Db 347 QVK-EKYSFVSEVEPNDDPLDSNVAHQKPFESGSDKISKEVVPSSLACEWSQLTSLGLNG 405
```



QY 110 IPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTVEVDGKLYGRGATDNKGP 169  
Db 87 -----ESVSDLALVAVGGYRGELHPLSDVDLLILSRKKLPDDQAQKVGELLT----- 134  
QY 170 VLAW----INAVSAFRALEQ-----DLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFS 219  
Db 135 -LLWDVKLEVGHSVRTLEECLEGLSDLTVA TN-LIESRLIGDVAL--FLELQKH--- 186  
QY 220 GVDYIVISDNLWISQRKPAITYGTRGNSYFMEVEK---CRDQDFHSGTFFGGILHEPMADL 276  
Db 187 -----IFSDGFWPSEK-----FFAAKVEEQNVHRQRYHGT SYN--LEP--DV 224  
QY 277 VALLGSLVD-----SSGHILVPGIYDEVVP---LTHEEINTYK-----AIHL 315  
Db 225 KSSPGGLRDIHTLQWVARRHFGATSM-DEMVGFGFLTEARNELNECLHQLWRIRFALHL 283  
QY 316 DLEEYRNSRVEKFLDTKEEILMHLWRYPSLSIHGIEGAPDEPGTKTV-----IPGRV- 369  
Db 284 ELTRYDN-----RLLFDRQLSVARRL-----GYEGDGNQPIEHMMKDFFRVTRVS 329  
QY 370 -IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQYL 428  
Db 330 ELNQMLLOLFEAEIALTEDEKPRPIDDDFQLRGT----LIDLR-----DDTLFI 375  
QY 429 AAKRAIRTVFGTEPDMIRDGSTI 451  
Db 376 REPQAILRMFYI---MVRN-STI 394

RESULT 383  
AAM49743  
ID AAM49743 standard; protein; 903 AA.  
AC AAM49743;  
XX  
DT 17-JUN-2002 (first entry)  
DE Synechococcus sp MA19 cphA protein.  
XX  
KW Cyanophycin synthetase; cphA; cyanophycinase; cphB; cyanophycin;  
KW polyaspartic acid production; arginine production; plant protection;  
KW agricultural food supplement; paper; industry; textile; pigment; paint;  
KW polyaspartic acid cyanophycin graft polymer; ceramic; washing product;  
KW waste water treatment.  
XX  
OS Synechococcus sp.  
XX  
PN WO200212508-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 27-JUL-2001; 2001WO-EP008687.  
XX  
PR 09-AUG-2000; 2000DE-01038776.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Joentgen W, Steinbuechel A, Oppermann-Sanio FB, Aboulmagd E;  
XX WPI; 2002-303981/34.  
DR N-PSDB; ABA99887.  
XX

PT New cyanophycin synthase, useful for production of cyanophycin and its  
PT derivatives e.g. for food supplementation, comprises a high optimum  
PT temperature.  
XX  
PS Claim 1; Page 39-40; 40pp; German.  
XX  
CC This invention describes a novel cyanophycin synthase active at 35-  
CC 55plusoC from Synechocystis PCC6308 or Synechococcus sp. MA19. The products  
CC of the invention are used to prepare cyanophycin and its products,  
CC especially poly(aspartic acid) and arginine. Cyanophycin and its products

CC are useful as food supplements, in agriculture and/or plant protection,  
CC in the paper, textile, pigment, paint, ceramics, and washing product  
CC industries, and also for (waste) water treatment. The product of the  
CC invention is also useful for producing poly(aspartic acid) cyanophycin  
CC graft polymers. Nucleic acids that encode cyanophycin synthase can be  
CC used for recombinant production of the protein, and fragments of nucleic  
CC acids are used for identification and isolation of related genes. Since  
CC the protein of the invention is active at over 35 plusoC (known  
CC cyanophycin synthases require a lower temperature), processing is allowed  
CC at higher temperatures, providing better flexibility in conditions,  
CC significantly improved product yields and better reproducibility and  
CC economics. Modified forms of the protein may also have better stability  
CC (e.g. against proteases) in the cell or are resistant to feedback  
CC inhibition. The protein derived from PCC6308 has an optimum temperature  
CC for activity at 50 plusoC (over 250 nmole/min/ml). This sequence  
CC represents the Synechococcus sp MA19 cyanophycin synthetase cphA protein  
CC described in the method of the invention  
XX  
SQ Sequence 903 AA;

Query Match 3.7%; Score 98; DB 5; Length 903;  
Best Local Similarity 21.1%; Pred. No. 26;  
Matches 115; Conservative 73; Mismatches 189; Indels 168; Gaps 29;  
QY 6 GRMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYI-DLHQDEFVQTLKEWVAIESDS- 63  
Db 126 GRAAVRLCQ---SIVDRGRYHK-----ARAEQDLQDLKDLWRDAALGSPSTESIVKEAKR 177  
QY 64 ----VQVPVPRFRQEL-----FRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPV 113  
Db 178 GIPWMQLGARFLIQLGYGVNQKRIQATMTDQTGILGVELACDKEATKRILANAGIPVP-- 235  
QY 114 ILAELGSDPTKGTVC-FYGHLDVQPADRGDWLTDPYVLTVEVDGKLYGRGATDNKGPVLA 172  
Db 236 -----KGTVINFLDDLE-EAIEYVGGY---PIVIKPLDGN-HGRGITN---IQN 277  
QY 173 WINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDY--IVISDNL 230  
Db 278 WEEEAAYDAARQ---ISRSIIVE-----RYYQGRDHRVLVWDASS 315  
QY 231 WISQRKPAITYGT-RGNSYFMVEVKCRDQDFHSG-----TFG 266  
Db 316 AVAERVPAHVVDGRSTIAELIETNKDPNRGEGHDNLTKIELDRTSYQLLERQGYTLD 375  
QY 267 GILHEPMADLVALLGSLVDSSGHILV---PGIYDEVV----- 300  
Db 376 SIL--PQGEICYL RATANLSTGGIAVDRTDEIH PENVWL AQGVVKIVGLDIAGIDIVTPD 433  
QY 301 ---PLTE-----EEINTYKAHLDLEEYRNSR-----VEKFLFDTKEEILMHLWRYPSL 347  
Db 434 ISRPLREV DGVVVEVNAAPGFRMHVAPSQGTPRNVA AAVLDM LFPSEQSS-----RIPIL 488  
QY 348 SIHGIEG-----AFDEPGT---KTVIPGRVIGKF-----SIRLV---PH 380  
Db 489 SIIGTNGKTTTTRLLAHIFKQTKGVVGYTTDTGT YIGDFLVEAGDNTGPPSAQLILQDPT 548  
QY 381 MNVSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQYLA AKRAI--RTVF 438  
Db 549 VEVAVLETARGGILRSGLA-FHAANVGVLNVAADHLGIGIDITDIDQLAHLKSVVAEAVF 607  
QY 439 GTEPD 443  
Db 608 ---PD 609

RESULT 384  
ADM57193  
ID ADM57193 standard; protein; 1381 AA.  
XX  
AC ADM57193;  
XX  
DT 03-JUN-2004 (first entry)  
XX



DE A thaliana herbicide target protein SEQ ID NO: 4.

XX plant; herbicide; cress.

XX Arabidopsis thaliana.

XX WO2004022780-A2.

XX 18-MAR-2004.

XX 30-JUL-2003; 2003WO-EP008393.

XX 16-AUG-2002; 2002DE-01038434.

XX (META-) METANOMICS GMBH & CO KGAA.

XX Plesch G, Blau A, Daeschner K;

XX WPI; 2004-315575/29.

XX N-PSDB; ADM57192.

XX Identifying herbicides and growth regulators, comprises testing compounds for activity against specific nucleic acid or encoded proteins, also preparation of herbicide-tolerant plants.

XX Claim 1; Page 100-105; 205pp; German.

XX The present invention relates to a method for identifying substances with herbicidal activity from their ability to reduce or block the expression or activity of specific genes or nucleic acids or the amino acid sequences encoded by them. In particular, the sequences are from Arabidopsis thaliana. The method can identify herbicides with species-independent activity and can be used to screen combinatorial libraries. The present sequence is a protein of the invention.

XX Sequence 1381 AA;

Query Match 3.7%; Score 98; DB 8; Length 1381;

Best Local Similarity 19.3%; Pred. No. 51;

Matches 81; Conservative 55; Mismatches 125; Indels 158; Gaps 21;

QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEEGMEEAGSVALEELVEKE 213

Db 609 VYGKAYGN-----VFIGVQPTF-GYEGD-PMRLLFKSASPHHGFAYYSYVEK- 655

QY 214 KDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFM--VEVKCRDQDFHSGTFGGI--- 268

Db 656 -----IFKADAVLHFGTHGSLEFMPGKQVGMSDACFPDSLIGNIPNV 697

QY 269 ----LHEPMADLVALLGSLVDSSGHILVP----GIYDEVVPLTEEEINTYKAHLDLEBY 320

Db 698 YYAANNPSEATIAKRRSYANTISYLTPTPAENAGLYKGLKQLS-ELISSYQS----LKDT 752

QY 321 RNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGK---FSIRL 377

Db 753 GRGPQIVSSIIISTAKQ--CNLDKVDVLPDEGLELS---PKDRDSVVGKVKYKIMEIESRL 807

QY 378 VP---H-----MNVSAVEKQ-----VTRHLEDVF----- 398

Db 808 LPCGLHVIGEPPPSAMEAVATLVNIAALDRPEDEISALPSILAECVGREIEDVYRGSDKGI 867

QY 399 -----SKRNSSNKMVVSMT-----LGL---HPWIANIDTQY 427

Db 868 LSDVELLKEITDASRGAVSAFVEKTNKSGQVVDVSDKLTSLGFGINEPWPVEYLSNTKF 927

QY 428 LAAKR-AIRTVFG-----TPE-----DMIRDGSTIPIAK 455

Db 928 YRANRDKLRTVFGFLGELCKLVVMDNELGSLMQALEGKYVEPFGGDPINRPNKVLPTGK 986

RESULT 385

ADC10148

ID ADC10148 standard; protein; 1703 AA.

XX

AC ADC10148;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human NOVX polypeptide SEQ ID NO: 168.

XX

XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.

XX

OS Homo sapiens.

XX

PN WO2003000842-A2.

XX

PD 03-JAN-2003.

XX

PF 04-JUN-2002; 2002WO-US017443.

XX

04-JUN-2001; 2001US-0295607P.

PR

04-JUN-2001; 2001US-0295661P.

PR

06-JUN-2001; 2001US-0296404P.

PR

06-JUN-2001; 2001US-0296418P.

PR

07-JUN-2001; 2001US-0296575P.

PR

11-JUN-2001; 2001US-0297414P.

PR

12-JUN-2001; 2001US-0295573P.

PR

12-JUN-2001; 2001US-0297567P.

PR

14-JUN-2001; 2001US-0298285P.

PR

15-JUN-2001; 2001US-0298528P.

PR

18-JUN-2001; 2001US-0299133P.

PR

19-JUN-2001; 2001US-0299230P.

PR

21-JUN-2001; 2001US-0299949P.

PR

22-JUN-2001; 2001US-0300177P.

PR

26-JUN-2001; 2001US-0300883P.

PR

28-JUN-2001; 2001US-0301530P.

PR

28-JUN-2001; 2001US-0301550P.

PR

03-JUL-2001; 2001US-0302951P.

PR

31-JUL-2001; 2001US-0308890P.

PR

14-SEP-2001; 2001US-0322297P.

PR

25-SEP-2001; 2001US-0324669P.

PR

03-DEC-2001; 2001US-0337477P.

PR

14-DEC-2001; 2001US-0341562P.

PR

21-FEB-2002; 2002US-0358656P.

PR

21-FEB-2002; 2002US-0359122P.

PR

22-FEB-2002; 2002US-0358978P.

PR

22-FEB-2002; 2002US-0359034P.

PR

22-FEB-2002; 2002US-0359035P.

PR

22-FEB-2002; 2002US-0359121P.

PR

27-FEB-2002; 2002US-0359964P.

PR

01-MAR-2002; 2002US-0360858P.

PR

12-MAR-2002; 2002US-0363430P.

PR

12-MAR-2002; 2002US-0363676P.

PR

10-APR-2002; 2002US-0371346P.

PR

10-MAY-2002; 2002US-0379444P.

PR

04-JUN-2002; 2002US-00379444.

XX

(CURA-) CURAGEN CORP.

XX

Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;

Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;

Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;

Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;

Ort T, Padigar M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;

Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;

Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;

Burgess CE, Lepley DM;

XX

WPI; 2003-210149/20.

DR

N-PSDB; ADC10147.

DR

XX

New isolated NOVX polypeptides and nucleic acid molecules useful for

PT treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.  
XX  
PS Claim 1; SEQ ID NO 168; 772pp; English.  
XX  
CC The invention relates to novel isolated polypeptides, mature form of the  
CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to one of the  
CC polypeptides of the invention.  
XX  
SQ Sequence 1703 AA;  
  
Query Match 3.7%; Score 98; DB 7; Length 1703;  
Best Local Similarity 24.3%; Pred. No. 70;  
Matches 44; Conservative 36; Mismatches 69; Indels 32; Gaps 12;  
  
QY 320 YRNSRVEKFLFDTKKEIIMHL---WR--YPSL--SIHGIEGAFD-EPGTTKTVIPGRVI 370  
Db 120 HSNKAQYVRVSFDTKPDLLHLMTKEWQLPKLLISVHGGLQNFELOPKLKQVF-GKGL 178  
  
QY 371 GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPW--IANIDDTQYL 428  
Db 179 IKAAMTTGAWIFTGGVNTGVRHVGDALKDHASKSRGKI-CTIGIAPWGVENQED---- 233  
  
QY 429 AAKRAIRTVEGTEPDMIRDGTI--PIAKM-FQEI VHKSVVLIPLGAVDDGEHSQNEKIN 485  
Db 234 -----LIGR--DVVRPYQTMSNPMSKLTVLNSMHSHFILADNGTT--GKYGAEVKLR 281  
  
QY 486 R 486  
Db 282 R 282  
  
RESULT 386  
AAB66471  
ID AAB66471 standard; protein; 2111 AA.  
XX  
AC AAB66471;  
XX  
DT 09-APR-2001 (first entry)  
XX  
DE Protein encoded by Mycobacterium tuberculosis mas gene.  
XX  
KW Mycobacterium tuberculosis; attenuated microorganism;  
KW signature tagged transposon mutant; mutant library;  
KW mycobacterial infection; actinomycetales; antibacterial; immunostimulant;  
KW mas; myceroctic acid synthase; vaccine.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO200102555-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 06-JUL-2000; 2000WO-IB0000950.  
XX  
PR 06-JUL-1999; 99US-0142982P.  
PR 08-JUL-1999; 99US-0142833P.  
XX  
PA (INSP ) INST PASTEUR.  
XX  
PI Gicquel B, Guilhot C, Camacho L;  
XX  
DR WPI; 2001-091804/10.  
DR N-PSDB; AAF31641.  
XX

PT Screening a mutant library for mutants unable to grow under specific  
PT conditions and for identifying loci involved in pathogenicity, comprises  
PT using signature tagged transposon mutagenesis.  
XX  
PS Example 8; Page 148-155; 159pp; English.  
XX  
CC The present sequence is given in a specification relating to a method for  
CC screening a library of mutants. The method comprises constructing a  
CC library with insertions in genes and/or regulatory regions of the  
CC organisms of interest, where the insertion contains a tag and/or a  
CC transposon associated with a tag. The mutants are identified by  
CC hybridisation of the tags to known sequences. The method is useful for  
CC treating an individual suffering from a mycobacterial infection,  
CC suspected of being infected with a Mycobacterium, or having been exposed  
CC to an infectious Mycobacterium. It is also useful for identifying and  
CC isolating mutants of actinomycetales and for identifying compounds that  
CC have antibiotic activity. The method is used to identify mutants of  
CC microorganisms, preferably an actinomycetales, such as M. tuberculosis,  
CC M. bovis, M. leprae, M. avium, M. intracellulare and M.  
CC paratuberculosis, that is unable to grow under specific conditions. It is  
CC especially useful for identifying loci involved in pathogenicity. It is  
CC useful in constructing vaccines. The method can be used to screen  
CC multiple libraries concurrently. It can screen libraries of different  
CC organisms or different strains of the same organism  
XX  
SQ Sequence 2111 AA;  
  
Query Match 3.7%; Score 98; DB 4; Length 2111;  
Best Local Similarity 23.4%; Pred. No. 98;  
Matches 74; Conservative 46; Mismatches 140; Indels 56; Gaps 16;  
  
QY 65 QPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQ--QLPDGQSLPIPPVI-LAELGSD 121  
Db 1799 QPNPKARQTIEGLRAAGADIVVECG-NIAEPTADRLVSAATATGLPLRGLHSAAVVED 1857  
  
QY 122 PTKGTVC-----FYGLHDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPV 170  
Db 1858 ATLTNITDELIDRDWSPKVFSGWNLHRTLGP--LDWFCLFSSGAALLGSPQGAYAAA 1915  
  
QY 171 LAWINAVSAFRALEQDLNVN-----IKFIEGME-----EAGSVALEELVEKE 213  
Db 1916 NSWVDVFAHWRR-AQGLPVSAIAWGAWGEVGRATFLAEGGEIMITPEEGAYAFETLV--R 1972  
  
QY 214 KDRFFSGVDYIVISDNLWIS---QRKP-----AITYGTRGNSYFMVEVKCRDQDPHSGT 264  
Db 1973 HDRAVSG--YIPILGAPWLADLVRRSPWGEFASTQQRSGRSPKFRMELLSLPQDEWAGR 2030  
  
QY 265 FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPL---TEEEINTYKAIHLDLEEYR 321  
Db 2031 LRRLLVEQAS---VILRRITIDADRSFIEYGL-DSLGMLEMRTHVETETGIRLTPKVIATN 2086  
  
QY 322 NSSR-VEKFLFDTKBE 336  
Db 2087 NTARALAQYLAADTLAE 2102  
  
RESULT 387  
ABU31049  
ID ABU31049 standard; protein; 402 AA.  
XX  
AC ABU31049;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #16576.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Helicobacter pylori.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.





Db 63 -----GERLQHGKTHAQFWSLSLKNLDTGPRQHSFGNSGDL-----FLGAD- 105  
Qy 123 TKGTVCFYGHLDVQPADRGDWLTDPYVLTVDGK-----LYGRGATDNKGPVLAW 173  
Db 106 -----LDLATLAGLDGASLHIEETLFIIDRGTGQPTGP--SW 140  
Qy 174 INAVSAF---RALEQDLPVNIKFIIIEGMEEAAGSVALBELVEKEKDRFFSGVDYIVISDNL 230  
Db 141 QGAVGSYFGGAPLHNDIGANQLSLTWQQQ----- 170  
Qy 231 WISQRKPAITYGTRGNSYFMV-----EVKCRDQDFHS-----GTFGGIL-HEPMAD 275  
Db 171 WLGRLDShLGRTNARRYELLYNCETVVTCTNDPIIDASTGILPPPYGAWGGYKXRYATPT 230  
Qy 276 LVALLGSLV-----DSSGHILVPGIYDEVVPLTTEEEINTYKAHLDL 317  
Db 231 LYLHAGAFESNPVDYLKRRHGLDFGTDDASGTSLLGIGDK-----REESLDPYRS-HYEL 285  
Qy 318 BEYRN-SSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 376  
Db 286 NAYLNTANQVDPLTGASDHGSAGGFFKFQQLFWRADGGRLDSP-----RALGLFG-- 335  
Qy 377 LVPHMNVSAVEKQVTRHLEDV 397  
Db 336 ---SLSVSADDKQPFRRHFAEL 353

RESULT 389  
ABB76955  
ID ABB76955 standard; protein; 540 AA.  
XX ABB76955;  
AC  
XX  
DT 22-JUL-2002 (first entry)  
XX  
DE 4-Hydroxyphenylpyruvate oxidase mutant #2.  
XX  
KW 4-Hydroxyphenylpyruvate oxidase; enzyme; herbicide; weed control; mutein;  
mutant.  
XX  
OS Arthrobacter globiformis.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 98 /note= "Wild-type Ala substituted by Gly"  
FT  
XX  
PN FR2815969-A1.  
XX  
PD 03-MAY-2002.  
XX  
PF 30-OCT-2000; 2000FR-00013942.  
XX  
PR 30-OCT-2000; 2000FR-00013942.  
XX  
PA (AVET ) AVENTIS CROPSCIENCE SA.  
XX  
XX Zink O, Paget E, Rolland A, Sailland A, Freyssinet G;  
PI  
XX  
DR WPI; 2002-419041/45.  
N-PSDB; ABL57981.  
XX  
PT Rendering plants resistant to herbicides, useful for selective weed  
control, comprises by-passing the enzymatic pathway blocked by the  
herbicide.  
XX  
PS Claim 7; Page 93-95; 125pp; French.  
XX  
CC The present invention relates to a method for rendering plants tolerant  
to a herbicide by expressing an enzyme that by-passes the metabolic  
CC pathway inhibited by the herbicide. The method is used to impart  
CC resistance in plants to herbicides (e.g. isoxazoles or diketonitriles)

CC that inhibit 4-hydroxyphenylpyruvate dioxygenase, making possible use of  
CC such herbicides for selective weed control in crops. The present sequence  
CC is a protein sequence for a mutant of 4-hydroxyphenylpyruvate oxidase  
CC (HPPO), which was used to illustrate the invention  
XX  
SQ Sequence 540 AA;  
  
Query Match 3.7%; Score 97.5; DB 5; Length 540;  
Best Local Similarity 22.6%; Pred. No. 13;  
Matches 76; Conservative 43; Mismatches 141; Indels 77; Gaps 16;  
  
Qy 81 AADTLQRLGARVA--SVDMP-----QQLPDCQSLPIPPVILAEGLSDPTKGTVCIFYGH 132  
Db 35 AADAYYRASGRLAAGTTTYGPGYTNALTALAEAVQAQIPVVLVT--GDAPSSGARPW--- 89  
  
Qy 133 LDVQPADRGDGLTDPYVLTE-----VDGKLYGRGATDNKGPVLAWINAVSAFRA 182  
Db 90 -DVDQAAIAGGLGAATFTVTREAGSITQEAVEYALARRTAV-----VIAVPYDLSALEA 143  
  
Qy 183 LEQDLPVNIKFIE-----GMEEAAGSVALEELVEKEKDRFF-----SGVDYIVIS 227  
Db 144 AEEDLPVPPAASVDPDAIGGGLGRAAEVRAAEALLAGAKRPLILAGRGHAHLGAGAPELRELA 203  
  
Qy 228 DNLWISQRKPAITYGT-----RGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALL 280  
Db 204 DRL-----GALTAGTALALNLLQEGYLGA-----GGFGTDTAAGLMGE--ADVVLVA 250  
  
Qy 281 GSLVD-----SSGHILVPGI-----YDEVVPLTTEEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 251 GASLTPFTWRFGLIGPDATVIQIDTAMEPTDPRVDLF-----VSADAKAAAGRILRLDD 306  
  
Qy 333 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 369  
Db 307 AAGANASKAWRAEALK-RLAEGPCHHPGTAETTDGRL 342

RESULT 390  
ABB76990  
ID ABB76990 standard; protein; 560 AA.  
XX ABB76990;  
AC  
XX  
DT 22-JUL-2002 (first entry)  
XX  
DE 4-Hydroxyphenylpyruvate oxidase mutant #3.  
XX  
KW 4-Hydroxyphenylpyruvate oxidase; enzyme; herbicide; weed control; mutein;  
mutant.  
XX  
OS Arthrobacter globiformis.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 118 /note= "Wild-type Ala substituted by Gly"  
FT  
XX  
PN FR2815969-A1.  
XX  
PD 03-MAY-2002.  
XX  
PF 30-OCT-2000; 2000FR-00013942.  
XX  
PR 30-OCT-2000; 2000FR-00013942.  
XX  
PA (AVET ) AVENTIS CROPSCIENCE SA.  
XX  
XX Zink O, Paget E, Rolland A, Sailland A, Freyssinet G;  
PI  
XX  
DR WPI; 2002-419041/45.  
N-PSDB; ABL57981.  
XX  
PT Rendering plants resistant to herbicides, useful for selective weed  
control, comprises by-passing the enzymatic pathway blocked by the









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XX
PR 15-MAY-2001; 2001EP-00111774.
XX
XX (CELL-) CELLZONE AG.
XX
PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
PI Marzioch M, Schultz JD, Superti-Furga GD;
XX
DR WPI; 2003-250078/25.
DR N-PSDB; ACC60664.
XX
XX New isolated protein complexes useful for diagnosing a disease or
PT disorder, or as a target for an active agent of a pharmaceutical,
PT preferably a drug target in the treatment or prevention of disease or
PT disorder.
XX
PS Disclosure; SEQ ID NO 109; 17pp + Sequence Listing; English.
XX
XX The invention relates to multiprotein complexes from eukaryotes. Proteins
CC of the invention and DNA sequences encoding them are given in records
CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
CC obtainable by using a protein as a bait and isolating the set of proteins
CC which is attached thereto from cells. Such protein complexes may comprise
CC up to 30 distinct proteins. Protein complexes of the invention are useful
CC for diagnosing a disease or disorder, or as a target for an active agent
CC of a pharmaceutical, preferably a drug target in the treatment or
CC prevention of a disease or disorder. Note: The sequence data for this
CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM
XX
SQ Sequence 2000 AA;

Query Match          3.7%; Score 97.5; DB 6; Length 2000;
Best Local Similarity 21.2%; Pred. No. 1e+02;
Matches 112; Conservative 65; Mismatches 173; Indels 179; Gaps 27;

QY 13 LAVLLLLLLERGMFSSPPALLEKVFQYIDLHQD--EFVQTLKEWV-AIESDSVQVPVR 69
Db 1563 LALIIHIIHRGMHDSRANIKRACKIVGNMAILVDTKDLIPYLQQLIDEVEIAMVDPVN 1622
QY 70 FRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCVF 129
Db 1623 TR-----ATAARALGALVER--LGEEQFPD-----LIPRLDTLSDSKSG----- 1661
QY 130 YGHLDVQPADRGDGNLTDPYVLTEVDGKLYGRGAT--DNKGPVLAWINAVSAFRALEQD- 186
Db 1662 -----DR-----LGSAQALAEV---ISGLGLTKLDEMLPTI--LAGVTNFRAYIREG 1703
QY 187 -----LPV-----NIKFIIEGMEE-----AGSVALEELVEKEKDR 216
Db 1704 FMPLLLLFLPVCFGSQFAPYINQIIQPILSGLADNDENIRDTALKAGKLIVKNYATKAVDL 1763
QY 217 FFGVDYIVISDNLWISQKPAITYGTRGNSYFMV-----EVKCRDQDFHSGTFG-- 267
Db 1764 LLPELRCGMFDENDRIRLSSVQLT---GELLFQVTGISSRNEFSEEDGD-HNGEFSGKL 1818
QY 268 --ILHEPMAD--LVALLGSLVDSSGHI-----LVPG---IYDEVVPLTEEEINTY 310
Db 1819 VDLGQDRRRDRIALALFVCRNDTSGIVRATTVDIWKALVPNTPRAVKEILPTLTGMIVTH 1878
QY 311 KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSILSIHGEGAFDEPGTKTVPGRVI 370
Db 1879 LA-----SSSNV---LRNIAAQTLGLDLR-----RVG 1902
QY 371 GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVMVSMTL-----GLHP 417
Db 1903 GNALSQLLPSLEESLIETS-----NSDSRQGVCIALYELIESASTETISQFQS 1950
QY 418 WIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTTPIAKMFQEIIVHSVV 466
Db 1951 TIVNI-----IRTALIDESATVREAAALSF-DVFQDVGKTAV 1987

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RESULT 396  
ADK62602  
ID ADK62602 standard; protein; 2000 AA.  
XX  
AC ADK62602;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Disease treating protein complex-derived protein #427.  
XX  
KW protein complex; drug target; diagnosis.  
XX  
OS Unidentified.  
XX  
PN EPI338608-A2.  
XX  
XX 27-AUG-2003.  
PD  
PF 20-DEC-2002; 2002EP-00102902.  
XX  
PR 20-DEC-2001; 2001EP-00130253.  
XX  
PA (CELL-) CELLZOME AG.  
XX  
PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;  
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
PI Michon A, Leutwein C, Rick J;  
XX  
XX WPI; 2003-638460/61.  
DR N-PSDB; ADK62603.  
DR  
XX  
PT New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.  
XX  
PS Disclosure; SEQ ID NO 853; 13pp; English.  
XX  
CC The invention relates to novel protein complexes comprising a first and a  
CC second protein, or its derivative, fragment, homologue or variant. The  
CC proteins are selected from given protein complexes, which are not defined  
CC in the specification. The variants are encoded by nucleic acids that  
CC hybridize to the nucleic acids encoding the proteins under low stringency  
CC conditions. The protein complexes are useful as targets for an active  
CC agent of a pharmaceutical. These protein complexes are particularly  
CC useful as drugs targets for the treatment or preventing of a disease or  
CC disorder. The complexes and methods above are useful in diagnosing or  
CC screening for the presence of a disease or disorder or a predisposition  
CC for developing a disease or disorder in a subject. These are also useful  
CC in screening for a drug for treatment or prevention of a disease or  
CC disorder. The molecule that modulates the amount, activity or protein  
CC components of the complex is useful for the manufacture of a medicament  
CC for the treatment or prevention of a disease or disorder. This sequence  
CC corresponds to a protein of the invention. (Note: the sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained from the EPO in electronic format).  
XX  
SQ Sequence 2000 AA;

	Query Match	3.7%;	Score 97.5;	DB 7;	Length 2000;
	Best Local Similarity	21.2%;	Pred. No. 1e+02;		
	Matches 112;	Conservative 65;	Mismatches 173;	Indels 179;	Gaps 27;
Qy	13	LAVLLLLLERGMFSSPPPALLEKVFQYIDLHQD--EFVQTLKEWV-AIESDSVQPVPVR	69		
Dd	1563	LALIIHHIHRGHDRSANIKRKACKIVGNMAILVDTKDLIPYLQQLIDEVEIAMVDPVEN	1622		
Qy	70	FROELFRMMAVAADTLQRLGARVASVDMGFQQLPDDGQSPLPIPPVILAEGLSDPTKTGVCF	129		
Dd	1623	TR-----ATAARALGALVER--LGEEQFPD-----LIPRLDRTLSESKSG----	1661		
Qy	130	YGHLDVQPADRGDGWLTDPYVLTEVDGKLYCRGAT--DNKGPVLAWINAVSAFRALEQD-	186		

Db 1662 -----DR-----LGSQAALAEV---ISGLGLTKLDEMLPTI--LAGVTNFRAYIREG 1703

Qy 187 -----LPV-----NIKFIIEGME-----AGSVALEELVEKEKDR 216

Db 1704 FMPLLFLPVCFGSQFAPYINQIIPILSGLADNENIRDTALKAGKLIYKNYATKAVDL 1763

Qy 217 FFSGVYIVISDNLWISQRKPAITYGTRGNSYFMV-----EVKCRDQDFHSGTFGG-- 267

Db 1764 LLPELRGMFENDRIRLSSVOLT---GELLFQVTGISSRNEFSEEDGD-HNGEFSGKL 1818

Qy 268 --ILHEPMAD--LVALLGSLVDSSGHI-----LVPG---IYDEVVPLTEEEINTY 310

Db 1819 VDVLGQDRDRILAALFVCRNDTSGIVRATTVDIWKALVPNTPRAVKEILPTLTGMIVTH 1878

Qy 311 KAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVI 370

Db 1879 LA-----SSNV---LRNIAAQTLDLVR-----RVG 1902

Qy 371 GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVVMVMTL-----GLHP 417

Db 1903 GNALSQLEESLIETS-----NSDSRQGVCIALYELIESASTETISQFQS 1950

Qy 418 WIANIDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFOEIVHKSUV 466

Db 1951 TIVNI-----IRTALIDESATVREAAALSF-DVFQDVVGKTAV 1987

RESULT 397

ADJ69524

ID ADJ69524 standard; protein; 371 AA.

XX

AC ADJ69524;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human heat mitochondrial protein as a therapeutic target SeqID1330.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2003087768-A2.

XX

PD 23-OCT-2003.

XX

XX 04-APR-2003; 2003WO-US010870.

PF

XX 12-APR-2002; 2002US-0372843P.

PR

PR 17-JUN-2002; 2002US-0389987P.

PR

PR 20-SEP-2002; 2002US-0412418P.

XX

XX (MITO-) MITOKOR.

PA

PA (BUCK-) BUCK INST AGE RES.

XX

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

PI

XX WPI; 2003-845369/78.

DR

XX

XX Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX

PS Claim 1; SEQ ID NO 1330; 180pp; English.

XX

CC This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, nootropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytostatic activities. This polypeptide sequence is a human heart

CC mitochondrial protein of the invention.

XX SQ Sequence 371 AA;

Query Match 3.7%; Score 97; DB 7; Length 371;

Best Local Similarity 20.3%; Pred. No. 8.2;

Matches 66; Conservative 44; Mismatches 93; Indels 122; Gaps 16;

Qy 43 DLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQL 102

Db 68 ELHRLLETI--LKHWTTRYQSESA-----DLIHWLQSAKDRLEFWTQQSVTV---PQEL 114

Qy 103 PDG-QSLPIPPPVILAELGSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTVEVDG----- 156

Db 115 DTGNQLLRLLKKVDTATLRSE-----LSRIDSQWTD--LLTNIPAVQBEKL 156

Qy 157 -----KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALBEELV 210

Db 157 HQLQMDKLPSPRHAISE---VMSWIS-----LMENVI 184

Qy 211 EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY--FMVEVKCR----- 256

Db 185 QKDEDNIKNSIGYKAIHEYL-----QKYKGFKIDINCKQLTVDFFVNQSVL 229

Qy 257 ---DQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAI 313

Db 230 QISSQDVES-----XRSDKTDFABQLGAM-NKSWQIL-QGLVTEKIQLLGLELESW--- 278

Qy 314 HLDLEEYRNSRVEKFLFDTKBEIL 338

Db 279 ----SEYENNVCCLKTWFETQEKRL 299

RESULT 398

ADN17780

ID ADN17780 standard; protein; 4746 AA.

XX

AC ADN17780;

XX

DT 02-DEC-2004 (first entry)

XX

DE Bacterial polypeptide #433.

XX

KW Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.

XX

OS Bacteria.

XX

PN US2003233675-A1.

XX

PD 18-DEC-2003.

XX

PF 20-FEB-2003; 2003US-00369493.

XX





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QY 283 LVDSSGHILVPGIYDEVVPLTEEBINTYKAIHLDLEEVNRRSRVEKFLFDTKKEILMHLW 342
Db 208 -----FLENIEQIVEDLKIKNSQLGL-----
QY 343 RYPSLSIHGIEGAFDEPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRN 402
Db 230 --PTFVVTSILSGDENSPNKTADFAELV-----VDCRLTPELEEVEQVM 272
QY 403 SS-----NKMVSMTLGLHPWI---ANIDDTQYLAAKRAIRTVFGTEPDMIR 446
Db 273 SELAVQYHFTHEDIVTPVLSTLTDNQAPFIQLLTNLGAKTTAAGSNEQGF----- 324
QY 447 DGSTIPIAKMFQEIHKSVVLIPLGAVDGHSQ-----NEKINRWNYIEGKLFAPFLE 502
Db 325 -----FENVGIRTVVFGP-----GQHEQCHIANESIILEKLEEHIEILQSFYK 368
QY 503 MAQ 505
Db 369 MQE 371

RESULT 400
ABU23175
ID ABU23175 standard; protein; 421 AA.
XX
AC ABU23175;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #8702.
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Bordetella pertussis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Walj D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA27045.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 51099; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
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CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 421 AA;

Query Match 3.7%; Score 96.5; DB 6; Length 421;
Best Local Similarity 21.3%; Pred. No. 11;
Matches 66; Conservative 52; Mismatches 115; Indels 77; Gaps 15;

QY 79 AVAADTLQRLG-ARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCYGHLDVQP 137
Db 42 AMAGETNRLLSLAR-----EISPO--PDGRELD---MIAATGEQASSGMLAALQAEQVP 91
QY 138 ADRGDGW-----LTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180
Db 92 ARSYAGWQVPVRTDSSYTKARIKSIDDKRVLADLDA---GR-----VVIVTGF 136
QY 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ-RKPAI 239
Db 137 QGVDDD--GHITTLGRGSDTSAVAVAAAIKADECLIFTDVGVTYTTDPRVVPEARMVAV 194
QY 240 TYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299
Db 195 V--SFEEMLEMASIGSKVLQIRSVFEFAGKYHVP-----TRVLSLT-----DPL 236
QY 300 VPLTEEEINTYKAIHLDLEEVNRRSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEP 359
Db 237 IPL-EEEMRSGTLITFEEDKMEAAVVGIAF-SRDEAKITLLAVP-----DKP 283
QY 360 GTKTVIPGRV 369
Db 284 GIAYSILGPV 293

RESULT 401
ABB76954
ID ABB76954 standard; protein; 560 AA.
XX
AC ABB76954;
XX
DT 22-JUL-2002 (first entry)
XX
DE 4-Hydroxyphenylpyruvate oxidase mutant #1.
XX
KW 4-Hydroxyphenylpyruvate oxidase; enzyme; herbicide; weed control; mutein;
KW mutant.
XX
OS Arthrobacter globiformis.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 215
FT /note= "Wild-type Ala substituted by Thr"
XX
PN FR2815969-A1.
```







Db 1103 --FNGGIGTYIKAETESVADVGDGR--ANDPVRVNAVQRAKVIGEGG--NLG-----V 1149

Qy 178 SAFRALEQDL-----PVNKFIIEGMEEAGSVALEE---LVEKE 213

Db 1150 TALGRVEFDLSGGRINTDAMDNSAGVDCSDHEVNIKILIDSLVTAGKVKEERKHLES 1209

Qy 214 KDRFFSGVDYIVISDN-----LWISQRKPAITY--GTRG----- 245

Db 1210 TDE---VARLVLTDNEDQNDLIGTSRANAANMLSVHAMQIKYLVDERGVRNRELEALPSE 1265

Qy 246 -----NSYFMVEVKCR-----DQDFHSGTGGILHEPMAD-- 275

Db 1266 KEIQRSEAGIGLTSPELSTLMAHVKLALKEQMLATELPDQDFVSRLPYRFPKPLRERF 1325

Qy 276 -----LVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAI----- 313

Db 1326 TPEIRSHQLRREIVTMTLINDLVDTAGISYAFRIAEDIGVGPIDAIRTYVATDAIFGVGD 1385

Qy 314 -----HLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGEGAFD 357

Db 1386 VLRRIRAAANLSVLSDRMTLDRRLIDRAGRLLN-----YRPOPLAV----- 1428

Qy 358 EPGTKTIVPGRVIGKFSIR---LVPHM-----NVSAREKQVTRHLEDVFSKRNSNKM 407

Db 1429 -----GAEINRFAAKVKALTPRMSEWLGRGDDQAIVEQQATE-----FVSQGAPEDL 1474

Qy 408 VVSMTLGLHPW----IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVK 463

Db 1475 AYRVAVGLYRSLDIADIITELDPAEVADTYFSLMDRLGTGDLTAVSKLPQNDRW 1534

Qy 464 SVVLIPLG-----AVDDGEHSQNEKINRWNYIEGTLFAAFPLEMAQLH 507

Db 1535 SLARLAIRDDIYASLSLCLFDVLAVGEPDESGEEKIAEWEHISASRVERA-RIMLAIEH 1592

RESULT 405

ABU35909

ID ABU35909 standard; protein; 1622 AA.

XX AC ABU35909;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #21436.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Mycobacterium leprae.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX XX 21-MAR-2002; 2002WO-US009107.

XX PF 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA39779.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

XX

PS

XX

CC

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CC

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XX

SQ

Sequence 1622 AA;

Query Match

Best Local Similarity 3.7%; Score 96.5; DB 6; Length 1622;

Matches 121; Conservative 87; Mismatches 228; Indels 223; Gaps 27;

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Claim 25; SEQ ID NO 63833; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 1622 AA;

Query Match

Best Local Similarity 3.7%; Score 96.5; DB 6; Length 1622;

Matches 121; Conservative 87; Mismatches 228; Indels 223; Gaps 27;

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

QY 358 EPGTKTVIPGRVIGKFSIR---LVPHM-----NVSAVEKQVTRHLEDVFSKRNSNKM 407  
Db 1429 -----GAEINRFAAKVKALTPRMSEWLGRDDQAIVEQQATE-----FVSQGAPEDL 1474  
QY 408 VVSMTLGLHPW----IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHK 463  
Db 1475 AYRVAVGLYRYSLLDIIDIADITELDPAEVADTTYFSLMDRLGTGLLTAVSKLPQNDRWH 1534  
QY 464 SVVLIPLG-----AVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 1535 SLARLAIRDDIYASRLSLCFDVLAVGEPDESGEKIAEWEHISASRVERA-RLMLAEIH 1592

RESULT 406  
AAB18637  
ID AAB18637 standard; protein; 4551 AA.  
XX  
AC AAB18637;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Amino acid sequence of narbonolide synthase subunit 1 (PICAI).  
XX  
KW Narbonolide synthase; polyketide synthase gene; narbonolide polyketide;  
KW antibiotic; C12-hydroxylase; pick; desosamine biosynthesis;  
KW desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;  
KW picromycin biosynthesis.  
XX  
OS Streptomyces venezuelae.  
XX  
XX US6117659-A.  
PN  
XX  
PD 12-SEP-2000.  
XX  
PF 27-MAY-1999; 99US-00320878.  
XX  
PR 30-APR-1997; 97US-00846247.  
PR 06-MAY-1998; 98US-00073538.  
PR 28-MAY-1998; 98US-0087080P.  
PR 28-AUG-1998; 98US-00141908.  
PR 22-SEP-1998; 98US-0100880P.  
PR 08-FEB-1999; 99US-0119139P.  
PR 20-MAY-1999; 99US-0134990P.  
XX  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
XX  
PI Ashley G, Betlach MC, Betlach M, Tang L, Mcdaniel R;  
XX  
DR WPI; 2000-610844/58.  
XX  
PT New recombinant pick hydroxylase gene of Streptomyces venezuelae useful  
PT for converting ketolides to antibiotics and as antibiotics and  
PT intermediates in the synthesis of compounds with pharmaceutical value.  
XX  
PS Disclosure; Col 9-10; 117pp; English.  
XX  
CC The present sequence represents a narbonolide synthase subunit 1 (PICAI).  
CC The nucleotide sequence encoding it is used in the course of the  
CC invention. The specification describes a recombinant DNA compound  
CC expressing recombinant polyketide synthase genes in host cells for the  
CC production of narbonolide, narbonolide derivatives and polyketides that  
CC are useful as antibiotics and as intermediates in the synthesis of  
CC compounds with pharmaceutical value. The DNA compounds may also encode a  
CC C12-hydroxylase (pick), desosamine biosynthesis and desosaminyl  
CC transferase enzymes (useful for conversion of ketolides to antibiotics),  
CC and the beta-glucosidase enzyme (involved in picromycin biosynthesis).  
CC These compounds are also useful for increasing the antibiotic activity of  
CC a compound relative to the unhydroxylated compound. The recombinant host  
CC cells are useful as genetic systems that allow rapid engineering of the  
CC narbonolide polyketide synthase. These would be valuable for creating  
CC novel ketolide analogs for pharmaceutical applications  
XX  
SQ Sequence 4551 AA;

Query Match 3.7%; Score 96.5; DB 3; Length 4551;  
Best Local Similarity 19.9%; Pred. No. 4.4e+02;  
Matches 107; Conservative 64; Mismatches 170; Indels 197; Gaps 26;

QY 66 PVPFRQELFRMVAADT-LQRLGARVASVD---MGP-QQLPDGQ----- 106  
Db 3485 PTYSFRDRYWLDAADTAVDTAGLGTADHPLLAGVVSLEPDRDGLLLTGRLSLRTHP 3544  
QY 107 -----SLPIPPVILAELGSDPTKGTVCFCYGHLDVQPADRGDWLTDPYVLTE---- 153  
Db 3545 WLADHAVLGSVLLPGAAMVELAAHAESA-----GLRDVRELT-----LLEPLVLPEHGGV 3595  
QY 154 -----VDGKLYGRGATDNKGPV-----LAWINAVSAFRALEQ-DLPV--- 189  
Db 3596 ELRVTVGAPAGEPGESAGDGARFVSLHSRLADAPAGTAWSCHATGLLATDRPELPVAPD 3655  
QY 190 -NIKFIIEGMEERAGSVALEELVEKEKDR-----FFSGVDYIVISDNLWISQRK----- 236  
Db 3656 RAAMWPPQGAEE---VPLDGLYERLDGNGLAFGPLFQGLNAV-----WRYEGEVFADIA 3706  
QY 237 -PAITY-----GTRGNSYFMVEVKCRDQDFHSGTFGGILHEPM----- 273  
Db 3707 LPATTNATAPATANGGSAAAPYGIHPALLDASLHAIAVGGLVDEPELVVRVPFHWSGVT 3766  
QY 274 -----ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEBEINTYKAIHLD 316  
Db 3767 VHAAGAAAARVRLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLRPVTAD 3813  
QY 317 LEEYRNSSRVEKFLDTEKKEILMH--LWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 3814 ---QAAASRVGG-----LMHRVAVRYPVALASSGEQ---DPHATSYGPTAVLGKDE 3857  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 3858 LKVAALAESAGVE-----VGLYPDLAALSQ-DVAAGAPAP 3891  
QY 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIIVHKSVVLIPLGAVDDGEHS 479  
Db 3892 RTVLAPLPAGPADGGAEGVGTAVRTLELLQAWLADEHLAGTRLLLVTRGAVRDPES 3949

RESULT 407  
AAY67201  
ID AAY67201 standard; protein; 4551 AA.  
XX  
AC AAY67201;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Narbonolide synthase subunit 1 (PICAI) protein sequence.  
XX  
KW Narbonolide polyketide synthase; PKS; narbonolide synthase subunit 1;  
KW PICAI; antibiotic production; narbomycin; picromycin; ketolide.  
XX  
OS Streptomyces venezuelae.  
XX  
PN WO9961599-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 27-MAY-1999; 99WO-US011814.  
XX  
PR 28-MAY-1998; 98US-0087080P.  
PR 28-AUG-1998; 98US-00141908.  
PR 22-SEP-1998; 98US-0100880P.  
PR 08-FEB-1999; 99US-0119139P.  
XX  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
XX  
PI Ashley G, Betlach MC, Betlach M, Mcdaniel R, Tang L;  
XX  
DR WPI; 2000-072618/06.



DR N-PSDB; AAZ56001.

XX New recombinant DNA encoding a domain of narbonolide synthase, for production of ketolide antibiotics.

PT

XX Example 2; Page 11-12; 98pp; English.

PS

XX This is the Streptomyces venezuelae narbonolide synthase subunit 1, PICAI protein sequence. The invention relates to recombinant DNA containing a coding sequence for a narbonolide polyketide synthase (PKS). Polyketides are compounds synthesised from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules, and two thioester domains. Four proteins make up the narbonolide PKS (PICAI, PICAI, PICAI and PICAI). PICAI includes the loading module and extender modules 1 and 2, PICAI includes extender modules 3 and 4, PICAI includes extender module 5 and PICAI includes extender module 6 and a type II thioesterase domain. The second type II thioesterase domain is found on the PICB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid PKOS023-27 (see AAZ56001). Narbonolide is desosaminylated in S. venezuelae to yield narbomycin, the desosaminyl transferase enzyme is required for this conversion, and the desosamine biosynthetic genes are also found in cosmid PKOS023-27. The recombinant DNA of the invention is used to express, in transformed cells, narbonolide (or its derivatives) or other ketolides (particularly hybrids), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human or veterinary medicine

XX

SQ Sequence 4551 AA;

RESULT 408

ABG71661

ID ABG71661 standard; protein; 4551 AA.

XX

AC ABG71661;

XX

DT 21-JAN-2003 (first entry)

XX

DE S. venezuelae narbonolide synthase subunit 1, PICAI.

XX

KW Narbonolide polyketide synthase; PKS; desosamine biosynthetic gene; desosaminyl transferase gene; beta-glucosidase gene; antibiotic; pick hydroxylase gene; C12 hydroxylase gene; narbonolide; desosaminylated polyketide; narbomycin biosynthesis; PICAI; picromycin biosynthesis; narbonolide synthase subunit 1; enzyme.

XX

OS Streptomyces venezuelae.

XX

PN WO200297062-A2.

XX

PD 05-DEC-2002.

XX

PF 22-FEB-2002; 2002WO-US005642.

XX

PR 22-FEB-2001; 2001US-00793708.

XX

PA (KOSA-) KOSAN BIOSCIENCES INC.

XX

PI Ashley G, Betlach MC, Betlach M, Mcdaniel R, Tang L;

XX

DR WPI; 2003-041412/03.

XX

PT Preparation of polyketides by recombinant DNA technology, useful as antibiotics and as intermediates in the synthesis of pharmaceutical compounds.

PT

XX

PS Disclosure; Page 14-15; 127pp; English.

XX

CC The present invention relates to recombinant DNA sequences encoding for a narbonolide polyketide synthase (PKS) domain, and methods of producing polyketides by recombinant DNA technology. The recombinant DNA sequences are derived from Streptomyces venezuelae desosamine biosynthetic, desosaminyl transferase, beta-glucosidase, or pick (C12) hydroxylase genes. The method is useful for transforming a cell with a recombinant expression vector that encodes a functional beta-glucosidase gene, and therefore for increasing the yield of a desosaminylated polyketide in a cell. The recombinant methods and materials are useful for expressing polyketides with significant antibiotic activity, derived in whole or in part from the narbonolide PKS gene, and other genes involved in narbomycin and picromycin biosynthesis in recombinant host cells. The present sequence represents S. venezuelae narbonolide synthase subunit 1, PICAI

XX

SQ Sequence 4551 AA;

Query Match 3.7%; Score 96.5; DB 6; Length 4551;

Best Local Similarity 19.9%; Pred. No. 4.4e+02;

Matches 107; Conservative 64; Mismatches 170; Indels 197; Gaps 26;

QY 66 PVPRFRQELFRMMAVAADT-LQRLGARVASVD---MGP-QQLPDGQ----- 106

Db 3485 PTYSFRRDRYWLDAAPADTAVDTAGLGLGTADHPLLGAVVSLPDRDGLLLTGRSLRTHP 3544

QY 107 -----SLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPVVLTE---- 153

Db 3545 WLADHAVLGSVLLPGAAMVELAAHAESA-----GLRDVRELT-----LLEPLVLPHEGGV 3595

QY 154 -----VDGKLYGRGATDNKGPV-----LAWINAVSAFRALEQ-DLPV---- 189

Db 3596 ELRVTVGAPAGEPGGESAGDGARPVSLHSRLADAPAGTAWSCHATGLLATDRPELPVAPD 3655

QY 190 -NIKFIIEGMEEGAGSVALEELVEKEKDR-----FFSGVDYIVISDNLWISQRK----- 236

Query Match 3.7%; Score 96.5; DB 3; Length 4551;

Best Local Similarity 19.9%; Pred. No. 4.4e+02;

Matches 107; Conservative 64; Mismatches 170; Indels 197; Gaps 26;

QY 66 PVPRFRQELFRMMAVAADT-LQRLGARVASVD---MGP-QQLPDGQ----- 106

Db 3485 PTYSFRRDRYWLDAAPADTAVDTAGLGLGTADHPLLGAVVSLPDRDGLLLTGRSLRTHP 3544

QY 107 -----SLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPVVLTE---- 153

Db 3545 WLADHAVLGSVLLPGAAMVELAAHAESA-----GLRDVRELT-----LLEPLVLPHEGGV 3595

QY 154 -----VDGKLYGRGATDNKGPV-----LAWINAVSAFRALEQ-DLPV--- 189

Db 3596 ELRVTVGAPAGEPGGESAGDGARPVSLHSRLADAPAGTAWSCHATGLLATDRPELPVAPD 3655

QY 190 -NIKFIIEGMEEGAGSVALEELVEKEKDR-----FFSGVDYIVISDNLWISQRK----- 236

Db 3656 RAAMWPPQGAEE---VPLDGLYERLDGNGLAFGLPLFQGLNAV-----WRYEGEVFADIA 3706

QY 237 -PAITY-----GTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPM----- 273

Db 3707 LPATTNATAPATANGGSAAPYGIHPALLDASLHAIAVGLVDEPELVVPFHWGVT 3766

QY 274 -----ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 316

Db 3767 VHAAGAAARVRLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLRPVTAD 3813

QY 317 LEEYRNSSRVEKFLFTKEEILMH--LWRYPSLSIHGIEGAFDEPGTKTVIPGRVICKFS 374

Db 3814 ---QAAASRVGG-----LMHRVAWRPYALASSGEQ----DPHATSYGPTAVLGKDE 3857

QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMVMTLGLHPWIANIDTQYLAAKRAI 434

Db 3858 LKVAALLESAGVE-----VGLYPDLAALSQ-DVAAGAPAP 3891

QY 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIIVKSVVLIPLGAVDDGEHS 479

Db 3892 RTVLAPLPAGPADGGAGVGRGTAVRTLELLQAWLADEHLAGTLLLVTRGAVRDEGS 3949

Db 3656 RAAMWPPQGAEE---VPLDGLYERLDGNGLAFGLFQGLNAV-----WRYEGEVFADIA 3706

Qy 237 -PAITY-----GTRGNSYFMVEVKCRDQDFHSGTFGGILHEPM----- 273

Db 3707 LPATNATAPATANGGSAAPYGIHPALLDASLHAIAVGGGLVDEPELVVPFHWSGVT 3766

Qy 274 -----ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 316

Db 3767 VHAAGAAARVRLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLPVPTAD 3813

Qy 317 LEEYRNSRVEKFLFDTKEEILMH--LWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFS 374

Db 3814 ---QAAASRVGG-----LMHRVAVRPYALASSGEQ-----DPHATSYGPTAVLGKDE 3857

Qy 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRAI 434

Db 3858 LKVAALLESAGVE-----VGLYPDIAALSQ-DVAAGAPAP 3891

Qy 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIVHKS VWLIPLGAVDDGEHS 479

Db 3892 RTVLAPLPAGPADGGAEGVGTARTLELLQAWLADEHLAGTRLLLVTRGAVRDPES 3949

RESULT 409

ADA09400

ID ADA09400 standard; protein; 4551 AA.

XX AC ADA09400;

XX DT 06-NOV-2003 (first entry)

XX S. venezuelae narbonolide synthase subunit 1 (PICAI).

XX Kw Streptomyces venezuelae; Sv; narbonolide polyketide synthase; PKS;

XX Kw narbonolide PKS; narbomycin biosynthesis; picromycin biosynthesis;

XX Kw PKS gene cluster; picromycin; glycosylation; hydroxylation;

XX Kw C12 hydroxylase; Pick; desosamine biosynthesis;

XX Kw desosaminyl transferase enzyme; antibiotic; narbonolide synthase; PICAI.

XX OS Streptomyces venezuelae.

XX US6509455-B1.

XX PN 07-SEP-2000; 2000US-00657440.

XX PR 30-APR-1997; 97US-00846247.

XX PR 06-MAY-1998; 98US-00073538.

XX PR 28-MAY-1998; 98US-0087080P.

XX PR 28-AUG-1998; 98US-00141908.

XX PR 22-SEP-1998; 98US-0100880P.

XX PR 08-FEB-1999; 99US-0119139P.

XX PR 20-MAY-1999; 99US-0134990P.

XX PR 27-MAY-1999; 99US-00320878.

XX PA (KOSA-) KOSAN BIOSCIENCES INC.

XX PI Ashley G, Betlach MC, Betlach M, Mcdaniel R, Tang L;

XX DR WPI; 2003-352291/33.

XX PT Novel recombinant DNA compounds comprising coding sequences for

XX PT desosamine transferase gene of Streptomyces venezuelae, useful for

XX PT producing desosamine transferase which transfers desosamine to substrate

XX PT polyketides.

XX PS Disclosure; Col 9-12; 132pp; English.

XX CC The present invention relates to recombinant DNA compounds that encode

XX CC Streptomyces venezuelae (Sv) narbonolide polyketide synthases (PKSs). The

XX CC recombinant PKSs are derived from narbonolide PKS and other genes

CC involved in narbomycin and picromycin biosynthesis in recombinant host

CC cells. The invention also discloses the S. venezuelae PKS gene cluster

CC that results in the production of picromycin. Also disclosed are enzymes

CC such as those responsible for glycosylation and hydroxylation, (e.g. C12

CC hydroxylase (Pick)), desosamine biosynthesis, and desosaminyl transferase

CC enzymes. The recombinant narbonolide, narbonolide derivatives, and

CC polyketides are useful as antibiotics and as intermediates in the

CC synthesis of compounds for pharmaceutical applications. The present

CC sequence represents a subunit from S. venezuelae narbonolide synthase.

XX

SQ Sequence 4551 AA;

Query Match 3.7%; Score 96.5; DB 6; Length 4551;

Best Local Similarity 19.9%; Pred. No. 4.4e+02;

Matches 107; Conservative 64; Mismatches 170; Indels 197; Gaps 26;

Qy 66 PVPRFRQELFRMMAVAADT-LQRLGARVASVD--MGP-QQLPDGQ----- 106

Db 3485 PTYSFRRDRYWLDPAAADTAVDTAGLGTADHPLLGAVVSLPDRDGLLTGRLSLRTHP 3544

Qy 107 -----SLPIPPVILAEELGSDPTKGTVCFCYGHLDVQPADRGDWLTDPPVLT----- 153

Db 3545 WLADHAVLGSVLLPEGAAMVELAAHAESA-----GLRDVRELT-----LLEPLVLPEHGGV 3595

Qy 154 -----VDGKLYRGATDNKGPV-----LAWINAVSAFRALEQ-DLPV--- 189

Db 3596 ELRVTVGAPAGEPGGESAGDARGPVSLHSLRADAPAGTAWSCHATGLLATDRPELPVAPD 3655

Qy 190 -NIKFIIEGMEEGAGSVALEELVEKEKDR-----PFSGVDYIVISDNLWISQRK----- 236

Db 3656 RAAMWPPQGAEE---VPLDGLYERLDGNGLAFGLFQGLNAV-----WRYEGEVFADIA 3706

Qy 237 -PAITY-----GTRGNSYFMVEVKCRDQDFHSGTFGGILHEPM----- 273

Db 3707 LPATNATAPATANGGSAAPYGIHPALLDASLHAIAVGGGLVDEPELVVPFHWSGVT 3766

Qy 274 -----ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 316

Db 3767 VHAAGAAARVRLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLPVPTAD 3813

Qy 317 LEEYRNSRVEKFLFDTKEEILMH--LWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFS 374

Db 3814 ---QAAASRVGG-----LMHRVAVRPYALASSGEQ-----DPHATSYGPTAVLGKDE 3857

Qy 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRAI 434

Db 3858 LKVAALLESAGVE-----VGLYPDIAALSQ-DVAAGAPAP 3891

Qy 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIVHKS VWLIPLGAVDDGEHS 479

Db 3892 RTVLAPLPAGPADGGAEGVGTARTLELLQAWLADEHLAGTRLLLVTRGAVRDPES 3949

RESULT 410

ADH53444

ID ADH53444 standard; protein; 4551 AA.

XX AC ADH53444;

XX DT 25-MAR-2004 (first entry)

XX Streptomyces venezuelae narbonolide synthase subunit 1 protein, PICAI.

XX Kw Narbonolide polyketide synthase; PKS; desosamine;

XX Kw desosaminyl transferase; beta-glucosidase; pick hydrolase; antibiotic;

XX Kw pharmaceutical; gene therapy; antibacterial; infection; enzyme; PICAI.

XX OS Streptomyces venezuelae.

XX US2003162262-A1.

XX PD 28-AUG-2003.







QY 274 -----ADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAIHLD 316  
Db 3829 VHAAGAAAARVRLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLPVPTAD 3875  
QY 317 LEEYRNSSRVEKFLDFTKEEILMH--LWRYPSLSIHGIBGAFDEPGTKTVIPGRVIGKFS 374  
Db 3876 ---QAAASRVGG-----LMHRVAWRPYALASSGEQ----DPHATSYGPTAVLGKDE 3919  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 3920 LKVAALLESAGVE-----VGLYPDLAALSQ-DVAAGAPAP 3953  
QY 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIVHKSVVLIPLGAVDDGEHS 479  
Db 3954 RTVLAPLPAGPADGGAEGVRGTVARTLELLQAWLADEHLAAGTRLLLVTRGAVRDEGS 4011  
RESULT 413  
ADL91916  
ID ADL91916 standard; protein; 4613 AA.  
AC ADL91916;  
XX  
DT 20-MAY-2004 (first entry)  
DE Streptomyces macrolide biosynthetic protein - Pikr2.  
XX  
KW narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;  
KW medical application; industrial application;  
KW macrolide biosynthetic protein; pik.  
XX  
OS Streptomyces venezuelae.  
XX  
PN US2003194784-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 15-OCT-2002; 2002US-00271889.  
XX  
PR 17-APR-2001; 2001US-00836821.  
PR 18-MAY-2001; 2001US-00860846.  
PR 18-MAY-2001; 2001US-00861289.  
XX  
PA (SHER/) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
XX  
PI Sherman DH, Liu H, Xue Y, Zhao L;  
XX  
DR WPI; 2004-119267/12.  
DR N-PSDB; ADL91915.  
XX  
PT New isolated nucleic acid comprising a narbonolide polyketide synthase  
gene from Streptomyces narbonensis, useful for providing a  
polyhydroxyalkanoate monomer for medical and industrial applications.  
XX  
PS Disclosure; SEQ ID NO 31; 362pp; English.  
XX  
CC The invention comprises coding sequences for the narbonolide polyketide  
synthase gene from Streptomyces narbonensis. The DNA sequence of the  
invention are useful for providing polyhydroxyalkanoate monomer for  
medical and industrial applications. The present amino acid sequence  
represents a Streptomyces venezuelae macrolide (pik) biosynthetic  
protein.  
XX  
SQ Sequence 4613 AA;

Query Match 3.7%; Score 96.5; DB 8; Length 4613;  
Best Local Similarity 19.9%; Pred. No. 4.5e+02;  
Matches 107; Conservative 64; Mismatches 170; Indels 197; Gaps 26;

QY 66 PVPRFRQELFRMVAADT-LQRLGARVASVD---MGP-QQLPDGQ----- 106  
Db 3547 PTYSFRDRYWLDAADTAVDTAGLGLGTADHPLLGAVVSLPDRDGLLLTGRLSLRTHP 3606  
QY 107 -----SLPIPPVILAEGLSDPTKGTVCFCYGHLDVQPADRGDGLTDPYVLTE----- 153  
Db 3607 WLADHAVLGSVLLPGAAMVELAAHAAESA---GLRDVRELT-----LLEPLVLPEHGGV 3657  
QY 154 -----VDGKLYGRGATDNKGPV-----LAWINAVSAFRALEQ-DLPV--- 189  
Db 3658 ELRVTVGAPAGEPGGESAGDGARPVSLHSLRLADAPAGTAWSCATGLLATDRPELPVAPD 3717  
QY 190 -NIKFIIEGMEEAGSVALEELVEKEKOR-----PFGVDYIVISDNLWISQRK----- 236  
Db 3718 RAAMWPPQGAEE---VPLDGLYERLDGNGLAFGLFQGLNAV-----WRYEGEVFADIA 3768  
QY 237 -PAITY-----GTRGNSYFMVEVKCRDQDFHSGTFFGILHEPM----- 273  
Db 3769 LPATTNATAPATANGGSSAAAAPYGIHPALLDASLHAIAVGGGLVDEPELVRVPFHWSGVT 3828  
QY 274 -----ADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAIHLD 316  
Db 3829 VHAAGAAAARVRLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLPVPTAD 3875  
QY 317 LEEYRNSSRVEKFLDFTKEEILMH--LWRYPSLSIHGIBGAFDEPGTKTVIPGRVIGKFS 374  
Db 3876 ---QAAASRVGG-----LMHRVAWRPYALASSGEQ----DPHATSYGPTAVLGKDE 3919  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 3920 LKVAALLESAGVE-----VGLYPDLAALSQ-DVAAGAPAP 3953  
QY 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIVHKSVVLIPLGAVDDGEHS 479  
Db 3954 RTVLAPLPAGPADGGAEGVRGTVARTLELLQAWLADEHLAAGTRLLLVTRGAVRDEGS 4011  
RESULT 414  
ADL91934  
ID ADL91934 standard; protein; 11877 AA.  
XX  
AC ADL91934;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Streptomyces venezuelae pik gene cluster protein.  
XX  
KW narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;  
KW medical application; industrial application; pik gene cluster.  
XX  
OS Streptomyces venezuelae.  
XX  
PN US2003194784-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 15-OCT-2002; 2002US-00271889.  
XX  
PR 17-APR-2001; 2001US-00836821.  
PR 18-MAY-2001; 2001US-00860846.  
PR 18-MAY-2001; 2001US-00861289.  
XX  
PA (SHER/) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
XX  
PI Sherman DH, Liu H, Xue Y, Zhao L;  
XX  
DR WPI; 2004-119267/12.  
DR N-PSDB; ADL91933.  
XX  
PT New isolated nucleic acid comprising a narbonolide polyketide synthase





Db 4427 LPATNATAPATANGGSAAPYGIHPALLDASLHAIAVGLVDEPELVVRPFHWSGVT 4486  
QY 274 -----ADLVALLGSLVDSSGHILVPGIYDEVWPLTEEEINTYKAHLD 316  
Db 4487 VHAAGAAARVLASAGTDAVSL--SLTDGEGR-----PLVSVERLTLPVTAD 4533  
QY 317 LEEYRNSSRVEKFLDTEKEILMH--LWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFS 374  
Db 4534 ---QAAASRVGG-----LMHRVAWRPYALASSEQ----DPHATSYGPTAVLGKDE 4577  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 4578 LKVAALAESAGVE-----VGLYPDLAALSQ-DVAAGAPAP 4611  
QY 435 RTVFGTEPDMIRDGS-----TIPIAKMF---QEIVHKSVVLIPLGAVDDGEHS 479  
Db 4612 RTVLAPLPAGPADGGAEGVGTGVTARTLELLQAWLADEHLAGTRLLLVTRGAVRDPES 4669

RESULT 416  
ADS28138  
ID ADS28138 standard; protein; 485 AA.  
XX  
AC ADS28138;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #17171.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR WPI; 2004-061375/06.  
XX

PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 17171; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 485 AA;

QY Query Match 3.7%; Score 96; DB 8; Length 485;  
Best Local Similarity 21.4%; Pred. No. 15;  
Matches 105; Conservative 76; Mismatches 190; Indels 120; Gaps 29;

QY 34 LLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADT--LQRLGAR 91  
Db 72 ILERAVTYIEHEEEIVAIID---ELGGTRLKAAFEIGLVKNMIKEASTFPLRMEGKI 127  
QY 92 VASVDMGPQ---QLPDGQSLPIPPVILAEELGSDPTKGTVCYFGLHDVQPA-DRGCGWLT 146  
Db 128 LPSTENGKENRLRVPAVGVGVISPF-----NFFFLSVKSVAPALGAGNGVVL 176  
QY 147 DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPN-IKFIIEGMEEGSVA 205  
Db 177 KPHEETPITG-----GTLIAKI-----FE--EAGVPKGLLNVVVTEIDEIGNAF 218  
QY 206 LEELVEKEKDRFFSGVDYIVISDNL--WISQ-----RKPAITYGTRGNSYFMVEVKCRD 257  
Db 219 VEHPPIRIIS--FTG-----STNVGSHIGQLAVKHKPKLLELG--GNSAFLIPADA-D 267  
QY 258 QDF--HSGTFGGILHEPMDLVALLGSLVDSSGHILVP-GIYDEVVPLTEEEINTYKAIH 314  
Db 268 LDYAVQAATFSRFTHQ-----GQICMSANRIFVQRDQVYDEFV-----ERYTKVAS 313  
QY 315 LDLEEYRNSSRVEKFLDTEKEILMHLWRYPSSLHIGIEGAFDEPGTKTVPGRVIGKFS 374  
Db 314 LKVGDRDPRDPTETVIGPVMNRSQAETLK-----QAIESGI-AAGAKPVLHGAISGNM- 362  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANID-DTQYLAAKRA 433  
Db 363 --VEPTILIDA-----SPENAIQAEEELFGPVVCVIPFDTEEEAVEMA 402  
QY 434 IRTVFGTEPDM-----IRDGSTIPIAKMFOE-IVHKSQVLI---PLGAVDDGEHSQNEKIN 485  
Db 403 NDTKYGLSGAIHTANVERG--VEIAKRIQTGMHVNIDITINDEPIVAFGGEKHSGLGRLN 460  
QY 486 -RWNYIEGTKL 495  
Db 461 GEWSLEEFETTL 471

RESULT 417  
ABG12694  
ID ABG12694 standard; protein; 584 AA.  
XX  
AC ABG12694;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #12685.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX



QY	163	ATDNKGPVLAWINAVSAFRALEQD-----LPVNIKFIIEGMEEAGSVALEELVEKE	213
Db	185	PT--CWPGLDIIPSCALAHRIETELMGKFDGKLPDTPHMLR-----LAETVAH--	233
QY	214	KDRFFSGVDYIVISDNLWISQRKPAITYTRGNSYFMVEVKCRDQ-----DFHS	262
Db	234	-----DYDVI-----VIDSAPNLGIGT-----INVVCAADVLIPTPAELFDYTS	273
QY	263	G-TFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYR	321
Db	274	ALQFFDMLRDLKKN-VDLKGSQFDQ-----VEERSVIEDQMSMKR-----KENF	318
QY	322	NSSRVEKFLFDTKEEILMHLWRY----PSLSIHGIEGAFDEPGTKTV-----I	365
Db	319	REKRVKR-----NEQSLQELWHYVRRENLRRIIGVPESDGENGTKLENTLQDIVQENLPNL	373
QY	366	PGR-VIGKFSIRLVPHMNVA-----VEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPW	418
Db	374	PGRDTTKENFRPISLNMIDAKILNKILANQIOOHK-TFIHRDO-----VGFIIPGMOGW	427

**RESULT 419**

ABB08760

ID ABB08760 standard; protein; 896 AA.

AC ABB08760;

DT 07-MAY-2002 (first entry)

DE Synechococcus cyanophycin synthetase SEQ ID NO 2.

Cyanophycin; synthase; enzyme; thermostable; feed supplement; plant;  
KW  
protection; paper; textile; pigment; paint; ceramic; washing;  
KW  
water treatment.

OS *Synechococcus elongatus*.

PN WO200212459-A2.

PD 14-FEB-2002.

27-JUL-2001; 2001WO-EP008690.

PR 09-AUG-2000; 2000DE-01038775.

PA (FARB ) BAYER AG.

PI Ziegler K, Lockau W, Ebert J, Piotukh K, Berg H;  
PI Volkmer-Engert R;

DR WPI; 2002-227149/28.

DR N-PSDB; ABL41216.

New cyanophycin synthase, useful in synthesis of cyanophycin and its downstream products, e.g. (poly) amino acids, has high heat stability, PT also related nucleic acid. PT

PS Claim 1; Page 23-25; 29pp; German. German.

The invention relates to a thermostable cyanophycin synthetase (I) with a temperature optimum 35-55°C. (I) is used for preparation of cyanophycin or its downstream products, especially poly(aspartic acid) and arginine. Cyanophycin and its products are useful as feed supplements, in plant protection and in the paper, textile, pigment, paint, ceramics, building materials and washing composition industries, also for (waste) water treatment. (I) has better heat stability than known enzymes, so allows production of cyanophycin at temperatures over 35°C (the usual maximum), resulting in greater flexibility in process control, improved yield and reduced risk of contamination

Sequence 896 AA;

Query Match      3.7%;    Score 96;    DB 5;    Length 896;

	Best Local Similarity Matches	23.7%; Conservative	Pred. No.	Mismatches	80;	Indels	46;	Gaps	9;
QY	56	WVAIESDSVQPVRFRQELFRMMAAADTLQRLGARVASVDMPGQQLPDQSPLPPPVIL	115	:   :	:  :   : :	:	:  :   : :	:	:
Dd	181	WFELSRSRIQL-GYGARSHRMQAATLSDRSSILAVELASDKEGAKRLLQDAQIPVP----	235	:   :	:  :   : :	:	:  :   : :	:	:
QY	116	AELGSDP TKGTVCFYGHLDVQPADRCGWLTDPYVLTEVDGKLYGRGATDNKG PVLAWIN	175	:	:  :   : :	:	:  :   : :	:	:
Dd	236	-----KGVIRYIEDLPEAIEEIGGY---PIVIKPLNGN-HGRGITID-----IN	276	:	:  :   : :	:	:  :   : :	:	:
QY	176	AVSAFRALEQDLVPNIKFIIEGMEEAGSVALBELVEKEKD RFFSGVDYIVISDN---	LWI 232	:  :   :	:  :   :	:	:  :   :	:	:
Dd	277	SLEAAE-----EAFEIASISKSVIVE----RYHAGRDFRLVVVGKVAV	318	:  :   :	:  :   :	:	:  :   :	:	:
QY	233	SQRKP AIT Y GTRGN SYFM VEV KCR D QDF H SG	263	:  :   :	:  :   :	:	:  :   :	:	:
Dd	319	AERVPAHVIGD- GHST I EE L IEKT NQ DP QR G	348	:  :   :	:  :   :	:	:  :   :	:	:

RESULT 420

AAU54438

ID AAU54438 standard; protein; 1267 AA.

AC AAU54438;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #15334.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

20-APR-2001: 2001WO-US012865.

PR 21-APR-2000: 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

PA (CORI-) CORIXA CORP.

PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI; 2001-616774/71.

DR N-PSDB; AAS59564.

PT Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris.

PS Example 1; SEQ ID NO 15633; 1069pp; English.

Sequences AAU39105-AAU68017 represent *Propionibacterium acnes* immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. *P. acnes* is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies





Db 338 NGQAVEGMEALPALVDEMELLVDVLPEHAMVVLSDEPMVRSRAADLVRTSEELGAGWA 397  
QY 313 -----IHLDEEYRNSRVEKFLFTDKEILMLHWRYPYSLSIHGIEGAFDEPGTKT 363  
Db 398 AAAGGQAPIDLAASGYRSLAQVRSHCLERG---MAWWSMSSFSL-----DSSATDV 446  
QY 364 VIPG-----RVIGKFSIRLVP-HMNVSAVEKQVTRHLED-----VFSKRNSNKNVVSMT 412  
Db 447 LVDDDDITSAPQTVNPQLVAVFPHGDDVEAAVKDLTARLDDGWTVLLCAEGEGMAKRMSEL 506  
QY 413 LGLHPWIAN-IDDTQYLAAKRAIRTV-----FGTEPDMIRDGSTIPIAK 455  
Db 507 LGEHNVAARLVDDVDPDATEPCVQVIRLHQRHGFAESVKLLVASTGDLAE 557

RESULT 422  
ABP73615  
ID ABP73615 standard; protein; 1448 AA.  
AC ABP73615;  
XX  
DT 30-JAN-2003 (first entry)  
XX  
DE Candida albicans essential protein SEQ ID NO 7452.  
XX  
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;  
KW signal transduction; DNA replication; cell division; growth;  
KW proliferation; Candida albicans; fungicide; antifungal.  
XX

OS Candida albicans.  
XX WO200253728-A2.  
PN  
XX 11-JUL-2002.  
PD  
PF 26-DEC-2001; 2001WO-US049486.  
XX  
PR 29-DEC-2000; 2000US-0259128P.  
PR 20-FEB-2001; 2001US-00792024.  
PR 22-AUG-2001; 2001US-0314050P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;  
XX  
DR WPI; 2002-566694/60.  
DR N-PSDB; ABZ32165.

Constructing strains for identifying gene products as effective targets  
for therapeutic intervention, by inactivating in the strain one allele of  
a gene and placing other allele of the gene under conditional expression.  
PS Claim 44; SEQ ID NO 7452; 167pp + Sequence Listing; English.  
XX  
CC The invention relates to constructing (M1) a strain of diploid fungal  
CC cells in which both alleles of a gene are modified, comprising modifying  
CC one allele by insertion or replacement by a cassette having an  
CC expressible selectable marker and modifying other allele by  
CC recombination, of a promoter replacement fragment with a heterologous  
CC promoter, so that expression of the second allele is regulated by the  
CC promoter. (M1) is useful for constructing a strain of diploid fungal  
CC cells in which both alleles of a gene are modified. The diploid fungal  
CC cells having both alleles modified are useful for identifying a gene that  
CC is essential to the survival or growth of a fungus, a gene that  
CC contributes to the virulence and/or pathogenicity of a fungus, a gene  
CC that contributes to the resistance of a diploid fungus to an antifungal  
CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
CC and for identifying a therapeutic agent for treatment of a mammalian  
CC disease. (M1) is useful for identifying a compound which modulates the  
CC activity of a gene product, preferably enzymatic activity, carbon  
CC compound catabolism, biosynthetic, transporter, transcriptional,  
CC translational, signal transduction, DNA replication and cell division  
CC activity. The method is useful for identifying a compound having the

CC ability to inhibit growth or proliferation of C. albicans cells and for  
CC treating infection by C. albicans. The present sequence is that of an  
CC essential Candida albicans protein used in the method of the invention.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied to Derwent by  
CC the European Patent Office  
XX  
SQ Sequence 1448 AA;

Query Match 3.7%; Score 96; DB 5; Length 1448;  
Best Local Similarity 20.3%; Pred. No. 84;  
Matches 66; Conservative 55; Mismatches 120; Indels 84; Gaps 16;  
QY 184 EQDLPVNIKFII--EGMEEAG---SVALEELVEKDKDRFFSGVDYIVISDNLWIS--QRK 236  
Db 279 EDDLTVKLTETIVTSSMIRAGIVKGISINNLMEQ-----WDYLQLSVAMYINSDSAN 330  
QY 237 PAITYGTRG-NSYFMVEVKCRDQDFHSGTFGGILHEPMDLVALLGSLVDSSGHILV--- 292  
Db 331 PALSTGGGAKSSKPIRAFQCRLKGKQGRFRG-----NLGKRVDGSGRTVISPD 380  
QY 293 PGI-YDEV-VPLTEEEINTYKAHLDLEEYRNSRVEKFLFTDKEILMLHWRYPYSLSIH 350  
Db 381 PNLKIDEAVPDRVAKVLTYPE--KCTRY-NKKKLQKLV----- 416  
QY 351 GIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVS---AVEKQVTRHLED-----VFSKRNS 403  
Db 417 -VNGPDIHPGANVYMKQNEPGKRNLRFGDRVKLAKTLQIGDVVERHIEDGDVVLNRPQS 475  
QY 404 SNKM-VVSMTGLLHPWIA-----NIDDTQYLAAKRAIRTVFGTEP 442  
Db 476 LHRLSILSHYAKIRPWRTRFRLNECVCTPNADFGDEMNLHVPQTTEARAEAINLMGVKN 535  
QY 443 DMIRDGSTIPIAKMFQEIYVHKSIVL 467  
Db 536 NLLTPKSGEPIAATQDFITGSYLI 560

RESULT 423  
AAE29910  
ID AAE29910 standard; protein; 1707 AA.  
XX  
AC AAE29910;  
XX  
DT 24-FEB-2003 (first entry)  
XX  
DE Human transporter and ion channel (TRICH) protein #10.  
XX

KW Human; transporter and ion channel; TRICH; neurodegenerative disorder;  
KW Parkinson's disease; Alzheimer's disease; muscular disorder; transgenic;  
KW myotonic dystrophy; catatononia; endocrine disorder; diabetes; cytostatic;  
KW Grave's disease; cancer; leukaemia; cervical; immunological; scleroderma;  
KW systemic lupus erythematosus; allergy; gastrointestinal; Crohn's disease;  
KW Goodpasture's syndrome; infection; cardiovascular; fungicide; nootropic;  
KW hepatic disease; cirrhosis; gene therapy; uropathic; anti-HIV; virucide;  
KW atherosclerosis; antiparasitic; protozoacide; antibacterial.  
XX

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 5..27 /note= "Transmembrane domain"  
FT Domain 204..228 /note= "Transmembrane domain"  
FT Domain 550..578 /note= "Transmembrane domain"  
FT Domain 865..893 /note= "Transmembrane domain"  
FT Domain 937..959 /note= "Transmembrane domain"  
FT Domain 975..995 /note= "Transmembrane domain"  
FT Domain 1005..1025







Matches	63;	Conservative	44;	Mismatches	120;	Indels	55;	Gaps	13;
QY	198	MEEAGSVALEELVEKEKDRFFSGVDYIVIS-DNLWISQRKPAITYGTRGNSYFMVEVKCR	256						
Db	92	MEKQDKWTRKNIKEYKTDSEFRHTGYVMAQIDGLYVGAKKRAILEGTPMTLFIQIQ----	147						
QY	257	DQDFHSGTGGILHEPMADLVALLGSLVDSS-----GHI-----LVPGIYDEVVPL	302						
Db	148	-----FLNSVGDLL-----DLIPSLPTKNGSLKVFKRWDMGHCSALIKVLPGF--ENVLF	196						
QY	303	TEEEINTYKAI-----HLD---LEEYRNSSRVEKFLDFTKKEILMHLWRYPSLS-----I	349						
Db	197	AHSSWYTYAAMLRIYKHWDFNIIDKDTSSRLS---FSSYPGFLESDDFYILSSGLILL	253						
QY	350	HGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVV	409						
Db	254	QTTNSVENKTLKQVIPETLLSWQVRVRVANMMADSG-----KRWADIFSKYNSGTNNQ	307						
QY	410	SMTLGLHPWIAN--ID-DTQYLAAKRAIRTVFGTEPDMIRDG	448						
Db	308	YMWLDLKKVKNHSLDKGTLYIVEQIPTTYVEYSEQTDVLRKG	349						
RESULT 427									
ADN04834									
ID	ADN04834 standard; protein; 506 AA.								
XX	ADN04834;								
XX	01-JUL-2004 (first entry)								
DT	Antipsoriatic protein sequence #597.								
XX	antipsoriatic; gene therapy; psoriasis; diagnosis.								
DE	Homo sapiens.								
XX	WO2004028479-A2.								
XX	08-APR-2004.								
XX	25-SEP-2003; 2003WO-US030907.								
PF	25-SEP-2002; 2002US-0414006P.								
XX	(GETH ) GENENTECH INC.								
XX	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI, Wu TD;								
XX	WPI; 2004-305105/28.								
DR	N-PSDB; ADN04833.								
XX	New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a mammal.								
PT	Claim 9; SEQ ID NO 1228; 3069pp; English.								
XX	The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.								
XX	Sequence 506 AA;								
Query Match									
Best Local Similarity 22.3%; Score 95.5; DB 8; Length 506;									
Matches 63; Conservative 44; Mismatches 120; Indels 55; Gaps 13;									
QY	198	MEEAGSVALEELVEKEKDRFFSGVDYIVIS-DNLWISQRKPAITYGTRGNSYFMVEVKCR	256						

Db	92	MEKQDKWTRKNIKEYKTDSEFRHTGYVMAQIDGLYVGAKKRAILEGTPMTLFIQIQ----	147
QY	257	DQDFHSGTGGILHEPMADLVALLGSLVDSS-----GHI-----LVPGIYDEVVPL	302
Db	148	-----FLNSVGDLL-----DLIPSLPTKNGSLKVFKRWDMGHCSALIKVLPGF--ENVLF	196
QY	303	TEEEINTYKAI-----HLD---LEEYRNSSRVEKFLDFTKKEILMHLWRYPSLS-----I	349
Db	197	AHSSWYTYAAMLRIYKHWDFNIIDKDTSSRLS---FSSYPGFLESDDFYILSSGLILL	253
QY	350	HGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVV	409
Db	254	QTTNSVFNKTLKQVIPETLLSWQVRVRVANMMADSG-----KRWADIFSKYNSGTNNQ	307
QY	410	SMTLGLHPWIAN--ID-DTQYLAAKRAIRTVFGTEPDMIRDG	448
Db	308	YMWLDLKKVKNHSLDKGTLYIVEQIPTTYVEYSEQTDVLRKG	349
RESULT 428			
ID	ADO20065	standard; protein; 506 AA.	
XX	AC	ADO20065;	
XX	DT	12-AUG-2004 (first entry)	
XX	DE	Human PRO polypeptide #487.	
XX	KW	Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.	
OS	Homo sapiens.		
XX	WO2004043361-A2.		
PN	27-MAY-2004.		
XX	06-NOV-2003; 2003WO-US035268.		
XX	08-NOV-2002; 2002US-0425235P.		
PF	(GETH ) GENENTECH INC.		
XX	Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM; Wood WI, Wu TD;		
XX	WPI; 2004-420067/39.		
DR	N-PSDB; ADO20064.		
XX	Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or spondyloarthropathy.		
PS	Claim 7; SEQ ID NO 974; 1731pp; English.		
XX	The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating		







CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
CC or physiology, altered endoreduplication, biochemistry, signal  
CC transduction, storage lipid mobilisation and/or altered photosynthesis,  
CC each relative to the corresponding wild type plants. Accordingly, these  
CC sequences can also be useful as positive or negative selectable markers  
CC during transformation of cells or tissues. The identified genes play a  
CC role in a variety of biological processes such as DNA replication, cell  
CC wall biosynthesis, nitrogen and/ or carbon metabolism or they function as  
CC transcription factors. This polypeptide sequence is thale cress protein  
CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing  
CC the E2Fa/DPa transcription factor, given in an exemplification of the  
CC invention.  
XX  
SQ Sequence 1029 AA;

Query Match 3.6%; Score 95.5; DB 8; Length 1029;  
Best Local Similarity 20.7%; Pred. No. 55;  
Matches 100; Conservative 69; Mismatches 170; Indels 145; Gaps 31;

QY 32 PALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVP-----RFRQELFRMMAVAADTLQR 87  
Db 233 PKITE---QFADLKRKLHTLSADEW-----DSIPEIGDYSLRNKKKFFSFVIPDITLLE 284  
QY 88 LGAR-----VASVD-----MGPPQLPDGQSLPIPPVILAEIGSDPTKGTV-----C 128  
Db 285 KAKKEKELVMALDPKSRAGGSETPWGQT--PVTDLTAVGEG--RGTVLSLKLDNLSDS 339  
QY 129 FYGHLDVQPADRGDGLWLT-D-PYVLTEVDGKLYGRG-----ATDNKGPVLAWINAV 177  
Db 340 VSGQTVVDP---KGYLTDLSKMKRTTDEEIIDRNPARLLYKSLTQSNPKNP-NGWI--- 391  
QY 178 SAFRALEQDLPVN-IKFIIE-GMEEA---GSVALEEL---VEKEKDRFFSGVDYIVISD 228  
Db 392 AARVEEVDGKIKAAARFQIQGCEECPKNEVDVLEACRLANPEDAKGVIAKGVKLIPNSV 451  
QY 229 NLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMAIDLVALGSLVDSSG 288  
Db 452 KLWLEAAK--LEHDVENKSRVLRK-----GLEHIP--DSVRL----- 484  
QY 289 HILVPGIYDEVVPLTEEE---INTYKAI-----HLD-----LEEYRNSSRVEKFLFDT 333  
Db 485 -----WKAVVELANEEDARILLHRAVECCPLHLELWVALARLEYAESKKV---LNKA 534  
QY 334 KEEILMH--LWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQ-V 390  
Db 535 REKLPEPAIW-ITAAKLEEANGKLDDEANDNTAMVGKIIDR-----GIKTLOREGV 584  
QY 391 TRHLEDVFSKRNSSNM-----VVSMTLGL-----HPWIANIDDTQYLAAKRAI 434  
Db 585 VIDRENWMSEAEACERVGSVATCQAIKNTIGIGVEEEDRKRTWVADADECKKRGSIETA 644  
QY 435 RTVF 438  
Db 645 RAIY 648

RESULT 432  
AAW89442  
ID AAW89442 standard; protein; 408 AA.  
XX  
AC AAW89442;

DT 18-MAR-1999 (first entry)  
XX  
DE Mycoplasma hominis arginine deiminase.  
XX  
KW Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritidis;  
KW Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;  
KW inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.  
XX  
OS Mycoplasma hominis.  
XX  
PN WO9851784-A1.

XX 19-NOV-1998.  
XX  
XX 12-MAY-1998; 98WO-US0009575.  
XX  
XX 12-MAY-1997; 97US-0046200P.  
PR 13-FEB-1998; 98US-00023809.  
XX  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
XX Clark MA;  
XX  
XX WPI; 1999-045227/04.  
XX  
PT New compound comprising arginine deiminase - covalently bonded via  
PT linking group to polyethylene glycol, to enhance the half life of  
PT arginine by this modification.  
XX  
PS Claim 6; Fig 1; 30pp; English.  
XX  
XX The present sequence represents Mycoplasma hominis arginine deiminase.  
CC The present invention describes: (1) a compound comprising arginine  
CC deiminase (AD) covalently bonded via linking group to polyethylene glycol  
CC (PEG), and having a molecular weight 12-40 kDa; and (2) a composition as  
CC above, but where the linking group is selected from a malimide group, an  
CC amide group, an imide group, a carbamate group, an ester group, an epoxy  
CC group, a carboxyl group, a hydroxyl group, a carbohydrate, a tyrosine  
CC group, a cysteine group and/or a histidine group. AD can be used in the  
CC treatment of tumours, e.g. melanomas, hepatomas and sarcomas, and to  
CC inhibit metastasis. The modified AD has an enhanced circulating half life  
XX  
SQ Sequence 408 AA;

Query Match 3.6%; Score 95; DB 2; Length 408;  
Best Local Similarity 17.9%; Pred. No. 15;  
Matches 64; Conservative 59; Mismatches 134; Indels 100; Gaps 15;

QY 179 AFRALEQDLPVNI---KFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ 234  
Db 60 SFVKIMKDRGINVVVELTDLVAETYDLASKAAKEEFIE-----TFLEE 101  
QY 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMAIDLVALGSG---LVDSS 287  
Db 102 TVPVLTEANK-----KAVRAFLLSKPTHEMVEFMMSGITKVELGVESE 144  
QY 288 GHILV---PGIYDEVVPLTEEEINTYKAIHLDEEY---RNSSRVEKFLFDTKBEILMHL 341  
Db 145 NELIVDPMPLNYTRDPFA---SVNGVGTIHFMYIYVRRRETFLARFVRNHPKLVKTP 200  
QY 342 WRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEK----QVTRHLEDV 397  
Db 201 WYY-----DPAMKMPIEG---GDVFIYNNETLVVGVSERTDLDITLLAKNI 244  
QY 398 FSKRNSSNMVVSMT-----LGLHPWIANIDDTQYLAAKRAITVF-----GT 440  
Db 245 KANKEVEFKRIVAINVPKWTNLMHLDTWLTDKKNKFLYSPIA-NDVFKFWDYDLVNGGA 303  
QY 441 EPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGGEHSQNEKINRWNYIEGTKLFA 497  
Db 304 EPQPQLNG--LPLDKLLASIINKEPVLPIG---GAGATEMEIARETNFDGTNYLA 354

RESULT 433  
AAE16137  
ID AAE16137 standard; protein; 409 AA.  
XX

AC AAE16137;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mycoplasma hominis modified arginine deiminase (ADI) E112, S210.  
XX  
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;

KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour; mutant; mutein.  
XX  
OS Mycoplasma hominis.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 112 /note= "Wild type Lys substituted with Glu"  
FT Misc-difference 210 /note= "Wild type Pro substituted with Ser"  
FT  
XX  
XX  
PN WO200183774-A2.  
XX  
XX  
PD 08-NOV-2001.  
XX  
XX  
PF 02-MAY-2001; 2001WO-US014116.  
XX  
XX  
PR 04-MAY-2000; 2000US-00564559.  
XX  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
XX  
PI Ensor CM, Holtsberg FW, Clark MA;  
XX  
XX  
DR WPI; 2002-097497/13.  
XX  
XX  
XX Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
PS Example 1; Fig 2; 34pp; English.  
XX  
CC The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis modified ADI protein  
XX  
SQ Sequence 409 AA;  
  
Query Match 3.6%; Score 95; DB 5; Length 409;  
Best Local Similarity 18.1%; Pred. No. 15;  
Matches 64; Conservative 58; Mismatches 139; Indels 92; Gaps 13;  
  
QY 179 AFRALQDLPVNI---KFIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ 234  
Db 60 SFVKIMKDRGINVVVELTDLVAETYDLASKAAKEEFIE-----TFLEE 101  
  
QY 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGS-----LVDSS 287  
Db 102 TVPVLTEANK-----EAVRAFLLSKPTHEMVEFMMSGITKYELGVESE 144  
  
QY 288 GHILV---PGIYDEVVPLTEEEINTYKAHLDLEEY---RNSSRVEKFLFDTKKEILMHL 341  
Db 145 NELIVDPMNPPLYFTRDPFA---SVNGVGTIHFMRYYIVRRRETFLFARFVFRNHPKLVKTP 200  
  
QY 342 WRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN-----VSAVEKQVTRHL 394  
Db 201 WYYDPAMKMSIEG-----GDVFIYNNETLVVGVSERTDLDITITLLAKNIKANK 248  
  
QY 445 IRDGSTPIAKMFQEI VHKS VVLIPLGAVDGEHSQNEKINRWNYIEGPKLFA 497  
Db 308 QLNG--LPLDKLLASINKEPVLPIG---GAGATEMEIARETNFDCGTNYLA 354

AAE16136  
ID AAE16136 standard; protein; 409 AA.  
XX  
AC AAE16136;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mycoplasma hominis modified arginine deiminase (ADI) #2.  
XX  
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour; mutant; mutein.  
XX  
OS Mycoplasma hominis.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 210 /note= "Wild type Pro substituted with Ser"  
FT  
XX  
PN WO200183774-A2.  
XX  
XX  
PD 08-NOV-2001.  
XX  
XX  
PF 02-MAY-2001; 2001WO-US014116.  
XX  
XX  
PR 04-MAY-2000; 2000US-00564559.  
XX  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
XX  
PI Ensor CM, Holtsberg FW, Clark MA;  
XX  
XX  
DR WPI; 2002-097497/13.  
XX  
XX  
XX Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
PS Disclosure; Page 31-32; 34pp; English.  
XX  
CC The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis modified ADI protein  
XX  
SQ Sequence 409 AA;  
  
Query Match 3.6%; Score 95; DB 5; Length 409;  
Best Local Similarity 18.1%; Pred. No. 15;  
Matches 64; Conservative 58; Mismatches 139; Indels 92; Gaps 13;  
  
QY 179 AFRALQDLPVNI---KFIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ 234  
Db 60 SFVKIMKDRGINVVVELTDLVAETYDLASKAAKEEFIE-----TFLEE 101  
  
QY 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGS-----LVDSS 287  
Db 102 TVPVLTEANK-----KAVRAFLLSKPTHEMVEFMMSGITKYELGVESE 144  
  
QY 288 GHILV---PGIYDEVVPLTEEEINTYKAHLDLEEY---RNSSRVEKFLFDTKKEILMHL 341  
Db 145 NELIVDPMNPPLYFTRDPFA---SVNGVGTIHFMRYYIVRRRETFLFARFVFRNHPKLVKTP 200  
  
QY 342 WRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN-----VSAVEKQVTRHL 394  
Db 201 WYYDPAMKMSIEG-----GDVFIYNNETLVVGVSERTDLDITITLLAKNIKANK 248  
  
QY 395 EDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVF-----GTEPDM 444



Db 249 EVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIA-NDVFKFWDYDLVNGGAEPQP 307

QY 445 IRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFA 497

Db 308 QLNG--LPLDKLLASIIINKEPVLIPIG-----GAGATEMEIARETNFDGNTNYLA 354

RESULT 435

AAE16134

ID AAE16134 standard; protein; 409 AA.

XX AAE16134;

XX 26-MAR-2002 (first entry)

XX Mycoplasma hominis wild type arginine deiminase (ADI).

DE Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;

XX antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;

KW septic shock; tumour.

XX Mycoplasma hominis.

OS WO200183774-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014116.

PF 04-MAY-2000; 2000US-00564559.

XX (PHOE-) PHOENIX PHARMACOLOGICS INC.

PA Ensor CM, Holtsberg FW, Clark MA;

XX WPI; 2002-097497/13.

DR Modified arginine deiminase for improved manufacturing processes and for

XX treating cancer, is mutated to be free of a pegylation site at or

PT adjacent to its catalytic region.

XX Example 3; Fig 1; 34pp; English.

PS The invention relates to a modified arginine deiminase (ADI) for improved

XX manufacturing processes. The process comprises ADI modified to be free of

CC at least one pegylation site at or adjacent to its catalytic region. ADI

CC catalyses the conversion of arginine to citrulline and may be used to

CC eliminate arginine. ADI is useful for treating cancer, melanomas,

CC hepatomas, sarcomas, parasitic diseases, septic shock, and for treating

CC and inhibiting metastasis of tumour cells and other disease states. The

CC present sequence is Mycoplasma hominis wild type ADI

XX Sequence 409 AA;

QY Query Match 3.6%; Score 95; DB 5; Length 409;

Db Best Local Similarity 17.9%; Pred. No. 15;

Matches 64; Conservative 59; Mismatches 134; Indels 100; Gaps 15;

QY 179 AFRALEQDLPVNI-----KFIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ 234

Db 60 SFVKIMKORGINVVVELTDLVAETYDLASKAAKEEFIE-----TFLEE 101

QY 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLS-----LVDSS 287

Db 102 TVPVLTEANK-----KAVRAFLLSKPTHEMVEFMMSGITKYELGVSE 144

QY 288 GHILV---PGIYDEVVPLTEEEINTYKAIHLDLEEY---RNSSRVEKFLFDKKEILMHL 341

Db 145 NELIVDMPNLYFFTRDPFA----SVNGVGTIHFMYIVRRRETFLFARFVFRNHPKLVKTP 200

QY 342 WRYPVLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEK-----QVTRHLEDV 397

Db 201 WYY-----DPAMKMPIEG---GDVFIYNNETLVVGVVSERTDLDITLLAKNI 244

QY 398 FSKRNSSNKMVVSMT-----LGLHPWIANIDDTQYLAAKRAIRTVF-----GT 440

Db 245 KANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIA-NDVFKFWDYDLVNGGA 303

QY 441 EPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFA 497

Db 304 EPQPQLNG--LPLDKLLASIIINKEPVLIPIG-----GAGATEMEIARETNFDGNTNYLA 354

RESULT 436

ABG31996

ID ABG31996 standard; protein; 409 AA.

XX ABG31996;

AC ABG31996;

XX 06-AUG-2003 (revised)

DT 15-NOV-2002 (first entry)

XX M. hominus arginine deiminase gene, HOMADIPRO.

DE Arginine deiminase; cytostatic; ADI; polyethylene glycol; PEG; arginine;

XX citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;

KW auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.

XX Mycoplasma hominis.

OS WO200244360-A2.

XX 06-JUN-2002.

PN 19-SEP-2001; 2001WO-US029184.

PF 28-NOV-2000; 2000US-00723546.

XX (PHOE-) PHOENIX PHARMACOLOGICS INC.

PA Clark MA;

XX WPI; 2002-619003/66.

DR Compound for treating tumor such as melanoma, hepatoma or sarcoma in a

XX patient, comprises arginine deiminase covalently bonded by a linking

PT group such as succinimide to polyethylene glycol.

XX Example 1; Fig 1; 59pp; English.

PS The invention discloses a compound comprising arginine deiminase (ADI)

XX covalently bonded by a linking group to polyethylene glycol (PEG) having

CC a total weight average molecular weight of about 1000-50000. Also

CC disclosed is a method for enhancing the circulating half life or the

CC tumouricidal activity of arginine deiminase by modifying the arginine

CC deiminase by covalently bonding the arginine deiminase by a linking group

CC to PEG. Normal cells can synthesise arginine from citrulline in a 2 step

CC process catalysed by argininosuccinate synthase and argininosuccinate

CC lyase. In contrast, many cancerous cells do not express argininosuccinate

CC synthase and are, therefore, auxotrophic for arginine. Arginine deiminase

CC catalyses the conversion of arginine to citrulline and can be used to

CC eliminate arginine from the cancerous cells. The compound is useful for

CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or

CC for treating and inhibiting metastases in a patient. When compared to

CC native arginine deiminase the compound retains most of its enzymatic

CC activity, is far less antigenic, has a greatly extended circulating half-

CC life, and is much more efficacious in the treatment of tumours. The

CC sequence presented is the Mycoplasma hominus arginine deiminase gene,

CC HOMADIPRO. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 409 AA;

XX Query Match 3.6%; Score 95; DB 5; Length 409;

XX Best Local Similarity 17.9%; Pred. No. 15;

XX Matches 64; Conservative 59; Mismatches 134; Indels 100; Gaps 15;















Matches 98; Conservative 64; Mismatches 144; Indels 228; Gaps 26;

QY 31 PPALLEKVFQYI-----DLHQDEFVQTLKEWVAIESDSVQVPRFRQELF 75  
Db 80 PPELSEQ-FPYIRQLLDAYHIKRYELDNYEADDIIGTISK-----EADKAG-----F 125

QY 76 RMMAVAAD-----TLQRLGARVASVD-----MGPOQLPDGQSL--- 108  
Db 126 QTIITGDRDLTQLATDNVTIYYTKKGVTVDHYTFDFAEKYNGLTPNQIIDMKGLMGD 185

QY 109 ---PIPPVILAE LGS-----DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTQVD 155  
Db 186 TSDNIPGV--AGVGEKTAIKLLNQFDTVEGV---YEHL D-----EIS 222

QY 156 GKLYGRGATDNK-----GPVLAWINAVSAFRA-LEQDL-----PVNIKFI 194  
Db 223 GKKLKEKLQNSKEDALMSKELATINVDSPIEVKLEDTLMTHQDEQQEKIELFKLEFKQL 282

QY 195 IEGMEEAGSVALEELVEK--EKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVE 252  
Db 283 LSDIDQSASV--EDAIEKTFEIE TSDNIDF-----TSLKEAAIHFE L DGGNYLRNN 332

QY 253 VKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA 312  
Db 333 I-----LKFSLFTGKEHIVI-----NADDINNY-- 355

QY 313 IHL DLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIG- 371  
Db 356 --AELVSWLENPNTKKVYDAK-----KTYVASHRLGI 386

QY 372 ----KFSIRLV-----PHMNVSAVEKQVTRH----LEDVFSKRNSNKMVVSMTLGLHP 417  
Db 387 DIQNISFDIMLASIYIIPSR TISDVQSVSLYGQSFVKDDVSIYGKKFKVPEDDVLNP 446

QY 418 WIANIDDTQYLAAKRAIRTVFGTEPDMIRD-----GSTIPIAKMFQEI 460  
Db 447 YVASITDAIYFA-----KPNMDKQLEEYNQVELLADLELPLAKILSEM 489

RESULT 445  
ABBS2592  
ID ABB52592 standard; protein; 1376 AA.  
XX AC ABB52592;  
XX DT 11-FEB-2002 (first entry)  
XX DE Escherichia coli polypeptide SEQ ID NO 560.  
XX KW Escherichia coli; B2/D-A-; antiinflammatory; antibacterial;  
KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;  
KW systemic infection; non-diarrhoeal infection; septicaemia;  
KW pyelonephritis; antibiotic resistance.  
XX OS Escherichia coli.  
XX PN WO200166572-A2.  
XX PD 13-SEP-2001.  
XX PF 12-MAR-2001; 2001WO-EP003445.  
XX PR 10-MAR-2000; 2000FR-00003145.  
XX PR 02-FEB-2001; 2001FR-00001449.  
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;  
XX WPI; 2001-550253/61.  
XX DR A library of DNA fragments of Escherichia coli strains for the phylogenetic  
PT determination of a given strain comprises polynucleotides of nature B2/D+

PT A-  
XX Example 6; Fig 6; 646pp; English.  
CC The invention relates to a library of DNA fragments of Escherichia coli  
CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and  
CC encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature  
CC B2/D-A-. The polynucleotides have potential antiinflammatory,  
CC antibacterial and immunosuppressive activity as part of pharmaceutical  
CC compositions used to treat, palliate or prevent extra-intestinal E. coli  
CC infections. The polypeptides are useful for determining the phylogenic  
CC group of a given E. coli strain. These polypeptides can detect and treat  
CC an undesired development of E. coli, particularly an extra-intestinal  
CC infection that include systemic and non-diarrhoeal infections such as  
CC septicaemia, pyelonephritis and meningitis this is particularly  
CC advantageous as bacterial resistance is increasing with the more frequent  
CC use of broad spectrum antibiotics  
XX SQ Sequence 1376 AA;  
Query Match 3.6%; Score 95; DB 4; Length 1376;  
Best Local Similarity 21.3%; Pred. No. 96;  
Matches 74; Conservative 63; Mismatches 132; Indels 78; Gaps 21;

QY 119 GSDPTKG-TVCFYGH---LDVQ-PADRGDWL--TDPYVLTVDGKLY-GRGATDNKGPV 170  
Db 348 GSDLNAGKNLTFLGHNGQIDLENSVTQAGSILFTDDYTTVTSNGSTWGTGAGIIVDKDAS 407

QY 171 LAW-INAV---SAFRALEQDLPVNIKFIIEGMEEA--GSVALEELVEKEK-RFFSGVDY 223  
Db 408 VNQVNGVKGDNLHKIGEGTLVVGQGTGVNEGGLKVGDTVVLNQQAADSSGHVQAFSSVNI 467

QY 224 -----IVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLV 277  
Db 468 ASGRPTVVLADNQVNP DN--ISWGYRGG---VLDVNGNDLTFHKL N-----AADYG 514

QY 278 ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA IHL-----DLEEYRN--SSRVEKFLF 331  
Db 515 ATLGNSSDKTANITL-----DYQTRPADVKVNEWSSSNRGTGSLYIYNNPYTHTVDFYFIL 570

QY 332 DTKE-----EILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGK---FSIRLVPHM 381  
Db 571 KTSSYGWFFPTGQVSNHEWYV-----GHDQNSAQALLANRINNKG YLYHGKLLGNI 621

QY 382 NVS-----AVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 419  
Db 622 NFSNKATPGTTGALVMDGSANMSGTFTQENG-----RLTIQGH PVI 662

RESULT 446  
ABU48526  
ID ABU48526 standard; protein; 1416 AA.  
XX AC ABU48526;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #34053.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Treponema pallidum.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.







SQ Sequence 402 AA;  
Query Match 3.6%; Score 94.5; DB 4; Length 402;  
Best Local Similarity 23.1%; Pred. No. 16;  
Matches 68; Conservative 50; Mismatches 124; Indels 53; Gaps 13;  
QY 175 NAVSAFRALEQDLPV-----NIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD 228  
Db 102 NIAQLKQALNENAPTRIFLLENIRF-LKGEEN-----DENLAKD---LASLCDVFVND 151  
QY 229 NLWISQRKPAITYGTRGNSYFWMVEVKCRDQDFHSGTGGILHEPMA DLVALLGSLVDSSG 288  
Db 152 AFGTSHRKHASTYGTAKFAPIKVSGFLLKKEIDS--FYQAFNHPLRPLLLIVGGAKVSSK 209  
QY 289 HILVPGIYD--EVVPLTEEEINTY-KAIIHLDLEEYRNSRVEKFLFDTKKEIILMHLWRYP 345  
Db 210 LTLKNIULDIDKLIAGAMSNTFLKALGYDVQD---SSVEDALINDALELLQ----- 259  
QY 346 SLSIHGIEGAFDEPGTKTVIPGRVICKFSIRLVPHMNVSAVEKQVTRH-LEDV----- 397  
Db 260 -----SAKEKKVKVYLPIDAVTTDDILNPKHIKISPVQDIEPKHKIADIGPASLKL 310  
QY 398 FSK-RNSSNKMVWVSM TGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTI 451  
Db 311 FSEVIESAPTILWNGPLGVHEKQEFARGTTFLAHKIANITYAF----SLIGGGDTI 361  
RESULT 450  
AAG81837  
ID AAG81837 standard; protein; 478 AA.  
AC AAG81837;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE S. epidermidis open reading frame protein sequence SEQ ID NO:768.  
XX  
KW Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;  
KW endocarditis.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN WO200134809-A2.  
XX  
PD 17-MAY-2001.  
XX  
PF 09-NOV-2000; 2000WO-US030782.  
XX  
PR 09-NOV-1999; 99US-0164258P.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Kimmerly WJ;  
XX  
DR WPI; 2001-316495/33.  
DR N-PSDB; AAH52687.  
XX  
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis.  
XX  
PS Claim 18; Page 237; 2188pp; English.  
XX  
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)  
CC and (II) can have antibacterial activity and therefore can be used in  
CC vaccination. The nucleic acids (I) may be used to produce the S.  
CC epidermidis polypeptides (II) via the production of vectors containing  
CC them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to

CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5091 to AAH5098  
CC represent oligonucleotide sequences and primers which are used in the  
CC exemplification of the present invention. N.B. The present invention  
CC specifically claims all the polynucleotide sequences given in the  
CC sequence listing of the present specification, however the sequence  
CC in the disclosure for SEQ ID NO:4454 so even though sequences are given  
CC for SEQ ID NO:4455 to 4464  
XX  
SQ Sequence 478 AA;  
Query Match 3.6%; Score 94.5; DB 4; Length 478;  
Best Local Similarity 20.4%; Pred. No. 21;  
Matches 94; Conservative 70; Mismatches 167; Indels 129; Gaps 23;  
QY 34 LLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPRFRQELFRMNAV 80  
Db 41 LLGKDIQYKDLGLLIVDEEQRFGVRHKERIKTLKKNVDVLTLTATPIR TLH----- 92  
QY 81 AADTLQRLGARVASVDMGPQOLPDGSLPIPPVILAE-----LGSDPTKGTVCFYGH 132  
Db 93 ---MSMLGVR---DLSVIETPPENRFPVQTYVLEQNTNFIKEALERELSRDGOVFYLY 144  
QY 133 LDVQ---PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL P 188  
Db 145 NKVQSIYEKREQLRLMPDANIAV-AHQMTER---DLEETMLSFINH-----EYDIL 193  
QY 189 VNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTR-GNS 247  
Db 194 VTTIIETGVDVPNA---NTLIIIEEADRF--GLS QLY-----QLRGRVGRSSRIGYA 240  
QY 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMA DL-VALLGSLVDSSGHILVPGI-Y 296  
Db 241 YFLHPANKVLNETAEERLQAIKEFTELGSGFKIAMRDLNIRGAGNLLGKQQHGFIDSVGF 300  
QY 297 DEVVPLTEEEINTYKAI-----HLD-----LEEYRNSRV-- 326  
Db 301 DLYSQMLEEAVNEKRGIKEESPDAPDIEVELHLDAYLPAEYIQSEQAKIEIYKKLRKVET 360  
QY 327 EKFLFDTKEEILMHLWRYP-----SLSIH---GIEGAFDEPGTKTVIPGRVIGK 372  
Db 361 EEQLFDVKDELIDRFNDYPIEVERLLDIVEIKVHALHAGVELIKDKGKSIQII----- 413  
QY 373 FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMT 412  
Db 414 LSPKATEDINGEELFKQ-TQPLGRAMKVGQNNAMNVTILT 452  
RESULT 451  
ADK60222  
ID ADK60222 standard; protein; 590 AA.  
XX  
AC ADK60222;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Angiogenesis differentially expressed protein GS-P46.  
XX  
KW vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;  
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;  
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;  
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;  
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;  
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;  
KW ischemia; angina; myocardial infarction; chronic heart disease;  
KW cardiac congestion; macular degeneration; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
PN FR2836687-A1.  
XX

PD 05-SEP-2003.  
XX 11-APR-2002; 2002FR-000004546.  
PF 04-MAR-2002; 2002FR-00002717.  
XX (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
XX Colin S, Schneider C, Al Mahmood S;  
PI WPI; 2004-013912/02.  
XX N-PSDB; ADK60472.  
DR Compositions for diagnosing, prognosing and treating angiogenic disorders  
PT including tumor vascularization and heart disease, comprise nucleic acid  
PT or polypeptide differentially expressed in angiogenesis.  
XX  
PS Claim 7; SEQ ID NO 98; 424pp; French.  
XX  
CC The invention relates to a novel pharmaceutical composition active on  
CC angiogenesis comprising an endothelial cell nucleic acid whose expression  
CC is induced by an angiogenic factor and inhibited by an angiostatic agent  
CC or its complement or fragment, a polypeptide sequence encoded by the  
CC nucleic acid or its fragment, a molecule capable of inhibiting expression  
CC of the nucleic acid or a molecule which binds to the polypeptide  
CC sequence. The invention is used to diagnose, prognose or treat an  
CC angiogenic disorder in a mammal, particularly a human. The disorder is  
CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,  
CC endometriosis associated with neovascularization, restenosis due to  
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral  
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,  
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
CC myocardial infarction, chronic heart disease, cardiac congestion or  
CC macular degeneration due to age or osteoporosis. This sequence  
CC corresponds to a protein encoded by a differentially expressed DNA used  
CC in the composition of the invention.  
XX  
SQ Sequence 590 AA;  
  
Query Match 3.6%; Score 94.5; DB 8; Length 590;  
Best Local Similarity 18.1%; Pred. No. 29;  
Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;  
  
QY 23 GWFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76  
Db 7 GQRGPPSPGPA-----AQPAPPPRRRARSALLGA 36  
  
QY 77 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 136  
Db 37 LLAASAAAARVRCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSLDTD 82  
  
QY 137 PADRGDGLTDPYVLTVEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183  
Db 83 ---GDMYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSHSLQQLPWLNXSSCLSLLRST 137  
  
QY 184 -----EQDLPVNIKFIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236  
Db 138 PAASYEEELPPDPSELTIEARFQPLLPETMTKSKDGFL-GVSRLLALSGLRNWTAAS 196  
  
QY 237 PAITYGTR-----GNSYFMVEVKRD----- 257  
Db 197 PSAVFATRHFPQFLPPGQELGEPWIIIPSELNMTGYLSNNRFFPPPPKGKGVIIHRL 256  
  
QY 258 QDFHSGTGGILHEPNMADLVALLGSLVD-----SSG 288  
Db 257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYITVMFRIHAEFQLSPEPDPFSPQAFTG 315  
  
QY 289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEVNRSRVEKFLFDTKKEILMH-- 340  
Db 316 HILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNMEVD 358

QY 341 LWRYPSTLSIHGIEGA-----FDEPGT--KTVIPG-----RVIGKF 373  
Db 359 IGYIPQMELEATGSPSPVSLDEGDMIDSHLPSEPLQFVFEEIKWQQLSWEERARL 418  
QY 374 SIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVMVMTLGLHPWIANIDDTQYLAAKRA 433  
Db 419 EVAMYPFKKVSYLP-----FTEAFDRAKAENKLVSILL---WGA-LDDQSCXGSGRT 467  
QY 434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVVLIPGLGAVDDGEHSQNEKI 484  
Db 468 LRETVLESSPILTLNLSFISTWSLVKELELQNKQ-----ENSSHQKL 511  
  
RESULT 452  
ADK60523  
ID ADK60523 standard; protein; 590 AA.  
XX  
AC ADK60523;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Angiogenesis differentially expressed protein GS-P46.  
XX  
KW vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;  
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;  
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;  
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;  
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;  
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;  
KW ischemia; angina; myocardial infarction; chronic heart disease;  
KW cardiac congestion; macular degeneration; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
PN FR2836686-A1.  
XX  
PD 05-SEP-2003.  
XX  
PF 04-MAR-2002; 2002FR-00002717.  
XX  
PR 04-MAR-2002; 2002FR-00002717.  
XX  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
XX  
PI Colin S, Schneider C, Al Mahmood S;  
XX  
DR WPI; 2004-013911/02.  
DR N-PSDB; ADK60773.  
XX  
PT Compositions containing nucleic acid or polypeptide differentially  
PT expressed in angiogenesis are useful to diagnose, prognose and treat  
PT angiogenic disorders including tumor vascularization and heart disease.  
XX  
PS Claim 7; SEQ ID NO 98; 405pp; French.  
XX  
CC The invention relates to a novel pharmaceutical composition active on  
CC angiogenesis comprising an endothelial cell nucleic acid whose expression  
CC is induced by an angiogenic factor and inhibited by an angiostatic agent  
CC or its complement or fragment, a polypeptide sequence encoded by the  
CC nucleic acid or its fragment, a molecule capable of inhibiting expression  
CC of the nucleic acid or a molecule which binds to the polypeptide  
CC sequence. The invention is used to diagnose, prognose or treat an  
CC angiogenic disorder in a mammal, particularly a human. The disorder is  
CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,  
CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,  
CC endometriosis associated with neovascularization, restenosis due to  
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral  
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,  
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
CC myocardial infarction, chronic heart disease, cardiac congestion or  
CC macular degeneration due to age or osteoporosis. This sequence



CC	corresponds to a protein encoded by a differentially expressed DNA used	
CC	in the composition of the invention.	
XX		
SQ	Sequence 590 AA;	
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	OS
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	PN
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	PD
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	PA
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	PA
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	PI
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	RESULT 453	
	ADP73146	
XX	ID ADP73146 standard; protein; 590 AA.	
AC	ADP73146;	
XX		
DT	12-AUG-2004 (first entry)	
XX		
DE	Angiogenesis inhibitor human protein sequence, GS-P46.	
XX		
KW	Inhibitor; angiogenesis; antisense nucleic acid; immunisation;	
KW	angiogenic disorder; antiangiogenic; angiogenesis stimulator; cytostatic;	
KW	dermatological; antiarthritic; antirheumatic; antiinflammatory;	
KW	vasotrophic; hypotensive; ophthalmological; antipsoriatic; cardiant;	
KW	gene therapy; antisense gene therapy; tumour vascularisation;	
KW	retinopathies; rheumatoid arthritis; Crohn's disease; atherosclerosis;	
KW	ovarian hyperstimulation; psoriasis; endometriosis; restenosis;	
KW	tissue granulation; peripheral vascular disorder; hypertension;	
KW	vascular inflammation; Raynaud's disease; aneurism; arterial restenosis;	
KW	thrombophlebitis; lymphadenopathy; lymphedema; ischaemia; angina;	
KW	myocardial infarction; chronic heart disease; congestive heart disease;	
XX	macular degeneration; human.	
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ-----ELAKTLGTD---GLFLFSSSLDTD 82	XX
Qy	137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183	XX
Db	83 ---GDWYIS-PEEFKPIAEKLTGSCSVTQTGVQWCSSHSLQPLPWLNXSSCLSLRST 137	XX
Qy	184 -----EQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236	XX
Db	138 PAASVEEELPPDPSEETLTIEARFPQLLPETMTKSKDGF-L-GVSRLALSGLRNWTAAS 196	XX
Qy	237 PAITYGTR-----GNSYFMVEVKCRD----- 257	XX
Db	197 PSAVEATRHQFPFLPPPGQELGEPWIIIPSELMSFTGYLSNNRFPYPPPKGKEVIIHRL 256	XX
Qy	258 QDFHSGTGGILHEPMADLVALLGSLVD-----SSG 288	XX
Db	257 SMFHPRPFVKTRFAPQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDPFPWFSPAQFTG 315	XX
Qy	289 HILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMH-- 340	XX
Db	316 HIILSKDATHVRDFRLFVP-----NHRSLNVDME-----WLYGASESSNNMEVD 358	XX
Qy	341 LWRYPSLSIHGIEGA----FDEPGT--KTVIPG-----RVIGKF 373	XX
Db	359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFVEEIKWQELSWEEAARRL 418	XX
Qy	374 SIRLVHNMVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDDTQYLAAKRA 433	XX
Db	419 EVAMYPPKKVSILP-----FTEAFDRAKAENKLVHSILL----WGA-LDDQSCXSGRT 467	XX
Qy	434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKI 484	XX
Db	468 LRETVLESSPILTLTNESFISTWSLVKELEELQNKK-----ENSSHQKL 511	XX
	Query Match 3.6%; Score 94.5; DB 8; Length 590;	
	Best Local Similarity 18.1%; Pred. No. 29;	
	Matches 108; Conservative 73; Mismatches 190; Indels 225; Gaps 29;	
Qy	23 GMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQP--VPRFRQE-----LFR 76	XX
Db	7 GORGPPSPGPA-----AQPAPPPRRRARSLLALGA 36	XX
Qy	77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136	XX
Db	37 LLAATAAAAVRVCARHAEAAQAARQ	



Db 37 LLAIAAAAAVRCARHAEAAQAARQ-----ELAKTLGTD-----GLFLPSSLDTD 82

Qy 137 PADRGDGLTDPYVLTVEVDGKLYGRGATDNKG-----PVLAWINAVSAFRAL--- 183

Db 83 ---GDMYIS-PEEFKPIAEKLTGSCSVTQTGVQWCHSSSLQPQLPWLANKSSCLSLRST 137

Qy 184 -----EQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD-NLWISQRK 236

Db 138 PAASYEEELPPDPSEETLTIEARFQPLLPEMTKSKDGFL-GVSRALSLGLRNWTAAS 196

Qy 237 PAITYGTR-----GNSYFMVEVKCRD----- 257

Db 197 PSAVFATRHFPQFLPPCQQLGEPWIIIPSELSMFTGYLSNNRFYPPPPKGEVLIHRL 256

Qy 258 QDFHSGTFGGILHEPMADLVALLGSLVD-----SSG 288

Db 257 SMFHPRPFVKTRFAQG-AVACLTAISDFYTYVMFRIHAEFQLSEPPDFPFWFSPAQFTG 315

Qy 289 HILVPGIYDEV-----VPLTEEEINTYKAIHLDLLEYRNSRVEKFLFDTKBEILMH-- 340

Db 316 HIILSKDATHVRDFLFPV-----NHRSLNVDME-----WLYGASESSNMEVD 358

Qy 341 LWRYPSSLIHGIEGA-----FDEPGT--KTVIPG-----RVIGKF 373

Db 359 IGYIPQMELEATGPSVPSVILDEGSMIDSHLPSGEPLQVFEEIKWQQLSWEAAARL 418

Qy 374 SIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRA 433

Db 419 EVAMYPFKKVSYLP-----FTEAFDRAKAENKLVHSILL---WGA-LDDQSCXGSGRT 467

Qy 434 IR-TVFGTEP--DMIRDG--STIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQNEKI 484

Db 468 LRETVLESSPILTLNESFISTWSLVKLEELQNKQ-----ENSSHQKL 511

RESULT 454  
ADS44317  
ID ADS44317 standard; protein; 662 AA.

XX ADS44317;  
XX  
DT 02-DEC-2004 (first entry)  
DE Bacterial polypeptide #22747.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
XX bacterial polypeptide.

OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
DR WPI; 2004-061375/06.

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SQ

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 22747; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transforming plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 662 AA;

Query Match 3.6%; Score 94.5; DB 8; Length 662;

Best Local Similarity 19.1%; Pred. No. 34;

Matches 86; Conservative 61; Mismatches 166; Indels 137; Gaps 21;

Qy 99 PQLPDGQSLPIPPVIL--AELGSDPTKGTV-CFYGHL-----DVQPADR---- 140  
Db 254 PRYCPPAVVNPEHPLFLLYTSGTGPKGVVHCTGGYLLGAAATCKYVFDLHPTDRMGCA 313

Qy 141 GD-GWLT-DPYVLTEVDGKLYGRGAT-----DNKGPVLAWINAVSAF 180  
Db 314 GDVGWITGHTYI--VYGPLMLGAATLVFESTPAYPDYSRYWSVVERHRLTQWYIAPTAI 370

Qy 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFF--SGVDYIVISDNLW----- 231  
Db 371 RLLQKAGNEFVKHRRSSRLVLGSVG--EPIAPESFMWYEVVGEKRCACAVADTYQTETGS 428

Qy 232 -----ISQRKPAITYGTRGNSYFMVEVKCRD----QDFHSGTGGIL----- 269  
Db 429 HIVTSLGPVTPMKP---GSATLPFFGIDAVIIDPLTGKIIIEGNDVEGVLAIRSPWPSAA 484

Qy 270 -----HEPMADLVALL-----GSLVDSSGHILVPGIYDEVVPLTEEBEINTYKAIH 314  
Db 485 RTVWRGHDRYIDTYLKPYPGFYFTGDGATRDKGYIWIWIRGRVDDVVNISGHLST----- 539

Qy 315 LDLEEYRNSRVEKFLFDTKKEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 540 -----AEIEAALLSHDAVAESAVGVHDE-----LTGQAVNAF- 572

Qy 375 IRLVPHMNVSA-VEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQY-LAAKR 432  
Db 573 ILLKPGYEATVELEKELIMAVRSTIGPFASPRKLIFS-----DLPKTRSGKIMRR 622

Qy 433 AIRTVEGTEDMIRDGSTIPIAKMFQEIYVH 462  
Db 623 ILRKILAGEVDQIGDLSTLADPKVVEHIIH 652

RESULT 455  
AAG81127



CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 787 AA;  
  
Query Match 3.6%; Score 94.5; DB 6; Length 787;  
Best Local Similarity 20.4%; Pred. No. 45;  
Matches 104; Conservative 68; Mismatches 180; Indels 159; Gaps 29;  
  
QY 18 LLLERGMFSSPPPALLEKVFQYIDLH-----QDFVQTLKEWVAIESDSVQPVP 68  
Db 263 IVLERQKALGIVPPDTLSPINPYLDVPGNGETWPLQD---TVRPWDSLSDE----- 312  
QY 69 RFRQELF-RMMAVAADTLQRLGARV-----ASVDMGPQ-Q 101  
Db 313 --EKLCFRMAEVFAGFLSYTDAQIGRILDYLBESGQLDNTIIVISDNGASGEGGPNGS 370  
QY 102 LPDGQ-----SLPIPPVILAEGLSDPTKGTVCYFGHLDVQPADRGDW---LTDPYVL 151  
Db 371 VNEGKFENGVIDTVAESMKLFDHLGGPQT-----YNHYPI-----GWAMAFNTPY-- 415  
QY 152 TEVDGKLYGRGATDNKG----PVLAWINAVSAFFALEQDLPVNIKFI-----IEGMEEA 201  
Db 416 -----KLFKRYASHEGGIADPAIISWPNGIAAHGEI-RDNYVNVSDITPTVYDLLGMTTP 469  
QY 202 GSVALEELVEKEKDRFFSGVDYI-VISDNLWISQKKPAITYGTRGNSYEMVEVKCRDQDF 260  
Db 470 GTV--KGIPQKPM-----GVSFIAALAD-----PAADTGKTTQFTYMLGTR---GIW 512  
QY 261 HSGTGGGILHEPM-----ADLVALLGSLVD--SSGHILV---PGIYDEVVPLTEESIN 308  
Db 513 HEGWFANTIHAATPAGWSNMFNADRWELFHIAADRSQCHDLAAEHDPKLEELKALWFSEAA 572  
QY 309 TYKAIHL-DLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPPTKTVIPG 367  
Db 573 KYNGPLPLADLNLLETWTRSRPYLVSERASYVY---YPCDADVGI-----GAAVEIRG 621  
QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRH-----LEDVFSKRNSSNKMVVSMT 412  
Db 622 R---SFAVLADVTTIDTTGAEGVLFKHGGAGHGHVLFVRDGRHLHYVYNFLGERQQLVSSS- 677  
QY 413 LGLHPWIANIDDTQYLAAKRAIRTVFGTEPD '443  
Db 678 -----GPVPSGRHLLGVRYLRT--GTVPN 699  
  
RESULT 457  
ABB70130  
ID ABB70130 standard; protein; 983 AA.  
XX  
AC ABB70130;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 37182.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.

XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
DR N-PSDB; ABL14233.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 37182; 2lpp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 983 AA;  
  
Query Match 3.6%; Score 94.5; DB 4; Length 983;  
Best Local Similarity 18.8%; Pred. No. 63;  
Matches 113; Conservative 87; Mismatches 209; Indels 193; Gaps 30;  
  
QY 48 EFVQTLKEWVA---IESDSVQVPVPRFQEL-----FRMMAVAADTLQRLGARV-AS 94  
Db 149 DFLEESTDYAADYSSEGSSVTHSPRHRSTTTIGSPLAREFRATAKMAQVIQRFSGSMEGR 208  
QY 95 VDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT-----VCFYG---HL---DV 135  
Db 209 IDEHPENGSAACS--PPELSTQQQLEALQANELRRKREARQALRVFVQLVHLKSGSDL 265  
QY 136 QPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAWINA-----VSAFR- 181  
Db 266 VAMDKNG--LSDPYVKFKVGGRLHLKSRTHRDLPVWDEVFIVPIEDFPQPIIVKVFYD 323  
QY 182- --ALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLW-ISQKPA 238  
Db 324 DWGLQDDFMGSAKLDLTQLELGAEDIHLQLCDSSGNGGSLGEILNLTLWPRSQEDKE 383  
QY 239 IT-----YGTR-----GNSY-----FMVEVKCRDQDFHSGTGGILHEPMAD 275  
Db 384 MTCVKVTHNDIWSRARIMLGNWPGCKRAPRMVLKHVRRQHEELREQ-----LEQGCDD 438  
QY 276 LVALLG-----LVDSSGHILVPGIYDEVV-----PLTEE--EIN- 308  
Db 439 LMEVAESYFPDVLQHFQNSKLAESSKR-LKSQIWSVVTTILLVKAKDPLAEDGSKLND 497  
QY 309 TYKAIHLDLEEYRNSR-----VEKF---LFDTKKEILMHLWRYPSL----- 347  
Db 498 THEKFRLGNEKYKSSWTERWLEQFDLHLFDEDDQNLLEIALWNRNTLYGKAIIDLVSFQR 557  
QY 348 -SIHGIEGAFDEPPTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFS-KRNSSN 405  
Db 558 ENTHGIWKPLED-----CPGEV-----HMLTISGTTALETISDLKAFKEDPRE 601



QY 406 KMVVSMTGLHPWIANIDTQYLAAKRAIRTVFG----- 439  
Dd 602 AQLRERYKFLRCLQNLRDVGHLTVK-----VFGATGLAAADIGKSDPFCVLELGNARL 656  
QY 440 -TEPDMIRGSTIPIAKMFOR-----IVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGT 493  
Dd 657 QTQTDNVKDITQVLEITVFDEDRDHRVFLGKLVIPLRIKSG-----VKRWYTLKDX 709  
QY 494 KL 495  
Dd 710 NL 711

RESULT 458  
ABU43125  
ID ABU43125 standard; protein; 1169 AA.  
XX  
AC ABU43125;  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #28652.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA46995.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 71049; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1169 AA;

Query Match 3.6%; Score 94.5; DB 6; Length 1169;  
Best Local Similarity 20.4%; Pred. No. 83;  
Matches 94; Conservative 70; Mismatches 167; Indels 129; Gaps 23;  
QY 34 LLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80  
Dd 732 LLGKDIQYKDLGLLIVDEEQFGVRHKEIKTKKNVDVLTLTATPIPTLH----- 783  
QY 81 AADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAE-----LGSDPTKGTVCFYGH 132  
Dd 784 ----MSMLGVR----DLSVIETPPENRFPQTVVLEQNTNFKEALERELSRDGOVFYLY 835  
QY 133 LDVQ----PADRGDWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP 188  
Dd 836 NKVQSIYEKREQLRLMPDANIAV-AHGQMTER---DLEETMLSFINH-----EYDIL 884  
QY 189 VNIKFIIEGMEEAAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTR-GNS 247  
Dd 885 VTTTIIETGVDVNA---NTLIIIEADRF--GLSQLY-----QLRGRVGRSSRIGYA 931  
QY 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMDL-VALLGSLVDSSGHILVPGI-Y 296  
Dd 932 YFLHPANKVLNETAEERLQAIKEFTELGSGFKIAMRDLNIRGAGNLLGKQHQGFIDSVGF 991  
QY 297 DEWVPLTEEEINTYKAI-----HLD-----LEEYNSSRV-- 326  
Dd 992 DLYSQMLEEAVNEKRGIKEESPDAPDIEVELHLDAYLPAEYIQSEQAKIEIYKKLRKQVET 1051  
QY 327 EKFLFDTKKEEILMHLWRYP-----SLSIH----GIEGAFDEPGTKTVIPGRVIGK 372  
Dd 1052 EEQLFDVKDELIDRFNDYPIEVERLLDIVEIKVHALHAGVELIKKGKSIQII----- 1104  
QY 373 FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNNKMVVSMT 412  
Dd 1105 LSPKATEDINGEELFKQ-TQPLGRAMKVGQVQNNAMNVTLT 1143

RESULT 459  
ABU24351  
ID ABU24351 standard; protein; 1253 AA.  
XX  
AC ABU24351;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #9878.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Clostridium botulinum.  
OS  
XX WO200277183-A2.  
PN  
XX 03-OCT-2002.  
PD  
XX 21-MAR-2002; 2002WO-US009107.  
PF  
XX 21-MAR-2001; 2001US-00815242.  
PR























XX 04-NOV-2004 (first entry)  
XX Staphylococcus epidermis polypeptide seqid 5267.  
DE antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
XX recombinant expression vector; infection; computer readable medium;  
KW computer based system.  
KW Staphylococcus epidermidis.  
XX US2004147734-A1.  
XX 29-JUL-2004.  
XX 01-DEC-2003; 2003US-00724972.  
XX 08-NOV-1997; 97US-0064964P.  
PR 13-AUG-1998; 98US-00134001.  
PR 29-NOV-1999; 99US-00450969.  
XX (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
XX Doucette-Stamm L, Bush D;  
PI WPI; 2004-580138/56.  
XX N-PSDB; ADS02200.  
DR New isolated polypeptide and encoding nucleic acid derived from  
XX Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
PT treating an S. epidermidis bacterial infection.  
XX Claim 17; SEQ ID NO 5267; 741pp; English.  
PS The invention describes an isolated nucleic acid comprising a nucleotide  
XX sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
CC given in the specification. Also described are: a recombinant expression  
CC vector; a cell comprising a recombinant expression vector of (1);  
CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection, comprising a nucleic acid cited above and a carrier; treating  
CC a subject for S. epidermidis infection; a recombinant or substantially  
CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
CC sample; a computer readable medium having recorded in it the nucleotide  
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
CC system for identifying fragments of the Staphylococcus genome of  
CC commercial importance; a computer based system for identifying fragments  
CC of the Staphylococcus plasmids of commercial importance; identifying  
CC commercially important nucleic acid fragments of the Staphylococcus  
CC genome and/or plasmids; and identifying an expression modulating fragment  
CC of the Staphylococcus genome and/or plasmids. The methods and  
CC compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of an Staphylococcal epidermidis bacterial  
CC infection. This is the amino acid sequence of a S. epidermis protein of  
CC the invention.  
XX  
SQ Sequence 823 AA;  
Query Match 3.6%; Score 94; DB 8; Length 823;  
Best Local Similarity 24.2%; Pred. No. 53;  
Matches 61; Conservative 32; Mismatches 101; Indels 58; Gaps 13;  
The  
QY 269 LHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEBEINTYK-----AIHLDLLEYRNS 323  
Db 393 LPDKAIDLIDEASSKVLKSH-TTPSNLKEI----EQEIDKVKNEKDAAVH--AQEFENA 445  
QY 324 -----SRVEKFLFDTKBEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 376

Db 446 ANLRDKQSKLEKQYEDAKNE-----WKNAQ---GGLDTALSENIAEVIAGWT----- 490  
QY 377 LVPHMNVSAVEKQVTRHLEDVFSKR-----NSSNMKVSVMTGLGHPWIANIDDTQYL 428  
Db 491 GIPLTKINETESDRLNLEDTLHKRVIGQNDVANSISKAVRRARAGLKDKPRPICSFIFL 550  
QY 429 A-----AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPLGAV--DDGE 477  
Db 551 GPTGVGKTELARALAESMFEGDDAMIR-----VDMSEFMKHAVSRVLVGAPPGYVGHDDG- 605  
QY 478 HSQNEKINRWNY 489  
Db 606 GOLTEKVRKPY 617  
RESULT 471  
ABM67688  
ID ABM67688 standard; protein; 852 AA.  
XX  
AC ABM67688;  
XX 20-NOV-2003 (first entry)  
DT Photorhabdus luminescens protein sequence #785.  
XX  
DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX Photorhabdus luminescens.  
XX WO200294867-A2.  
PN 28-NOV-2002.  
XX 07-FEB-2002; 2002WO-IB003040.  
PF 07-FEB-2001; 2001FR-00001659.  
XX (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
XX WPI; 2003-148459/14.  
DR Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
PT Claim 2; SEQ ID NO 785; 1205pp; French.  
XX The invention relates to the isolation of genes and their encoded  
PS proteins from Photorhabdus luminescens. The isolated sequences are  
XX sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.











XX	PR	09-APR-1999;	99US-0128706P.
XX	PA	(GENO-) GENOME THERAPEUTICS CORP.	
XX	PI	Breton GL;	
XX	DR	WPI; 2003-895291/82.	
DR	DR	N-PSDB; ADF03725.	
XX	XX	New Proteus mirabilis polypeptides and polynucleotides, useful as	
PT	PT	reagents for diagnosis of bacterial disease, as components of	
PT	PT	antibacterial vaccines, as targets for antibacterial drugs, or as	
PT	PT	biocontrol agents for plants.	
XX	PS	Disclosure; SEQ ID NO 8182; 870pp; English.	
XX	CC	The invention relates to new Proteus mirabilis polypeptides and	
CC	CC	polynucleotides. The invention also relates to antibodies against the	
CC	CC	polypeptides, methods for producing the polypeptides, a method of	
CC	CC	generating vaccines for immunising an individual against P. mirabilis,	
CC	CC	method for evaluating a compound for the ability to bind a P. mirabilis	
CC	CC	polypeptide and a method for screening test compounds for anti-bacterial	
CC	CC	activity. The polypeptides and polynucleotides are useful as molecular	
CC	CC	targets for diagnosing, preventing and treating pathological conditions	
CC	CC	resulting from bacterial infection, as reagents for diagnosis of	
CC	CC	bacterial diseases, as components of antibacterial vaccines, as targets	
CC	CC	for antibacterial drugs or as bio-control agents for plants. This	
CC	CC	sequence represents a Proteus mirabilis polypeptide of the invention.	
XX	XX	Sequence 412 AA;	
SQ			
Query Match 3.6%; Score 93.5; DB 7; Length 412;			
Best Local Similarity 20.5%; Pred. No. 20;			
Matches 84; Conservative 61; Mismatches 154; Indels 111; Gaps 20;			
QY	88	LGARVASVDMGQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRG-----	141
Db	56	LGKVGSGIS---QNFKDGSG-----ITTNRPDTVAISGGFPRIEDSNGGVFYSRN	103
QY	142	-----DGLWLT-----PYVLTEVDGK-LYGRGATDNKGPVLAWINAVSAFRALEQD	186
Db	104	GEFGKDKNGYLTNMQGMRITGYPVQVNDGKVVQKGATPT--PIIPTDMNNASATDKMD	161
QY	187	LPVNIKFIIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN	246
Db	162	MTVN-----LNSAEAAIDQTHKFDPKDNDY-----NFSNV-----TTYDSLGN	202
QY	247	SY-----FMVEVKRD-----QDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYD	297
Db	203	EHNLNLFVFKTKDNEWSVYAQDTTGT-----EPAQD-----LGKLVYKDN-----GVLD	246
QY	298	EWVP-LTEEEINTYKAIH-LDLEEYRNSSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGA	355
Db	247	ETAPKLNFTTVAYKGSQPMDEMNFSGTQOKVAESSVSKLAQNGYQAGEFTNFRIEPD	306
QY	356	FDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKNMNVSMTLGL	415
Db	307	GSIMATYSNQSQVVQG--IALANFANPGLSSQG-----DNMWSETNGSGSPIGVV----	356
QY	416	HPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS V	465
Db	357	-----ACSGVFGLTNNALAESNV---DMSQELVNMI V	386
RESULT 478			
ADQ35183			
ID	ADQ35183 standard; protein; 431 AA.		
XX			
AC	ADQ35183;		
XX			
DT	07-OCT-2004 (first entry)		
XX			

DE	Human TRIP13 amino acid sequence SEQ ID NO:11.
XX	
KW	thyroid hormone receptor interacting protein 13; TRIP13;
KW	thyroid hormone receptor interacting protein 13 modulator;
KW	TRIP13 modulator; antineoplastic; cytostatic; cancer therapy; cancer;
KW	breast cancer; colon cancer; lung cancer; prostate cancer; tumour; human;
KW	chromosome 5.
XX	
OS	Homo sapiens.
XX	
PN	WO2004058050-A2.
XX	
PD	15-JUL-2004.
XX	
PF	19-DEC-2003; 2003WO-US040701.
XX	
PR	20-DEC-2002; 2002US-0434918P.
PR	17-APR-2003; 2003US-0463577P.
XX	(AVAL-) AVALON PHARM.
PA	Augustus M, Horrigan S, Cain C, Strovel JW;
XX	
PI	WPI; 2004-525766/50.
XX	N-PSDB; ADQ35177, ADQ35178.
DR	
DR	Identifying modulators of thyroid hormone receptor interacting protein 13
XX	(TRIP13) gene or polypeptide, for treating cancer, by contacting a TRIP13
PT	-expressing cell with a compound, and detecting a change in gene
PT	expression or activity.
PT	
XX	Claim 9; SEQ ID NO 11; 64pp; English.
PS	
XX	The present invention describes a method for identifying an agent that
CC	modulates thyroid hormone receptor interacting protein 13 (TRIP13) gene
CC	or TRIP13 polypeptide biological activity. The method comprises: (a)
CC	contacting a test compound with a cell that expresses a TRIP13 gene or
CC	with a TRIP13 polypeptide; and (b) determining a change in the gene
CC	expression or biological activity, where a change in the expression or
CC	biological activity indicates modulation of gene or biological activity,
CC	thus identifying the test compound as a gene modulating agent. Also
CC	described: (1) a method for identifying an antineoplastic agent; (2) a
CC	method for detecting the cancerous status of a cell comprising detecting
CC	elevated expression in the cell of at least one gene corresponding to a
CC	polynucleotide comprising a sequence of 2602, 2034, 1908, 2538, 2240, or
CC	1672 bp (SEQ ID NO: 1-6, ADQ35173 to ADQ35178), where an elevated
CC	expression indicates the cancerous status of the cell; (3) a method for
CC	detecting a cancer-linked gene; (4) a method for detecting cancer or a
CC	disposition toward developing cancer; (5) a method for monitoring the
CC	progress of cancer therapy in a patient; (6) a method for determining the
CC	likelihood of success of cancer therapy in a patient; (7) a method for
CC	producing test data with respect to the anti-neoplastic activity of a
CC	compound; (8) a method for determining the progress of treatment for a
CC	patient afflicted with cancer, following commencement of a cancer
CC	treatment on the patient; (9) a method for determining survival prognosis
CC	of a patient afflicted with cancer; (10) a method for determining the
CC	likelihood of survival of a patient afflicted with cancer, following
CC	commencement of a cancer treatment on the patient; and (11) a method for
CC	diagnosing cancer. The TRIP13 modulator has cytostatic activity. The
CC	method is useful for identifying an agent that modulates the TRIP13 gene
CC	or TRIP13 polypeptide biological activity. Agents identified from the
CC	method are useful for treating a cancer (e.g. cancer of breast, colon,
CC	lung or prostate tissues) to cause a reduction in cancerous activity of
CC	the cell. TRIP13 genes are useful as diagnostic marker for tumour state,
CC	stage and grade, as a prognostic marker to predict response to therapy,
CC	as a target for therapeutic molecule, or as a marker for screening for
CC	drug activity based on the activity of the protein, transcriptional state
CC	of the gene or target genes activated by TRIP13. The human TRIP13 gene is
CC	located on chromosome 5, more specifically to region 5p15. The present
CC	sequence represents a TRIP13 protein, which is used in the
CC	exemplification of the present invention.
XX	Sequence 431 AA;
SQ	



Query Match 3.6%; Score 93.5; DB 8; Length 431;  
Best Local Similarity 20.1%; Pred. No. 22;  
Matches 74; Conservative 59; Mismatches 129; Indels 107; Gaps 19;

QY 158 LYGRGATDNKGPVL-----AWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEEL 209  
Db 3 LPGVGQTQRRGQTFTDPPYVHGGWIEVST---AKKEDINLSVR-----KL 44

QY 210 VEXEKDRFFSGVDYIIVISDNLWISQKPKAITYGTRGNSYFMVEVKCRD----- 257  
Db 45 LNRHN-----IVFGDYTWTEFDEPFLTRNVQSVSIIDTELKVKDSQPIDLSACTVA 95

QY 258 -----QDFHSGTGGILHEPMADLVALLGSLVDSSGHILVP-----GIYDEVVPLTSEEIN 308  
Db 96 LHIFQLNEDGPSSSENLEETEENIIA-----ANHWVLPAAEFHGLWDSLV--YDVEVK 145

QY 309 TYKAIHLDLLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGT-KTVIPG 367  
Db 146 SHLLDYVMTLLFSDKNVNSNLITWNRVVLH-----GPPGTGKTSCLK 189

QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK-RNSSNMVVSMTLGLHPMIAN----- 421  
Db 190 ALAQKLTIRLSSRYRYQL-IEINSH--SLFSKWFSESGKLVTKMFQKIQDLDDKDALV 246

QY 422 ---IDDTQYL-AAKRAIRTVFGTEP-DMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDG 476  
Db 247 FVLIDEVESLTAARNACRA--GTEPSDAIRVVNAV-LTQIDQIKRHSNVVILTTSNI--- 300

QY 477 EHSQNEKIN 485  
Db 301 -----TEKID 305

RESULT 479  
ABO74061  
ID ABO74061 standard; protein; 472 AA.  
XX  
AC ABO74061;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #6236.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
PF 18-FEB-1999; 99US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
XX  
PR 27-JUL-1998; 98US-0094190P.  
XX  
RA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
DR WPI; 2003-615309/58.  
DR N-PSDB; ABD07632.  
XX  
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 22807; 455pp; English.  
XX  
CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,

CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 472 AA;

Query Match 3.6%; Score 93.5; DB 7; Length 472;  
Best Local Similarity 25.1%; Pred. No. 25;  
Matches 50; Conservative 25; Mismatches 73; Indels 51; Gaps 9;

QY 30 PPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLG 89  
Db 5 FVPRLAEK-----HQEKA-----TIMHTIQLQQSPSFAVELHQ---AASGRLGQIE 47

QY 90 ARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGLDVPADRGDWLTDPY 149  
Db 48 ARQVATPSEAQQLAQRQDAPKGEGLLARLGAALVRPFVAIM-----DWL---- 91

QY 150 VLTEVDGKLYGRGATDNKGPVL-----AWINAVSAFR--ALEQDLPVNIKFIEGMEEAGS 203  
Db 92 -----GKLLGSHARTGPQPSQDAQPAVMSSAVVFKQMVLLQALPMTLK----GLDKASE 141

QY 204 VA--LEELVEKEKDRFFSG 220  
Db 142 LATLTPEGLAREHSRLASG 160

RESULT 480  
ABP38493  
ID ABP38493 standard; protein; 535 AA.  
XX  
AC ABP38493;  
XX  
DT 24-JUL-2002 (first entry)  
XX  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3338.  
XX  
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
XX antibacterial; gene therapy.  
OS Staphylococcus epidermidis.  
XX  
PN US6380370-B1.  
XX  
PD 30-APR-2002.  
XX  
PF 13-AUG-1998; 98US-00134001.  
XX  
PR 14-AUG-1997; 97US-0055779P.  
XX  
PR 08-NOV-1997; 97US-0064964P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2002-381255/41.  
XX  
DR N-PSDB; ABN91038.  
XX  
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis  
PT polypeptide, useful for diagnosing and treating bacterial infections.  
XX  
PS Disclosure; SEQ ID NO 3338; 267pp; English.  
XX

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
CC antibacterial activity and can be used in gene therapy. The sequences can  
CC also be used in the diagnosis and treatment of bacterial infections,  
CC particularly S. epidermidis infections. The sequences can be used to  
CC screen for compounds able to interfere with the S. epidermidis life cycle  
CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from the USPTO web site

XX SQ Sequence 535 AA;

Query Match 3.6%; Score 93.5; DB 5; Length 535;  
Best Local Similarity 20.4%; Pred. No. 30;  
Matches 94; Conservative 70; Mismatches 167; Indels 129; Gaps 23;

QY 34 LLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPRFRQELFRMAV 80  
Db 98 LLGKDIQYKDLGLLIVDEEQRFVGRHKEIKTKGNVDVLTATPIPTLH----- 149  
QY 81 AADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE-----LGSDPTKGTVCFYGH 132  
Db 150 ----MSMLGVR---DLSVIETPPENRFPVQTYVLEQNTNFIKEALERLSRDGQVFYLY 201  
QY 133 LDVQ----PADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP 188  
Db 202 NKVQSIYEKREQLQMLMPDANIAV-AHQQMTER---DLEETMLSFINH-----EYDIL 250  
QY 189 VNIKFIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPKAITYGTR-GNS 247  
Db 251 VTTIITETGVDVPNA---NTLIIIEADRF--GLSQLY-----QLRGRVGRSSRIGYA 297  
QY 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMADL-VALLGSLVDSSGHILVPGI-Y 296  
Db 298 YFLHPANKVLNETAEERLQAIKEFTELGSGFKIAMRDNLNIRGAGNLLGKQHGFDISVGF 357  
QY 297 DEVVPLTEEEINTYKAI-----HLD-----LEEYRNSRV-- 326  
Db 358 DLYSQMLEEAVNEKRGIKERSPDAPDIEVELHLDAYLPAEYIQSEQAKIEIYKLRKVET 417  
QY 327 EKFLDFTKEEILMHLWRYP-----SLSIH---GIEGAFDEGCTKTVIPGRVIGK 372  
Db 418 EEQLFDVKDELIDRENDYPIEVERLLDIVEIKVHALHAGVELIKDKGKSIQII----- 470  
QY 373 FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKNVVSMT 412  
Db 471 LSPKATEDINGEELFKQ-TQPLGRAMKVGQVQNNAMNVTILT 509

RESULT 481  
ADS04661  
ID ADS04661 standard; protein; 535 AA.  
XX  
AC ADS04661;  
XX  
DT 04-NOV-2004 (first entry)  
DE  
DE Staphylococcus epidermis polypeptide seqid 3956.  
XX  
XX antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
KW recombinant expression vector; infection; computer readable medium;  
KW computer based system.  
XX  
OS Staphylococcus epidermidis.  
XX  
XX US2004147734-A1.  
PN  
XX  
PD 29-JUL-2004.  
XX  
XX 01-DEC-2003; 2003US-00724972.  
PF  
XX 08-NOV-1997; 97US-0064964P.  
PR

PR 13-AUG-1998; 98US-00134001.  
PR 29-NOV-1999; 99US-00450969.  
XX  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
XX  
PI Doucette-Stamm L, Bush D;  
XX  
XX WPI; 2004-580138/56.  
DR N-PSDB; ADS00889.  
XX  
PT New isolated polypeptide and encoding nucleic acid derived from  
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
PT treating an S. epidermidis bacterial infection.  
XX  
PS Claim 17; SEQ ID NO 3956; 741pp; English.  
XX

CC The invention describes an isolated nucleic acid comprising a nucleotide  
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
CC given in the specification. Also described are: a recombinant expression  
CC vector; a cell comprising a recombinant expression vector of (1);  
CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection, comprising a nucleic acid cited above and a carrier; treating  
CC a subject for S. epidermidis infection; a recombinant or substantially  
CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
CC sample; a computer readable medium having recorded in it the nucleotide  
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
CC system for identifying fragments of the Staphylococcus genome of  
CC commercial importance; a computer based system for identifying fragments  
CC of the Staphylococcus plasmids of commercial importance; identifying  
CC commercially important nucleic acid fragments of the Staphylococcus  
CC genome and/or plasmids; and identifying an expression modulating fragment  
CC of the Staphylococcus genome and/or plasmids. The methods and  
CC compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of an Staphylococcus epidermidis bacterial  
CC infection. This is the amino acid sequence of a S. epidermis protein of  
CC the invention.

XX SQ Sequence 535 AA;

Query Match 3.6%; Score 93.5; DB 8; Length 535;  
Best Local Similarity 20.4%; Pred. No. 30;  
Matches 94; Conservative 70; Mismatches 167; Indels 129; Gaps 23;

QY 34 LLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPRFRQELFRMAV 80  
Db 98 LLGKDIQYKDLGLLIVDEEQRFVGRHKEIKTKGNVDVLTATPIPTLH----- 149  
QY 81 AADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE-----LGSDPTKGTVCFYGH 132  
Db 150 ----MSMLGVR---DLSVIETPPENRFPVQTYVLEQNTNFIKEALERLSRDGQVFYLY 201  
QY 133 LDVQ----PADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP 188  
Db 202 NKVQSIYEKREQLQMLMPDANIAV-AHQQMTER---DLEETMLSFINH-----EYDIL 250  
QY 189 VNIKFIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPKAITYGTR-GNS 247  
Db 251 VTTIITETGVDVPNA---NTLIIIEADRF--GLSQLY-----QLRGRVGRSSRIGYA 297  
QY 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMADL-VALLGSLVDSSGHILVPGI-Y 296  
Db 298 YFLHPANKVLNETAEERLQAIKEFTELGSGFKIAMRDNLNIRGAGNLLGKQHGFDISVGF 357  
QY 297 DEVVPLTEEEINTYKAI-----HLD-----LEEYRNSRV-- 326  
Db 358 DLYSQMLEEAVNEKRGIKERSPDAPDIEVELHLDAYLPAEYIQSEQAKIEIYKLRKVET 417







Db 98 LGSEAAQHPPEVRGLWQTCGELMFSLPRLHLGLGKEGITYTFSGNCTMEDAKLAQDF 157  
QY 97 MGPOQLP-----DQSLPIPPVILAE-LGSDPT-----KGTVCFYG 131  
Db 158 LDSQNL SAYNTRLFKEVDGEGKPYEVRLASVLGSEPSLDSEVTSKLSYEFRGSPQVT 217  
QY 132 HLDVQP-----ADRGDWLTDPPVLTVDGKL--YGRGA---TDNKGVPV 170  
Db 218 RGDYAPILQKVVEQLEKAKAYAANSHQOMLAQYIESFTQGSIEAHKRGRSFWIQDKGPI 277  
QY 171 L-AWINAVSAFRALEQDLPVNIKPIIEG---MEEAGSVALEELVEK----- 212  
Db 278 VESYIGFIESYRD-----PFSRGEFEGFVAVVNKAMSAKFERLVASAEQLLKELPWPPT 332  
QY 213 -EKDRF---FSGVDYIVIS-----DNLWISQ-----RKPAITYGTRGN 246  
Db 333 FEKDKFLTPDFTSLDVLTFAGSGIPAGINIPNYDDLROTEGFKNVSLGNVLAVAYATQRE 392  
QY 247 SYPMVEVKCRDQDFHSGTGGILHEPMDLVALGSLVDSSGHILVPGIYDE----- 298  
Db 393 KLTFLEED--DKOLYI-LWKGPSFDVQVGLHELLG---HSGKLFV---QDEKGA FNFDQ 443  
QY 299 ---VVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTK-----EELMLHLW 342  
Db 444 ETVINPETGEIQISW-----YRSGE-----TWDSKFSTIASSEYECRAESVGLYLC 489  
QY 343 RYPS-LSIHGIEGA 355  
Db 490 LHPQVLEIFGFEGA 503

RESULT 485  
ABU33126  
ID ABU33126 standard; protein; 763 AA.  
XX AC ABU33126;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #18653.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Legionella pneumophila.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA36996.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 61050; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 763 AA;

Query Match 3.6%; Score 93.5; DB 6; Length 763;  
Best Local Similarity 19.6%; Pred. No. 53;  
Matches 73; Conservative 57; Mismatches 137; Indels 105; Gaps 17;  
QY 141 GDGWLTDPPVLTVDG-----KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI-KF 193  
Db 127 GNGW----YQMLNMEGATLLLAMFLVGTWLTG--LSWIKAIELIGCYTLNLTFLDKF 180  
QY 194 IIEGM-----BEAGSVALEELVEKEKDRFFSGVDYIVISD 228  
Db 181 IRKGMQIISENFENKEKLKTLIKTEQLPKPDNEKKKSVPKLFQDKKDEKEKATPVLIA- 239  
QY 229 NLWISQRKPAITYGTRGNSY-----FMVEVKCRDQDFHSGTGGILHEPMDL 276  
Db 240 ----SEEKPEIVKPT--NEFKEIRPPKTTIPGALPSLSLLDKGQPKPMGGYTHEELES 293  
QY 277 VALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEE 336  
Db 294 SR-----DVEQHLLDFGIQADVAVHGPVVT--RPELQLAAGVKVSKLTALAKDLARS 345  
QY 337 ILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLE- 395  
Db 346 LSV-----ISVRVVE-----VIPGKTV--VGLELPNH-----SRQVVRLSDV 380  
QY 396 ---DVFSKRNSNKMVMVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 452  
Db 381 LSADVYQQAHSPLSLALGVDIGGHPMVVDL-----AKMPHLLVAGT-----TGSGKSVG 429  
QY 453 IAKMFQEIIVHKS 464  
Db 430 INAMILSILFKA 441

RESULT 486  
ADC26275  
ID ADC26275 standard; protein; 1459 AA.  
XX  
AC ADC26275;  
XX  
DT 18-DEC-2003 (first entry)  
XX





DR WPI; 2003-029926/02.  
DR N-PSDB; ACA24307.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 48361; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1487 AA;

Query Match 3.6%; Score 93.5; DB 6; Length 1487;  
Best Local Similarity 18.8%; Pred. No. 1.5e+02;  
Matches 84; Conservative 61; Mismatches 136; Indels 167; Gaps 24;  
QY 99 PQQLPDQSLPIPPVILAEELGSDPTKGTVCYGHLDVQPADRGDW-----L 145  
DB 701 PEDIED--SLDTDIIAYIQLGA---GSVCRINNFIQIEIGDTATGWKPAKPKDSFTESKKY 754  
QY 146 TDPYVLTVDGKL-----YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195  
DB 755 TDTQILA-VDGKIELSVKTKVENLGIGANNLYSYTSSLNTLYPSPTIERQMSLHGFLV 813  
QY 196 EGMEEAGSVALEELVEKEKDRF-FSGVDYIVISDNLWI--SQRKPAITYGTRGNSYFMVE 252  
DB 814 GSQNGGAMRIPNIPIPGKYTVSG-----WIKGSQNTP----- 848  
QY 253 VKCRDQDFHSGTGGILHEPMADLVALLGSLVD--SSGHILVPGIYD-----EVV 300  
DB 849 -----VGFTDVCDSENVIVKSTADNQSFKHTFNVT 881  
QY 301 PLTEEEINTYKAHLDLEBYRNSRVEKFLFTKKEILMHLW-----RYPSSL 348  
DB 882 KNTEEKQDVNFVDIERIDWA-YIWKQDFKVEAGE--IATAWSPNFQDAVYKGAETNSQ 938  
QY 349 IHGIEGAFDEPGTKTV-----IPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 403  
DB 939 ISWVEGKI---TSIVKEKINTVDGRVTGLAS-----RVEQTEKSITSVVGDI-GVINS 986  
QY 404 SNKMVWSMTLGLHPMTIANIDDTQYLAAKRAIRTVFGTEPDMIRGDSITPIAKMFQEIIVHK 463

Db 987 TTNRHISKRIDLRGW-----DNNKFF-----PLVI-----SIP-----VYHK 1018  
QY 464 SVVLI--PLGA-----VDDGEHSQN 481  
Db 1019 TRVEISRPLDAGYKPSYGYTHDGGFSMN 1046  
RESULT 488  
ADM97582  
ID ADM97582 standard; protein; 1488 AA.  
XX  
AC ADM97582;  
XX  
DT 01-JUL-2004 (first entry)  
XX Human calcium-independent alpha-latrotoxin receptor.  
DE  
XX receptor; human; calcium-independent alpha-latrotoxin receptor;  
KW homologue; cardiant; cytostatic; antiinflammatory; haematological;  
KW gastrointestinal; hepatotropic; nootropic; neuroprotective; vasotropic;  
KW gynaecological; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2004031235-A1.  
XX  
PD 15-APR-2004.  
XX  
XX 07-OCT-2003; 2003WO-EP011059.  
PF  
XX 07-OCT-2002; 2002US-0416270P.  
PR 08-APR-2003; 2003US-0460967P.  
XX  
PA (FARB ) BAYER HEALTHCARE AG.  
XX  
XX Smolyar A;  
XX  
DR WPI; 2004-347961/32.  
DR N-PSDB; ADM97581.  
XX  
PT New polynucleotide encoding a calcium-dependent alpha-latrotoxin receptor  
PT polypeptide, useful for treating diseases, e.g. cardiovascular disorder,  
PT cancer, inflammatory disease, or respiratory disease.  
XX  
XX Claim 2; Fig 2; 147pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC calcium-independent alpha-latrotoxin receptor (homologue 1). The  
CC sequences are useful for the preparation of a medicament for modulating  
CC the activity of a calcium-dependent alpha-latrotoxin receptor in a  
CC disease, such as cancer, a gastrointestinal or liver disorder, a CNS  
CC disorder, a cardiovascular disorder, an inflammatory disease, a  
CC hematological disease, or respiratory diseases, a reproductive disorder  
CC or a genitourinary disorder. The polypeptides may also be used to  
CC identify compounds which may act as activators or inhibitors at the  
CC enzyme's active site, to raise specific antibodies which can block the  
CC enzyme and effectively reduce its activity, as a bait protein in a two-  
CC hybrid or three-hybrid assay to identify other proteins which bind to or  
CC interact with the human methionine aminopeptidase-like protein  
CC polypeptide and modulate its activity, and for immunization of mammals.  
CC The present sequence is the protein of the invention.  
XX  
SQ Sequence 1488 AA;  
Query Match 3.6%; Score 93.5; DB 8; Length 1488;  
Best Local Similarity 20.4%; Pred. No. 1.5e+02;  
Matches 100; Conservative 63; Mismatches 159; Indels 167; Gaps 25;  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGFQQLPDGQSLP-----IPPV-----ILA 116  
Db 417 ELFKTIIISTTSTTSQKGPMSSTTV-AGSQEGSKGTKPPPAVSTTKIPITNIPPLPERFCE 475  
QY 117 ELGSDPTKGTVCYGHLDVQPADRGDWLTDPYVLTVDGKLYGRGATDNKGPVLA---- 172

Db 476 ALDSKGIKWPQTQGMVVERPCPKGTRG-TASYLC-----MISTGTWNPKGPDLSNCTS 528

Qy 173 -WINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSG-----VDY 223

Db 529 HWNQLAQ-----KIRGENAASLA-NELAKHTKGPVFAQDVSSSVRLMEQ 573

Qy 224 IVISDNLWISQKPAITYGTRGNSYFMV---EVKCRDQDFHSGTGGILHEPMDLVAL 280

Db 574 LVDILDAQLELKPS-EKDSAGRSYNKLQKREKTCR-----AYL 611

Qy 281 GSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHLDLEEVNSSRVEKFLFDTKEEILMH 340

Db 612 KAIVDTVDNLLRP-----EALSWK--HMNSSEQAHTATM---LLDTLE----- 650

Qy 341 LWRYPSLSIHGIEGAFD-----EPGKTVPGRVIGKFSIRLVPHMNVSAVEKQV---- 390

Db 651 -----EGAFVLADNLEP-TRVSM-----TENIVLEAVLSTEGQIQDFK 690

Qy 391 -----TRHLEDVFSKRNSNM-----VVSMTLGLHPWIANIDDTQYLAKRAIR 435

Db 691 FPLGIKAGSSIQLSANTVKQNSRNLAKLVFIYRSLG-----QFLSTENA-- 737

Qy 436 TVFGTEPMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINR 486

Db 738 -TIKLGADFIGRNSTIAVNSHVISVINKESSRVYLTDPVLFTLPHIDPDNYF-NANCSF 795

Qy 487 WNYIEGTKL 495

Db 796 WNYISERTWM 804

RESULT 489

ABU49364

ID ABU49364 standard; protein; 1613 AA.

XX

AC ABU49364;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #34891.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Vibrio cholerae.

XX

PN W0200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR N-PSDB; ACA53234.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 77288; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 1613 AA;

Query Match 3.6%; Score 93.5; DB 6; Length 1613;

Best Local Similarity 18.9%; Pred. No. 1.7e+02;

Matches 110; Conservative 74; Mismatches 211; Indels 187; Gaps 25;

Qy 32 PALLEKVFQYI---DLHQDEFVQTLKEWVAIESDSVQVPRFRQELF----- 75

Db 9 PVLEKVVQLIQDKLELAQQLVTQLGQHLFSNISQDDLVERNESDLYGAVLSLWHHINE 68

Qy 76 -----RMMAVAADTLQRLGARVASVDMGPPQQLPDGSL-PIPPVILAELGSDP---TKGT 126

Db 69 KKADERSVRVFNPTVSRQGWQ-STHTIVEIVLPSDFLVDISIKMALSRLGLASHMLNGP 127

Qy 127 VCFYGHLD--VQPADRCGWLTDPPVLTVEVDGKLYGRGATDNKGPVLAWIN----- 175

Db 128 AHIAHDDGSIKSINQEGEQLTSMFHI-EVDRLLSXEEMTELKNELLDILHDTALVVKDW 186

Qy 176 -----AVSAFRALEQDLPV-----NIKFIIEGMEEAGSVALEELV 210

Db 187 KPNATKLEQVINQLEADKKQIPVEAERLQETIQFLRWLGNHNFMTMGYKEF-----DLV 240

Qy 211 EKEKDR-----FFS-----GVDYIVISDNLWISQKPAITYGTRGNSYFMVEV 253

Db 241 EKNGDTELTPTKDTGLGFLSDNERVRSVKLSQFPDSARLEAKKPFLLILTGNKQSR-- 298

Qy 254 KCRDQDFHSGTGGILHEP-MADLVALLGSLVDSGGHIL-----VPGIYD-----EVV 300

Db 299 -----HRPAYTDYIGI--KKFDAKGKVGIEHRFTGLYTSAVYNQSVEGI 340

Qy 301 PLTTEBIN-----TYKAHLDLEEVNSSRVEKFLFDTKEEILMHLWRYPSL 347

Db 341 PLIREKVGRILAAAGYRQGSYAYKALHNILENYPDE-----LLQAREEELLEVMG---- 391

Qy 348 SIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK----- 400

Db 392 ---GVVQMQRDRLRLFRVKDPFGRRFFSCMV-YVTKERYNTELRRKTKQVFKQYFGCEQD 447

Qy 401 -----RNSSNKMVSVMTLGLHPWIANIDDTQYLAKRAIRTVF 438

Db 448 VEFTTYFSESPLARTHYIVRVNNDNNINVDVKKIEQNLMEASTSWDD----RLAEAIVANF 503









Db 1321 KV 1322

RESULT 494

ADS93536

ID ADS93536 standard; protein; 1732 AA.

XX

AC ADS93536;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human MRCK2 protein sequence SegID2.

XX

KW human protein kinase; MCRK2;

KW myotonic dystrophy kinase-related Cdc42 binding kinase 2; 1q42;

KW chromosome 1; pkinase\_C domain; DAG-PE; CNH domain;

KW cytoskeleton reorganisation; cytostatic; antiinflammatory;

KW antiarteriosclerotic; ophthalmological; antipsoriatic; antiasthmatic;

KW antiparkinsonian; antirheumatic; antiarthritic; neuroprotective;

KW muscular-Gen; osteopathic; cardiovascular-Gen; immunosuppressive;

KW cerebroprotective; vasotropic; anticonvulsant; anti-HIV; MRCK2-modulator;

KW gene therapy; inflammation; cancer; arteriosclerosis; psoriasis; asthma;

KW Parkinson's disease; rheumatoid arthritis; spinal cord injury;

KW muscle condition; osteoporosis; graft versus host disease;

KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;

KW epilepsy; ischaemia; reperfusion; breast cancer; ovarian cancer;

KW glioblastoma; non-Hodgkin's lymphoma; colorectal cancer;

KW non-small cell lung cancer; brain cancer; Kaposi's sarcoma;

KW pancreatic cancer; liver cancer; tumour; human; enzyme.

XX

OS Homo sapiens.

XX

PN WO2004033638-A2.

XX

PD 22-APR-2004.

XX

PF 07-OCT-2003; 2003WO-US031591.

XX

PR 07-OCT-2002; 2002US-0416257P.

XX

PA (AMHP ) WYETH.

PA (LIUW/) LIU W.

PA (WULL/) WU L.

XX

PI Liu W, Wu L;

XX

DR WPI; 2004-340908/31.

DR N-PSDB; ADS93535, ADS93537.

XX

PT New isolated polypeptide, useful for preventing or treating a myotonic dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease e.g., inflammation, cancer, arteriosclerosis, psoriasis, and Parkinson's disease.

XX

PS Claim 8; SEQ ID NO 2; 242pp; English.

XX

CC This invention relates to a novel isolated human protein kinase, MCRK2. The sequence shows homology to rat myotonic dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2). The gene encoding the novel kinase is localised to human in locus 1q42 of human chromosome 1. The novel protein kinase comprises multiple functional/structural domains that include a kinase domain, a pkinase C domain, a DAG-PE binding domain and a CNH domain. The protein may function as a downstream effector of Cdc42 in cytoskeleton reorganisation. The invention may be useful for the production of cytostatic, antiinflammatory, antiarteriosclerotic, ophthalmological, antipsoriatic, antiasthmatic, antiparkinsonian, antirheumatic, neuroprotective, muscular-Gen, osteopathic, cardiovascular-Gen, immunosuppressive, cerebroprotective, vasotropic, anticonvulsant or anti-HIV activity acting as myotonic dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2)-inhibitors or MRCK2-Modulator. In addition, the disclosed sequences may be used for gene therapy. The invention may be useful for preventing or treating an myotonic dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease in a

[illegible]



FT /note= "Protein kinase domain"  
FT 238. .404  
FT /note= "Protein kinase domain"  
FT 344. .372  
FT /note= "Protein kinase C terminal domain"  
FT 772. .793  
FT /note= "Leucine zipper domain"  
FT 779. .800  
FT /note= "Leucine zipper domain"  
FT 786. .807  
FT /note= "Leucine zipper domain"  
FT 1051. .1100  
FT /note= "Phorbol esters/diacyl glycerol binding domain"  
FT 1064. .1122  
FT /note= "Phorbol esters/diacyl glycerol binding domain"  
FT 1121. .1239  
FT /note= "PH domain"  
FT 1266. .1550  
FT /note= "CNH domain"  
FT 1653. .1728  
FT /note= "Protein kinase domain"  
FT  
XX WO200246384-A2.  
PN  
XX  
XX  
PD  
XX  
PF  
XX  
XX  
PR 06-DEC-2000; 2000US-0254034P.  
PR 07-DEC-2000; 2000US-0251814P.  
PR 14-DEC-2000; 2000US-0255756P.  
PR 15-DEC-2000; 2000US-0256172P.  
PR 22-DEC-2000; 2000US-0257416P.  
PR 10-JAN-2001; 2001US-0260912P.  
PR 25-JAN-2001; 2001US-0264664P.  
PR 02-FEB-2001; 2001US-0266017P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yue H, Ding L, Lal PG, Griffin JA, Gururajan R, Baughin MR;  
PI Ison CH, Ramkumar J, Tribouley CM, Swarnakar A, Burford N;  
PI Bandman O, Thornton M, Khan FA, Walia NK, Nguyen DB, Elliott VS;  
PI Xu Y, Lu Y, Hafalia AJA, Yao MG, Gandhi AR, Arvizu C, Forsythe I;  
XX  
DR WPI; 2002-519665/55.  
DR N-PSDB; AAD40758.  
XX  
PT Novel human kinase and phosphatase polypeptide, useful in diagnosis,  
PT prevention or treatment of cardiovascular, immune system, neurological,  
PT growth, developmental, lipid and cell proliferative disorders.  
XX  
PS Claim 74; Page 190-194; 219pp; English.  
XX  
CC The present invention relates to novel human kinase and phosphatase (KAP)  
CC proteins and polynucleotides encoding such proteins. Sequences of the  
CC invention are useful for treating or preventing disorders associated with  
CC aberrant expression of KAP where the disorders include cardiovascular  
CC disorders (e.g., atherosclerosis, hypertension, vasculitis), immune  
CC system disorders (e.g., acquired immunodeficiency syndrome (AIDS), gout,  
CC anaemia, asthma, diabetes mellitus, multiple sclerosis), neurological  
CC disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's  
CC disease, Parkinson's disease), growth and developmental disorders (e.g.,  
CC cirrhosis, hepatitis, psoriasis), lipid disorders (e.g., fatty liver,  
CC Gaucher's disease, obesity) and cell proliferative disorders (e.g.,  
CC arteriosclerosis, myelofibrosis and cancer). They are useful for drug  
CC screening techniques and to analyse the proteome of a tissue or cell  
CC type. KAP sequences are useful for creating knock-in humanised animals or  
CC transgenic animals to model human diseases, in somatic or germline gene  
CC therapy, to generate a transcript image of a tissue or cell type, for  
CC detecting differences in the chromosomal location due to inversion, or  
CC translocation among normal, carrier or affected individuals and as  
CC hybridisation probes for mapping naturally occurring genomic sequences.  
CC The present sequence is human KAP-19 protein

XX SQ Sequence 1770 AA;  
Query Match 3.6%; Score 93.5; DB 5; Length 1770;  
Best Local Similarity 19.9%; Pred. No. 1.9e+02;  
Matches 60; Conservative 40; Mismatches 119; Indels 83; Gaps 12;  
QY 109 PIPP-VILAEIGSDPTKGT-VCFYGHLDV-QPADRGDGLTDPYVLTEVDGKLYGRGATD 165  
Db 1101 PVPPEQTKGPLGIDPQKGIGTAYEGHVRIPKAGVKKGW----- 1139  
QY 166 NKGVPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIV 225  
Db 1140 -----QRALAIVCDFKLFYDIAEGKASQPSVVISQVIDMRDEEF--SVSSVL 1185  
QY 226 ISDNLWISQRKPAITYGTRGNSYFMVEVKC-----RDQDFHSGTGGILHEPMADLVALL 280  
Db 1186 ASDVIHASRKDIPICIFRVTASQLSASNNKCSILMLADTENEKNKWGVLSE----LHKIL 1241  
QY 281 GSLVDSSGHILVP-GIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFD-TKEEIL 338  
Db 1242 KKNKFRDRSVYVPKEAYDSTLPLIK---TTQAAAAIIDHERIALGNEEGLFVVHVTKDEII 1298  
QY 339 -----MHLWRYPSLSIHGIEGAF----DEPGTKTVIPG 367  
Db 1299 RVGDNKKIHQIELIPNDQLVAVISGRNRHVLFPMSALDGRETDFFYKLSKGCQTVTSG 1358  
QY 368 RV 369  
Db 1359 KV 1360  
RESULT 496  
ID AAB94961 standard; protein; 214 AA.  
XX AAB94961;  
AC AAB94961;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:16507.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX Homo sapiens.  
XX  
PN EPI074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-00116126.  
XX  
PR 29-JUL-1999; 99JP-00248036.  
PR 27-AUG-1999; 99JP-00300253.  
PR 11-JAN-2000; 2000JP-00118776.  
PR 02-MAY-2000; 2000JP-00183767.  
PR 09-JUN-2000; 2000JP-00241899.  
XX (HELI-) HELIX RES INST.  
PA  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX  
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-  
PT length cDNAs defined in the specification, and for the detection and/or  
PT diagnosis of the abnormality of the proteins encoded by the full-length  
PT cDNAs.  
XX  
PS Claim 8; SEQ ID NO 16507; 2537pp + Sequence Listing; English.  
XX The present invention describes primer sets for synthesising 5602 full-  
CC



PT Human cell cycle and proliferation proteins and polynucleotides are used  
PT to treat, diagnose and prevent immune, developmental and cell signaling  
PT disorders and cell proliferative disorders including cancer.  
XX  
PS Claim 1; Page 158; 205pp; English.  
XX  
CC Sequences AAB60453-AAB60506 represent 54 human cell cycle and  
CC proliferation proteins (CCYPR), which are encoded by AAF59590-AAF59643.  
CC CCYPR and agonists of CCYPR are used to treat diseases or conditions  
CC associated with decreased expression of functional CCYPR, while CCYPR  
CC antagonists are used to treat diseases or conditions associated with  
CC overexpression of functional CCYPR. Monoclonal or polyclonal antibodies  
CC to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or  
CC radioimmunoassays to detect CCYPR. CCYPR itself may be used to detect  
CC compounds e.g., antibodies, oligonucleotides and proteins (receptors)  
CC that specifically bind to CCYPR, and in drug screening methods to  
CC identify compounds that modulate the activity of CCYPR. CCYPR nucleotides  
CC can be used to generate transgenic animal models of human disease, and  
CC can be used in gene therapy in target cells with genetic abnormalities  
CC with respect to the expression of CCYPR for the treatment or prevention  
CC of a disorder associated with CCYPR. Diseases which can be diagnosed,  
CC treated and prevented using CCYPR proteins, nucleic acids, agonists or  
CC antagonists include immune, developmental and cell signalling disorders,  
CC and cell proliferative disorders including cancer. Specific examples of  
CC these disorders include anaemia, epilepsy, arteriosclerosis, asthma,  
CC cancer, allergies, diabetes mellitus, disorders of the menstrual cycle  
CC and infections caused by bacteria  
XX

SQ Sequence 255 AA;

Query Match 3.5%; Score 93; DB 4; Length 255;  
Best Local Similarity 25.3%; Pred. No. 11;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;  
QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAFD-EPGKTVIPGRVIGKFSIRLVPHM 381  
Db 7 FDTKPDLLHLMTKEWQLPCLJISVHGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65  
QY 382 NVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439  
Db 66 FTGGVNTGVIRHVGDAKDASHKSRGKI-CTIGIAPNGIVENQED-----LIG 112  
QY 440 TEPDMIRDGSTI--PIAKM-FQEI VHKS VVLIPLGA VDDGGEHSQNEKINR 486  
Db 113 R--DVVRPYQTMSPMSKLTVLNSMHSFILADNGTT--GKYGAEVKLRR 158

RESULT 499  
ADC96791  
ID ADC96791 standard; protein; 398 AA.  
XX  
AC ADC96791;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE E. faecium protein sequence SEQ ID 6418.  
XX  
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.  
XX  
OS Enterococcus faecium.  
XX  
PN US6583275-B1.  
XX  
PD 24-JUN-2003.  
XX  
PF 30-JUN-1998; 98US-00107532.  
XX  
PR 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX

PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-799836/75.  
DR N-PSDB; ADC93137.  
XX

PT New isolated nucleic acid derived from Enterococcus faecium encoding an  
PT Enterococcus faecium polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.  
XX

PS Example 1; SEQ ID NO 6418; 243pp; English.

XX The invention relates to an isolated nucleic acid derived from  
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.  
XX

SQ Sequence 398 AA;

Query Match 3.5%; Score 93; DB 7; Length 398;  
Best Local Similarity 19.8%; Pred. No. 21;  
Matches 86; Conservative 53; Mismatches 125; Indels 170; Gaps 21;  
QY 119 GSDPTKGTVCFYGHLDVQPADRG---DGWLTDP-----YVLTEVDGKLYGRGATD-- 165  
Db 4 GSDK--TVMIHGGF-----RGNWNGIVTBEYDFYKAGYNLLFVDSRATNSGGDYV 54  
QY 166 -----NKG PVLAWIN-----AVSAFRALEQDLPVNIKFIEG----- 197  
Db 55 TYGQYESDDVLYWINQEVRRERPSQKILLYGSGMGAATMSVLAKDIPNVKGIENCGFA 114  
QY 198 -----MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY 248  
Db 115 SIDEQLRFTYSQT VAPALPDAIKNQLD-----IIGD-----QEHEDLPMLLKQYY 160  
QY 249 FMVEVKCRDQDFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN 308  
Db 161 F-----DQEMHLDT-----KAALPTI--GMSDSLPLKLIHGTADDVVPVS----- 198  
QY 309 TYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGR 368  
Db 199 -----NAQKLYELSGGYKDLL-----VEGA----- 219  
QY 369 VIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKR-----NSSNMVSMTLGLHPWIANI 422  
Db 220 --GHGKAQEVDH---AAYTKHVTDFLKVVFHDQINVKYVDENKSL-----LKDQ 264  
QY 423 DDTQYLAA-----KRAIRTVFGTEPDMIRDGSTIPIAKMFOEIV-----HKSVVLIPLG 471  
Db 265 DEIQLYGAYGENYMTQKTFEGYELANVEG-----PTGIFNETIPTIIFYKKIPVAPPK 320  
QY 472 AVDDGEHSQNEKIN 485  
Db 321 KQDPTENADNKGKN 334

RESULT 500  
AAW01044  
ID AAW01044 standard; protein; 501 AA.







CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 646 AA;
	Query Match 3.5%; Score 93; DB 6; Length 646;
	Best Local Similarity 20.3%; Pred. No. 45;
	Matches 83; Conservative 61; Mismatches 139; Indels 126; Gaps 18;
QY	115 LAELGSDPT-KGTVCFYGHLDVQPADRGDGLTDPVVLTEVDGKLYGR--GATDNKGP-- 169
Db	24 LAELDINVTDKDSVLEGELELALMLGEDLSQENGNNVIEDKLTQVLATKLDKSPSE 83
QY	170 VLAWINAVSAFRALEQDLPVNI-----KFIEGMEEAGSVALEELVEKEKDRFFS 219
Db	84 IIMKLMKGMTATINQEISFEIAALAAKDYGFELTVAESDDTEALEIEALMEIEEDK--- 140
QY	220 GVDYIVISDNLWISQKPAIT---YGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADL 276
Db	141 -----EEDL--KPRPPVVVMGHVDHGKTSLLDAI--RKTDVISGEAGGITQHIGASE 189
QY	277 VALLGS---LVDSSGH-----ILVPGIYDEVVPLTBBEINTYKAIHLD 316
Db	190 VKINGHKIVFLDTPGHEAFTSMRARGAQVTDIALLVVAADDGIMPQTVEAINHAKAAGVP 249
QY	317 L-----EEYRNSSRVKEKFLDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGR 368
Db	250 LIVAINKIDKPGANPKVKQELAD--QGLLVEDW-----GGE 284
QY	369 VIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDDTQYL 428
Db	285 VIA-----VP-----VSAKKKEGIDTLLEMVL-----LVAEMEELRAN 317
QY	429 AAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGE 477
Db	318 PNKRAVGTVIEAELDKGRG----PVA-----TVLVQGGTLTVGD 352
RESULT 504	
ID	AAU35250
XX	AAU35250 standard; protein; 686 AA.
AC	AAU35250;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	Enterococcus faecalis cellular proliferation protein #537.
XX	
KW	Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW	antibacterial; drug design.
XX	
OS	Enterococcus faecalis.
XX	
PN	WO200170955-A2.
XX	
PD	27-SEP-2001.
XX	
PF	21-MAR-2001; 2001WO-US009180.
XX	
PR	21-MAR-2000; 2000US-0191078P.
PR	23-MAY-2000; 2000US-0206848P.
PR	26-MAY-2000; 2000US-0207727P.
PR	23-OCT-2000; 2000US-0242578P.
PR	27-NOV-2000; 2000US-0253625P.
PR	22-DEC-2000; 2000US-0257931P.
PR	16-FEB-2001; 2001US-0269308P.
XX	
PA	(ELIT-) ELITRA PHARM INC.
XX	
PI	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI	Yamamoto RT, Xu HH;
XX	
DR	WPI; 2001-611495/70.
DR	N-PSDB; AAS53109.

Db	468 TSAVANAYD-----MVINGYEVGGGVRI 491
RESULT 503	
ABU25463	
ID	ABU25463 standard; protein; 646 AA.
XX	
AC	ABU25463;
XX	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #10990.
XX	
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX	
OS	Clostridium difficile.
XX	
PN	WO200277183-A2.
XX	
PD	03-OCT-2002.
XX	
PF	21-MAR-2002; 2002WO-US009107.
XX	
PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
PA	(ELIT-) ELITRA PHARM INC.
XX	
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX	
DR	WPI; 2003-029926/02.
DR	N-PSDB; ACA29333.
XX	
PT	New antisense nucleic acids, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 53387; 1766pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for
CC	proliferation; (7) identifying a compound that influences the activity of
CC	the gene product or that has an activity against a biological pathway
CC	required for proliferation, or that inhibits cellular proliferation; (8)
CC	identifying a gene required for cellular proliferation or the biological
CC	pathway in which a proliferation-required gene or its gene product lies
CC	or a gene on which the test compound that inhibits proliferation of an
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC	compound's activity; (11) a culture comprising strains in which the gene
CC	product is overexpressed or underexpressed; (12) determining the extent
CC	to which each of the strains is present in a culture or collection of
CC	strains; or (13) identifying the target of a compound that inhibits the
CC	proliferation of an organism. The antisense nucleic acids are useful for
CC	identifying proteins or screening for homologous nucleic acids required
CC	for cellular proliferation to isolate candidate molecules for rational
CC	drug discovery programs, or for screening homologous nucleic acids
CC	required for proliferation in cells other than S. aureus, S. typhimurium,
CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC	the target prokaryotic essential genes. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at











Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;

QY       331 FDTKEEILMHL-----WR--YPSL---SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381  
            |||| :||| | : ||| : ||| : ||| : ||| : ||| : ||| :  
Db       7 FDKPDLULLHMTKEWQLPLKLISVHGGLQNFELOPKLKQVF-GKGLIKAAAMTTGAWI 65

QY       382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW--IANIDTQYLAAKRAIRTVEF 439  
            | | | | | | | | | : : : : | : | : | : | : | : | :  
Db       66 FTGGVNTGVIRHVGDALKDHASKSRGKI-CTIGIAPWGIVENQED-----LIG 112

QY       440 TEPDMIRDGSTI--PIAKM-FQEIVHKSVVLIPLGAVDDGEHSQNEKINR 486  
            | : | : | : | : | : | : | : | : | : | : | : | :  
Db       113 R--DVVRPYQTMSNPFMSKLTVLNSMHSHFILADNGTT--GKYGAEVKLR 158

RESULT 509  
AAU02393  
ID AAU02393 standard; protein; 778 AA.  
XX  
AC AAU02393;  
XT  
DT 29-AUG-2001 (first entry)  
XX Human novel melastatin-like protein #7.  
DE  
XX Human; melastatin-like protein; tumour progression inhibitor; cancer;  
KW tumour growth; metastasis.  
XW Homo sapiens.  
OS WO200132870-A1.  
XX 10-MAY-2001.  
PD 31-OCT-2000; 2000WO-US029851.  
XX  
PF 01-NOV-1999; 99US-0162678P.  
PR  
XX (LEXI-) LEXICON GENETICS INC.  
PA Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;  
XX WPI; 2001-291053/30.  
DR N-PSDB; AAS03111.

Nucleic acids encoding human proteins that share structural similarity with mammalian melastatin proteins, and which function as tumor progression inhibitors, useful for treating cancers.

PS Disclosure; Page 44-46; 129pp; English.  
XX

The present sequence representing human melastatin-like protein #7 is 1 of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full length cDNA sequence for melastatin-like protein is also described (AAS03147). The melastatin-like proteins are tumour progression inhibitors sharing structural and functional similarity with mammalian melastatin proteins. The novel melastatin-like proteins were found to be expressed in inter alia, human cell lines, adult brain, pituitary, prostate, thymus, thyroid, testis, kidney, and gene trapped human cells. The nucleic acids encoding melastatin-like proteins and the polypeptides themselves may be used for treating cancer by inhibiting tumour growth and metastasis. The melastatin-like polynucleotide and polypeptide sequences can be used in therapeutic, diagnostic and pharmacogenomic applications

XX  
SQ Sequence 778 AA;

Query Match 3.5%; Score 93; DB 4; Length 778;  
Best Local Similarity 25.3%; Pred. No. 61;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;

QY       331 FDTKEEILMHL-----WR--YPSL---SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381  
            |||| :||| | : ||| : ||| : ||| : ||| : ||| : ||| :  
            | : | : | : | : | : | : | : | : | : | : | : | :







QY 74 LFRMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFG-H 132  
Db 341 VFLVSQASSENSTSIGVRNADADLACEVLNEEFAGEISPIQAEKNLATVAIVGEN 400  
QY 133 LDVQPADRGDGLWLTDPVYLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIK 192  
Db 401 MKHTPG-----IAGKLFGLTRNG-----INVIACAQGASE---TNIS 435  
QY 193 FIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVE 252  
Db 436 FVVD-----SKSLRKSLSNVIHDSFFLS-EYQVL--NLFI----- 466  
QY 253 VKCRDQDFHSGTGGILHEPNADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA 312  
Db 467 --C-----GVGTVGSLVEQIRQQKKL--MVENGLKLVVGIIDATKAM-----FSR 510  
QY 313 IHLDEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK 372  
Db 511 AGFDLANYRE-----ELKEK-----GVDSSLDTIRDE-IIGNMIFNS 546  
QY 373 FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSVMTLGLHPWIANIDDTQYLAAGR 432  
Db 547 VFVDCTASPDIASLYKDFLQHNISV---AANKIAASSA-----YENYRELKLIARQR 596  
QY 433 AIRTVEGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDG 476  
Db 597 GVKYLFETNV-----GAGLPIINTINDLIHSGDKILKIEAVLSG 635

RESULT 515  
AAU02400  
ID AAU02400 standard; protein; 813 AA.  
XX  
AC AAU02400;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human novel melastatin-like protein #14.  
XX  
KW Human; melastatin-like protein; tumour progression inhibitor; cancer;  
KW tumour growth; metastasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200132870-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 31-OCT-2000; 2000WO-US029851.  
XX  
PR 01-NOV-1999; 99US-0162678P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;  
XX  
DR WPI; 2001-291053/30.  
DR N-PSDB; AAS03118.  
XX  
PT Nucleic acids encoding human proteins that share structural similarity  
PT with mammalian melastatin proteins, and which function as tumor  
PT progression inhibitors, useful for treating cancers.  
XX  
PS Disclosure; Page 66-67; 129pp; English.  
XX  
CC The present sequence representing human melastatin-like protein #14 is 1  
CC of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full  
CC length cDNA sequence for melastatin-like protein is also described  
CC (AAS03147). The melastatin-like proteins are tumour progression  
CC inhibitors sharing structural and functional similarity with mammalian  
CC melastatin proteins. The novel melastatin-like proteins were found to be  
CC expressed in inter alia, human cell lines, adult brain, pituitary,  
CC prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.  
CC themselves may be used for treating cancer by inhibiting tumour growth  
CC and metastasis. The melastatin-like polynucleotide and polypeptide  
CC sequences can be used in therapeutic, diagnostic and pharmacogenomic

CC The nucleic acids encoding melastatin-like proteins and the polypeptides  
CC themselves may be used for treating cancer by inhibiting tumour growth  
CC and metastasis. The melastatin-like polynucleotide and polypeptide  
CC sequences can be used in therapeutic, diagnostic and pharmacogenomic  
CC applications  
XX  
SQ Sequence 813 AA;  
  
Query Match 3.5%; Score 93; DB 4; Length 813;  
Best Local Similarity 25.3%; Pred. No. 65;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;  
  
QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAFD-EPGKTKVIPGRVIGKFSIRLVPHM 381  
Db 7 FDTKPDLLLHLMTKEWQLPQLLISVHGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65  
QY 382 NVSAVEKQVTRHLEDVFSKRNSSNMVSVMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439  
Db 66 FTGGVNTGVIRHVGDALKDHASKSRGKI-CTIGIAPWGIVENQED-----LIG 112  
QY 440 TEPDMIRDGSTI--PIAKM-FQEIIVHKSVVLIPLGAVDDGGEHSQNEKINR 486  
Db 113 R--DVVRPYQTMSPMSKLTVLNSMHSHFILADNGTT--GKYGAEVKLR 158  
  
RESULT 516  
AAU02388  
ID AAU02388 standard; protein; 823 AA.  
XX  
AC AAU02388;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human novel melastatin-like protein #2.  
XX  
KW Human; melastatin-like protein; tumour progression inhibitor; cancer;  
KW tumour growth; metastasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200132870-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 31-OCT-2000; 2000WO-US029851.  
XX  
PR 01-NOV-1999; 99US-0162678P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;  
XX  
DR WPI; 2001-291053/30.  
DR N-PSDB; AAS03106.  
XX  
PT Nucleic acids encoding human proteins that share structural similarity  
PT with mammalian melastatin proteins, and which function as tumor  
PT progression inhibitors, useful for treating cancers.  
XX  
PS Disclosure; Page 27-29; 129pp; English.  
XX  
CC The present sequence representing human melastatin-like protein #2 is 1  
CC of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full  
CC length cDNA sequence for melastatin-like protein is also described  
CC (AAS03147). The melastatin-like proteins are tumour progression  
CC inhibitors sharing structural and functional similarity with mammalian  
CC melastatin proteins. The novel melastatin-like proteins were found to be  
CC expressed in inter alia, human cell lines, adult brain, pituitary,  
CC prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.  
CC The nucleic acids encoding melastatin-like proteins and the polypeptides  
CC themselves may be used for treating cancer by inhibiting tumour growth  
CC and metastasis. The melastatin-like polynucleotide and polypeptide  
CC sequences can be used in therapeutic, diagnostic and pharmacogenomic







Db	412	EVLWEKELPPGV	423	
RESULT 520				
ABM81745				
ID	ABM81745	standard; protein;	893	AA.
XX	ABM81745;			
AC	ABM81745;			
XX	18-NOV-2004	(first entry)		
DT				
XX	Tumour-associated antigenic target (TAT) polypeptide	PRO82586,	SEQ:4501.	
DE				
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;			
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;			
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;			
KW	central nervous system cancer; bladder cancer; pancreatic cancer;			
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;			
KW	chromosome identification; chromosome mapping; gene mapping;			
KW	gene therapy; cytostatic.			
XX				
OS	Homo sapiens.			
XX				
PN	WO2004030615-A2.			
XX				
PD	15-APR-2004.			
XX				
PF	29-SEP-2003; 2003WO-US028547.			
XX				
PR	02-OCT-2002; 2002US-0414971P.			
XX				
PA	(GETH ) GENENTECH INC.			
XX				
PI	Wu TD, Zhang Z, Zhou Y;			
XX				
DR	WPI; 2004-347921/32.			
DR	N-PSDB; ACN39999.			
XX				
PT	New tumor-associated antigenic target polypeptides and nucleic acids,			
PT	useful in preparing a medicament for treating or detecting a			
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or			
PT	prostate cancer or tumor.			
XX				
PS	Claim 12; SEQ ID NO 4501; 7273pp; English.			
XX				
CC	The invention relates to human tumour-associated antigenic target (TAT)			
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are			
CC	overexpressed in cancer tissues compared to normal tissues, and may thus			
CC	serve as effective targets for the diagnosis and treatment of cancer in			
CC	mammals. The invention also relates to nucleic acid and polypeptide			
CC	sequences at least 80% identical to the TAT nucleic acids and			
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic			
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic			
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a			
CC	TAT polypeptide; and methods and compositions for the treatment or			
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,			
CC	antibodies, antagonists, binding molecules and compositions are useful			
CC	for diagnosing or treating a cell proliferative disorder associated with			
CC	increased TAT expression, particularly cancers such as breast cancer,			
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder			
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central			
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be			
CC	used as hybridisation probes, in chromosome and gene mapping, in			
CC	chromosome identification and in gene therapy. The present sequence			
CC	represents a TAT polypeptide of the invention			
XX				
SQ	Sequence 893 AA;			
Query Match 3.5%; Score 93; DB 8; Length 893;				
Best Local Similarity 20.6%; Pred. No. 75;				
Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;				
QY	32	PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPFRFQ	72	

Db	206	PAVFEVLDLVD	AVILTEKTAHLRARNFRD	FRGVSRRRTGEEWLVTVQDTEAHVPDVHE	265
QY	73	ELFRMMAVAAD	TLQRLGARVASVDMGFPQQLPDGQSLPIPPVILAE	LGSD-PTKGTVCFYG	131
Db	266	EVLGVVPITT	-----LGNHNYCVILDPVG-PDGKN	-----QLGQKRVVKGESFF-	309
QY	132	HLDVQPADRG	WLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA	FRALQDLPN-	190
Db	310	---LQPGEQLE	QIGQDVVYLSQQGLL-----LRALQPLEEGE	DEEKVSH	351
QY	191	-----IKFI	-----IEGMEEAGSVALEEL-----VEKEKDRFFS	GVDIYIVISD	228
Db	352	QAGDHWLIRG	PLEYVPSAKVEVVEERQAIPLDENEGIYVQDVKTG	KVRAVIGSTYMLTQD	411
QY	229	N-LWISQRKPAI	239		
Db	412	EVLWEKELPPGV	423		
RESULT 521					
ADSI17662					
ID	ADSI17662	standard; protein;	893	AA.	
XX					
AC	ADSI17662;				
XX					
DT	16-DEC-2004	(first entry)			
XX					
DE	Human major vault protein (MVP).				
XX					
KW	vault; carrier molecule; major vault protein; MVP;				
KW	vault poly-ADP ribose polymerase; VPARP; toxin.				
XX					
OS	Homo sapiens.				
XX					
PN	WO2004081533-A2.				
XX					
PD	23-SEP-2004.				
XX					
PF	10-MAR-2004; 2004WO-US007434.				
XX					
PR	10-MAR-2003; 2003US-0453800P.				
XX					
PA	(REGC ) UNIV CALIFORNIA.				
XX					
PI	Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;				
XX					
DR	WPI; 2004-690644/67.				
DR	N-PSDB; ADS17663.				
XX					
PT	Using vaults as carrier molecules to deliver substance(s) to an organism,				
PT	to a specific tissue, to specific cells, or to an environmental medium				
PT	comprises incorporating the substance(s) into the vaults and				
PT	administering them.				
XX					
PS	Disclosure; SEQ ID NO 1; 459pp; English.				
XX					
CC	The invention relates to a novel method of using vaults as carrier				
CC	molecules to deliver one, or more than one, substance to an organism, or				
CC	to a specific tissue or to specific cells, or to an environmental medium.				
CC	The method comprises providing vaults, incorporating the substance into				
CC	the vaults, and administering the vaults comprising the substance to the				
CC	organism, to the specific tissue, to the specific cells, or to the				
CC	environmental medium. The invention further comprises: a vault-like				
CC	particle, comprising a major vault protein (Mvp) or modified MVP, and/or				
CC	further comprising a vault poly-ADP ribose polymerase (VPARP) or a				
CC	portion of a VPARP, comprising at least about 150 consecutive residues of				
CC	VPARP; a method of preventing damage by one, or more than one, substance				
CC	to an organism, to a specific tissue, to specific cells, or to an				
CC	environmental medium by sequestering the substance within a vault-like				
CC	particle; a method of delivering one or more than one substance,				
CC	particularly a sensor to an organism, to a specific tissue, to specific				
CC	cells, or to an environmental medium; a method of detecting a signal from				

CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Human major vault protein (MVP) of the invention.  
XX  
SQ Sequence 893 AA;

Query Match 3.5%; Score 93; DB 8; Length 893;  
Best Local Similarity 20.6%; Pred. No. 75;  
Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;  
QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQ 72  
Db 206 PAVFEEVLDLVDVILTEKTLHLRARNFRDVRGVSRRTGEWLVTVDTEAHVPDVHE 265  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSD-PTKGTVCFYG 131  
Db 266 EVLGWVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 309  
QY 132 HLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPN- 190  
Db 310 ---LQGEQLEQGIQDVVYVLSQQGLL-----LRALQPLEEGEDEEKVSH 351  
QY 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD 228  
Db 352 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIVQDVKTGKRAVIGSTYMLTQD 411  
QY 229 N-LWISQKPAI 239  
Db 412 EVLWEKELPPGV 423

RESULT 522  
AAW00733  
ID AAW00733 standard; protein; 896 AA.  
XX AAW00733;  
AC AAW00733;  
DT 05-DEC-1996 (first entry)  
XX Human major vault protein.  
DE Major vault protein; vault-related multidrug-resistance; VR-MDR;  
XX lung cancer; ovary carcinoma; tumour; prognosis; antisense; ribozyme;  
KW therapy; chemotherapy; cytotoxicity.  
XX Homo sapiens.  
OS WO9627611-A1.  
XX 12-SEP-1996.  
XX 06-MAR-1996; 96WO-EP001013.  
XX 06-MAR-1995; 95EP-00200543.  
XX (ALKU ) AKZO NOBEL NV.  
PA Scheper RJ, Scheffer GL;  
PI WPI; 1996-433405/43.  
XX N-PSDB; AAT33624.  
XX Identification of vault-related multi-drug resistance in cells - useful  
PT in the prognosis of treatment, e.g. in lung cancer or ovarian carcinoma.  
XX Claim 3; Page 72-74; 106pp; English.  
XX

CC The presence and amount of the 110 kDa major component protein (AAW00733)  
CC of the human cytoplasmic ribonucleoprotein vault is related to a novel  
CC type of multidrug-resistance, designated vault-related multidrug-  
CC resistance (VR-MDR). VR-MDR appears to a broad range of drugs, including  
CC cisplatin. This resistance is seen in a clinical setting and so provides  
CC a marker for prognosis of treatment with chemotherapy. The vault protein  
CC sequence was deduced from a cDNA clone (AAT33624) derived from a MDR  
CC fibrosarcoma cell line. It can be expressed in transformed host cells.  
CC Antibodies raised against the vault protein are useful for inhibiting  
CC activity and thereby overcoming VR-MDR  
XX  
SQ Sequence 896 AA;

Query Match 3.5%; Score 93; DB 2; Length 896;  
Best Local Similarity 20.6%; Pred. No. 75;  
Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;  
QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPVPRFRQ 72  
Db 206 PAVFEEVLDLVDVILTEKTLHLRARNFRDVRGVSRRTGEWLVTVDTEAHVPDVHE 265  
QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSD-PTKGTVCFYG 131  
Db 266 EVLGWVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 309  
QY 132 HLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPN- 190  
Db 310 ---LQGEQLEQGIQDVVYVLSQQGLL-----LRALQPLEEGEDEEKVSH 351  
QY 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD 228  
Db 352 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIVQDVKTGKRAVIGSTYMLTQD 411  
QY 229 N-LWISQKPAI 239  
Db 412 EVLWEKELPPGV 423

RESULT 523  
ADK40909  
ID ADK40909 standard; protein; 900 AA.  
XX ADK40909;  
AC ADK40909;  
DT 06-MAY-2004 (first entry)  
XX Novel human kinase protein #16.  
DE cytotstatic; immunomodulator; cardiant; neuroprotective; nootropic;  
XX antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;  
KW analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;  
KW cancer; peripheral nervous system; central nervous system;  
KW Alzheimer's disease; Parkinson's disease; viral infection; prion infection;  
KW amyotrophic lateral sclerosis; pain; sexual dysfunction; mood disorder;  
KW ocular disease; migraine; cognition disorder; hypotension; hypertension;  
KW attention disorder; neurological disorder; dyskinesia;  
KW metabolic disorder; organ transplant rejection; enzyme.  
XX Homo sapiens.  
OS WO2003057841-A2.  
XX 17-JUL-2003.  
XX 31-DEC-2002; 2002WO-US041687.  
XX 31-DEC-2001; 2001US-0343169P.  
XX (GRIG/) GRIGORIEV I V.  
PA (SUDA/) SUDARSANAM S.  
XX Grigoriev IV, Sudarsanam S;  
PI













Db 113 R--DVVRPYQTMSNPMSKLTVLNSMHSHFILADNGTT--GKYGAEVKLRR 158

RESULT 530

ADSL17795 ID ADS17795 standard; protein; 921 AA.

XX AC ADS17795;

XX DT 16-DEC-2004 (first entry)

XX DE Polylysine + human major vault protein + HIV-Tat peptide.

XX KW vault; carrier molecule; major vault protein; MVP;  
XX vault poly-ADP ribose polymerase; VPARP; toxin.

OS Homo sapiens.

OS Human immunodeficiency virus 1.

OS Synthetic.

XX PN WO2004081533-A2.

XX PD 23-SEP-2004.

XX PF 10-MAR-2004; 2004WO-US007434.

XX PR 10-MAR-2003; 2003US-0453800P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;

XX DR WPI; 2004-690644/67.

XX DR N-PSDB; ADS17796.

XX PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.

XX PS Disclosure; SEQ ID NO 140; 459pp; English.

XX CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC Polylysine + human major vault protein + HIV-Tat peptide of the  
CC invention.

XX SQ Sequence 921 AA;

Query Match 3.5%; Score 93; DB 8; Length 921;  
Best Local Similarity 20.6%; Pred. No. 79;

Matches	52; Conservative	42; Mismatches	80; Indels	78; Gaps	12;
QY	32	PALLEKVFQYID-----LH-----	QDEFVQTLKEWVAIESDSVQVPFRFRQ	72	
Db	223	PAVFEVLDLVDVAVILTEKTLHLRARNFRD	FRGVSRRTGEEWLVTVDTEAHVPDVHE	282	
QY	73	ELFRMMAVAADTLQRLGARVASVDMGPQQL	PDGQSLPIPPVILAEIGSD-PTKGTVCFYG	131	
Db	283	EVLGVVPITT-----LGPVNYCVILDPVG	-PDGKN-----QLGQKRVVKGESFF-	326	
QY	132	HLDVQPADRGDGLTDPYVLTVDGKLYGRG	ATDNKGPVLAWINAVSAFRALEQDLPVN-	190	
Db	327	---LQPGEQLEQIGQDVVYLSEQQGLL-----	LRALQPLEEGEDEEKVSH	368	
QY	191	-----IKFI-----IEGMEEAGSVALEEL	-----VEKEKDRFFSGVDYIVISD	228	
Db	369	QAGDHWLIRGPLEYVPSAKVEVVEERQAIP	LDENEGIVVDVKTGKVRVIGSTYMLTQD	428	
QY	229	N-LWISQKPAI	239		
Db	429	EVLWEKELPPGV	440		

RESULT 531

AAU02395

ID AAU02395 standard; protein; 923 AA.

XX AC AAU02395;

XX DT 29-AUG-2001 (first entry)

XX DE Human novel melastatin-like protein #9.

XX KW Human; melastatin-like protein; tumour progression inhibitor; cancer;  
XX tumour growth; metastasis.

XX OS Homo sapiens.

XX PN WO200132870-A1.

XX PD 10-MAY-2001.

XX PF 31-OCT-2000; 2000WO-US029851.

XX PR 01-NOV-1999; 99US-0162678P.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;

XX DR WPI; 2001-291053/30.

XX DR N-PSDB; AAS03113.

XX PT Nucleic acids encoding human proteins that share structural similarity  
XX with mammalian melastatin proteins, and which function as tumor  
XX progression inhibitors, useful for treating cancers.

XX PS Disclosure; Page 49-51; 129pp; English.

XX CC The present sequence representing human melastatin-like protein #9 is 1  
CC of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full  
CC length cDNA sequence for melastatin-like protein is also described  
CC (AAS03147). The melastatin-like proteins are tumour progression  
CC inhibitors sharing structural and functional similarity with mammalian  
CC melastatin proteins. The novel melastatin-like proteins were found to be  
CC expressed in inter alia, human cell lines, adult brain, pituitary,  
CC prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.  
CC The nucleic acids encoding melastatin-like proteins and the polypeptides  
CC themselves may be used for treating cancer by inhibiting tumour growth  
CC and metastasis. The melastatin-like polynucleotide and polypeptide  
CC sequences can be used in therapeutic, diagnostic and pharmacogenomic  
CC applications

XX CC



XX PS Disclosure; SEQ ID NO 128; 459pp; English.

XX CC The invention relates to a novel method of using vaults as carrier

CC molecules to deliver one, or more than one, substance to an organism, or

CC to a specific tissue or to specific cells, or to an environmental medium.

CC The method comprises providing vaults, incorporating the substance into

CC the vaults, and administering the vaults comprising the substance to the

CC organism, to the specific tissue, to the specific cells, or to the

CC environmental medium. The invention further comprises: a vault-like

CC particle, comprising a major vault protein (MVP) or modified MVP, and/or

CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a

CC portion of a VPARP, comprising at least about 150 consecutive residues of

CC VPARP; a method of preventing damage by one, or more than one, substance

CC to an organism, to a specific tissue, to specific cells, or to an

CC environmental medium by sequestering the substance within a vault-like

CC particle; a method of delivering one or more than one substance,

CC particularly a sensor to an organism, to a specific tissue, to specific

CC cells, or to an environmental medium; a method of detecting a signal from

CC a sensor within an organism, or a specific tissue or specific cells; a

CC method of making vault-like particles; and a method of making vault-like

CC particles comprising one, or more than one, substance. The method or the

CC vault-like particles are useful for delivering substances to an organism,

CC or to a specific tissue or to specific cells, or to an environmental

CC medium. The vault-like particles are also useful for preventing damage by

CC a substance (e.g., toxin) to an organism, to a specific tissue, to

CC specific cells, or to an environmental medium. This sequence represents a

CC Polylysine + human major vault protein + antennapedia protein of the

CC invention.

XX SQ Sequence 926 AA;

Query Match 3.5%; Score 93; DB 8; Length 926;

Best Local Similarity 20.6%; Pred. NO. 79;

Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEVVAIESDSVQVPFRFRQ 72

Db 223 PAVFEEVLDLVDVILTEKTLHLRARNFRDPRGVSRRTGEELVTVDTEAHVPDVHE 282

QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQLPDQSLPIPPVILAELGSD-PTKGTVCFYG 131

Db 283 EVLGVPVPIIT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 326

QY 132 HLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVN- 190

Db 327 --LQGEQLEQGIQDVVYLSEQQGLL-----LRLAQPLEEGEDEEKVSH 368

QY 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDFRFGVDYIVISD 228

Db 369 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIYQDVKTGKRAVIGSTYMLTQD 428

QY 229 N-LWISQRKPAT 239

Db 429 EVLWEKELPPGV 440

RESULT 534

AAU02401

ID AAU02401 standard; protein; 938 AA.

XX AC AAU02401;

XX 29-AUG-2001 (first entry)

XX Human novel melastatin-like protein #15.

XX Human; melastatin-like protein; tumour progression inhibitor; cancer;

XX tumour growth; metastasis.

XX Homo sapiens.

XX WO200132870-A1.

XX 10-MAY-2001.

XX 31-OCT-2000; 2000WO-US029851.

XX PD 10-MAY-2001.

XX PF 31-OCT-2000; 2000WO-US029851.

XX PR 01-NOV-1999; 99US-0162678P.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;

XX WPI; 2001-291053/30.

XX N-PSDB; AAS03119.

XX Nucleic acids encoding human proteins that share structural similarity

PT with mammalian melastatin proteins, and which function as tumor

PT progression inhibitors, useful for treating cancers.

XX Disclosure; Page 68-70; 129pp; English.

XX The present sequence representing human melastatin-like protein #15 is 1

CC of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full

CC length cDNA sequence for melastatin-like protein is also described

CC (AAS03147). The melastatin-like proteins are tumour progression

CC inhibitors sharing structural and functional similarity with mammalian

CC melastatin proteins. The novel melastatin-like proteins were found to be

CC expressed in inter alia, human cell lines, adult brain, pituitary,

CC prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.

CC The nucleic acids encoding melastatin-like proteins and the polypeptides

CC themselves may be used for treating cancer by inhibiting tumour growth

CC and metastasis. The melastatin-like polynucleotide and polypeptide

CC sequences can be used in therapeutic, diagnostic and pharmacogenomic

CC applications

XX Sequence 938 AA;

Query Match 3.5%; Score 93; DB 4; Length 938;

Best Local Similarity 25.3%; Pred. No. 81;

Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;

QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAFD-EPGKTVIPGRVIGKFSIRLVPHM 381

Db 7 FDTKPDLILLHMTKEWQLELPKLLISVHGGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65

QY 382 NVSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439

Db 66 FTGGVNTGVIRHVGDALKDHASKSRGKI-CTIGIAPWGIVENQED-----LIG 112

QY 440 TEPDMIRDGSTI--PIAKM-FQEIIVHKSVVLIPLGAVDDGEHSQNEKINR 486

Db 113 R--DVVRPYQTMSNPMSKLTVLNSMHSFILADNGTT--GKYGAEVKLRR 158

RESULT 535

AAU02389

ID AAU02389 standard; protein; 948 AA.

XX AC AAU02389;

XX 29-AUG-2001 (first entry)

XX Human novel melastatin-like protein #3.

XX Human; melastatin-like protein; tumour progression inhibitor; cancer;

XX tumour growth; metastasis.

XX Homo sapiens.

XX WO200132870-A1.

XX 10-MAY-2001.

XX 31-OCT-2000; 2000WO-US029851.







CC specific cells, or to an environmental medium. This sequence represents a  
CC GAL4 peptide joined to human major vault protein (GAL4-MVP) of the  
CC invention.

XX Sequence 989 AA;

SQ Query Match 3.5%; Score 93; DB 8; Length 989;

Best Local Similarity 20.6%; Pred. No. 88;

Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPRFRQ 72

Db 302 PAVFEEVLDLVDVILTEKTLHRLARRNFRDVRGVSRRTEGEWLVTVDTEAHVPDVHE 361

QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSD-PTKGTVCFYG 131

Db 362 EVLGWVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 405

QY 132 HLDVQPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPN- 190

Db 406 ---LQPGEQLEQGIQDVVLSQQGLL-----LRLQPLEEGEDEEKVSH 447

QY 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD 228

Db 448 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIYVDVKTGKRAVIGSTYMLTQD 507

QY 229 N-LWISQRKPAI 239

Db 508 EVLWEKELPPGV 519

RESULT 539

ADS17769

ID ADS17769 standard; protein; 1000 AA.

XX ADS17769;

AC 16-DEC-2004 (first entry)

XX GAL4 + human major vault protein + HIV-Tat peptide.

XX vault; carrier molecule; major vault protein; MVP;

XX vault poly-ADP ribose polymerase; VPARP; toxin.

KW Homo sapiens.

XX Human immunodeficiency virus 1.

OS Synthetic.

OS WO2004081533-A2.

XX 23-SEP-2004.

XX 10-MAR-2004; 2004WO-US007434.

XX 10-MAR-2003; 2003US-0453800P.

XX (REGC ) UNIV CALIFORNIA.

XX Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;

PI WPI; 2004-690644/67.

XX N-PSDB; ADS17770.

XX Using vaults as carrier molecules to deliver substance(s) to an organism,

PT to a specific tissue, to specific cells, or to an environmental medium

PT comprises incorporating the substance(s) into the vaults and

PT administering them.

XX Disclosure; SEQ ID NO 108; 459pp; English.

XX The invention relates to a novel method of using vaults as carrier

CC molecules to deliver one, or more than one, substance to an organism, or

CC to a specific tissue or to specific cells, or to an environmental medium.

CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC GAL4 + human major vault protein + HIV-Tat peptide of the invention.

XX Sequence 1000 AA;

SQ Query Match 3.5%; Score 93; DB 8; Length 1000;

Best Local Similarity 20.6%; Pred. No. 89;

Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPRFRQ 72

Db 302 PAVFEEVLDLVDVILTEKTLHRLARRNFRDVRGVSRRTEGEWLVTVDTEAHVPDVHE 361

QY 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSD-PTKGTVCFYG 131

Db 362 EVLGWVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 405

QY 132 HLDVQPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPN- 190

Db 406 ---LQPGEQLEQGIQDVVLSQQGLL-----LRLQPLEEGEDEEKVSH 447

QY 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD 228

Db 448 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIYVDVKTGKRAVIGSTYMLTQD 507

RESULT 540

ADS17757

ID ADS17757 standard; protein; 1005 AA.

XX ADS17757;

AC 16-DEC-2004 (first entry)

XX GAL4+antennapedia protein+human major vault protein, GAL4-MVP-ANT.

XX vault; carrier molecule; major vault protein; MVP;

XX vault poly-ADP ribose polymerase; VPARP; toxin.

XX Homo sapiens.

OS Drosophila melanogaster.

OS Synthetic.

XX WO2004081533-A2.

XX 23-SEP-2004.

XX 10-MAR-2004; 2004WO-US007434.



10-MAR-2003; 2003US-0453800P.  
(REGC ) UNIV CALIFORNIA.  
Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
WPI; 2004-690644/67.  
N-PSDB; ADS17758.  
Using vaults as carrier molecules to deliver substance(s) to an organism, to a specific tissue, to specific cells, or to an environmental medium comprises incorporating the substance(s) into the vaults and administering them.  
Disclosure; SEQ ID NO 96; 459pp; English.  
The invention relates to a novel method of using vaults as carrier molecules to deliver one, or more than one, substance to an organism, or to a specific tissue or to specific cells, or to an environmental medium. The method comprises providing vaults, incorporating the substance into the vaults, and administering the vaults comprising the substance to the organism, to the specific tissue, to the specific cells, or to the environmental medium. The invention further comprises: a vault-like particle, comprising a major vault protein (MVP) or modified MVP, and/or further comprising a vault poly-ADP ribose polymerase (VPARP) or a portion of a VPARP, comprising at least about 150 consecutive residues of VPARP; a method of preventing damage by one, or more than one, substance to an organism, to a specific tissue, to specific cells, or to an environmental medium by sequestering the substance within a vault-like particle; a method of delivering one or more than one substance, particularly a sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium; a method of detecting a signal from a sensor within an organism, or a specific tissue or specific cells; a method of making vault-like particles; and a method of making vault-like particles comprising one, or more than one, substance. The method or the vault-like particles are useful for delivering substances to an organism, or to a specific tissue or to specific cells, or to an environmental medium. The vault-like particles are also useful for preventing damage by a substance (e.g., toxin) to an organism, to a specific tissue, to specific cells, or to an environmental medium. This sequence represents a GAL4+antennapedia protein+human major vault protein, GAL4-MVP-ANT of the invention.

Sequence 1005 AA;

Query Match	3.5%;	Score 93;	DB 8;	Length 1005;
Best Local Similarity	20.6%;	Pred. No. 90;		
Matches 52:	Conservative 42;	Mismatches 80;	Indels 78;	Gaps 12;

QY	32	PALLEKVFQYID-----LH-----	QDEFVQTLKEWVAIESDSVQVPVPRFRQ	72
DB	302	PAVFEEVLDLVDAILTEKTLHLRARNFRD	FGVSRRTGEEHLVTVDTEAHVPDVHE	361
QY	73	ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSD-PTKGTVCFYG	131	
DB	362	EVLGVVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESKFF-	405	
QY	132	HLDVQPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLFPN-	190	
DB	402	IRALPLPLEEGEDEEKVSH	447	

[illegible]

229 N-TSORKPAI 239

db 508 EVLWEKELPPGV 519

## RESULT 541

ADSI7701

IP ADS17701 standard; protein; 1024 AA.

[illegible]

ADSI7701;

16-DEC-2004 (first entry)

pNA binding peptide MS2 joined to human major vault protein (MS2-MVP).

vault; carrier molecule; major vault protein; MVP;  
vault poly-ADP ribose polymerase; VPARP; toxin.

Homo sapiens.  
Synthetic.

WO2004081533-A2.

23-SEP-2004.

10-MAR-2004: 2004WO-US007434:

10-MAR-2003: 2003US-0453800P.

(REGC ) UNIV CALIFORNIA-

Rome I.H. Kickhoefer VA. Raval-Fernandes S, Stewart PL;

WPT: 2004-690644/67.

N-PSDB: ADS17702.

Using vaults as carrier molecules to deliver substance(s) to an organism, to a specific tissue, to specific cells, or to an environmental medium comprises incorporating the substance(s) into the vaults and administering them.

Disclosure: SEQ ID NO 40: 459pp; English.

The invention relates to a novel method of using vaults as carrier molecules to deliver one, or more than one, substance to an organism, or to a specific tissue or to specific cells, or to an environmental medium. The method comprises providing vaults, incorporating the substance into the vaults, and administering the vaults comprising the substance to the organism, to the specific tissue, to the specific cells, or to the environmental medium. The invention further comprises: a vault-like particle, comprising a major vault protein (MVP) or modified MVP, and/or further comprising a vault poly-ADP ribose polymerase (VPARP) or a portion of a VPARP, comprising at least about 150 consecutive residues of VPARP; a method of preventing damage by one, or more than one, substance to an organism, to a specific tissue, to specific cells, or to an environmental medium by sequestering the substance within a vault-like particle; a method of delivering one or more than one substance, particularly a sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium; a method of detecting a signal from a sensor within an organism, or a specific tissue or specific cells; a method of making vault-like particles; and a method of making vault-like particles comprising one, or more than one, substance. The method or the vault-like particles are useful for delivering substances to an organism, or to a specific tissue or to specific cells, or to an environmental medium. The vault-like particles are also useful for preventing damage by a substance (e.g., toxin) to an organism, to a specific tissue, to specific cells, or to an environmental medium. This sequence represents a RNA binding peptide MS2 joined to human major vault protein (MS2-MVP) of the invention.

Sequence 1024 AA;

```
Query Match
3.5%: Score 93; DB 8; Length 1024;
```

Query Match	Best Local Similarity	Pred. No. 93;
2.50	20.6%	Pred. No. 93;

Best local similarity				
Matches	52;	Conservative	42;	Mismatches
			80;	Indels
			78;	Gaps
				12;

QY 32 PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQFVPRFRQ 72

327 PAVFEEVI.DI.VDAVII.TEKTAHLRARNFRD.FRGVSRRTGEEWLTVQDTEAHVPDVHE 396

72 EIERMMVAADTI.ORI.GARVASVDMGPOOLPDGOSLPIPPVILAEIGSD-PTKGTVC FYG 131

Db 397 EVLGVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 440  
Qy 132 HLDVQPADRGDWLTDPYVLTEDVGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVN- 190  
Db 441 ---LQPGEQLEQGIQDVYVLSQQGLL-----LRALQPLEEGEDEKVVSH 482  
Qy 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD 228  
Db 483 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIYVQDVKTGKRAVIGSTYMLTQD 542  
Qy 229 N-LWISQRKPAI 239  
Db 543 EVLWEKELPPGV 554

RESULT 542  
ADS17773  
ID ADS17773 standard; protein; 1040 AA.

XX ADS17773;  
DT 16-DEC-2004 (first entry)  
XX MS2 peptide + human major vault protein + antennapedia protein.  
DE vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.

XX Homo sapiens.  
OS Drosophila melanogaster.  
OS Synthetic.  
XX  
PN WO2004081533-A2.  
XX

PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX

DR WPI; 2004-690644/67.  
DR N-PSDB; ADS17774.  
XX  
PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.  
XX  
PS Disclosure; SEQ ID NO 112; 459pp; English.  
XX

CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or  
CC to a specific tissue or to specific cells, or to an environmental medium.  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like

CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC MS2 peptide + human major vault protein + antennapedia protein of the  
CC invention.  
XX  
SQ Sequence 1040 AA;

Query Match 3.5%; Score 93; DB 8; Length 1040;  
Best Local Similarity 20.6%; Pred. No. 95;  
Matches 52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;

Qy 32 PALLEKVFOYID-----LH-----QDEFVQTLKEWVAIESDSVQVPRFRQ 72  
Db 337 PAVFEEVLDLVDVILTEKTLHLRARNFRDFRGVSRRTGEWLTVQDTEAHVPDVHE 396  
Qy 73 ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSD-PTKGTVCIFYG 131  
Db 397 EVLGVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGESFF- 440  
Qy 132 HLDVQPADRGDWLTDPYVLTEDVGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVN- 190  
Db 441 ---LQPGEQLEQGIQDVYVLSQQGLL-----LRALQPLEEGEDEKVVSH 482  
Qy 191 -----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD 228  
Db 483 QAGDHWLIRGPLEYVPSAKVEVVEERQAIPLDENEGIYVQDVKTGKRAVIGSTYMLTQD 542  
Qy 229 N-LWISQRKPAI 239  
Db 543 EVLWEKELPPGV 554

RESULT 543  
ADS17765  
ID ADS17765 standard; protein; 1045 AA.

XX ADS17765;  
DT 16-DEC-2004 (first entry)  
XX GAL4 + human major vault protein + human EGF peptide.  
DE vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.

XX Homo sapiens.  
OS Synthetic.  
XX  
PN WO2004081533-A2.  
XX

PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.

XX (REGC ) UNIV CALIFORNIA.  
XX Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX  
DR WPI; 2004-690644/67.  
DR N-PSDB; ADS17766.

XX Using vaults as carrier molecules to deliver substance(s) to an organism,  
XX to a specific tissue, to specific cells, or to an environmental medium  
XX comprises incorporating the substance(s) into the vaults and  
XX administering them.  
PS Disclosure; SEQ ID NO 104; 459pp; English.







Db 7 FDTKPDLLHLMTKEWQLEPLKLLISVHGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65

QY 382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439

Db 66 FTGGVNTGVIRHVGDALKDHASKRGKI-CTIGIAPWGIVENQED-----LIG 112

QY 440 TEPDMIRDGSTI--PIAKM-FQEIIVHKSVVLIPLGAVDDGGEHSQNEKINR 486

Db 113 R--DVVRPYQTMSPMSKLTVLNSMHSFILADNGTT--GKYGAEVKLR 158

RESULT 547

AAU02396

ID AAU02396 standard; protein; 1109 AA.

XX

AC AAU02396;

XX

DT 29-AUG-2001 (first entry)

XX

DE Human novel melastatin-like protein #10.

XX

XX Human; melastatin-like protein; tumour progression inhibitor; cancer;

KW tumour growth; metastasis.

XX

OS Homo sapiens.

XX

PN WO200132870-A1.

XX

PD 10-MAY-2001.

XX

PF 31-OCT-2000; 2000WO-US029851.

XX

PR 01-NOV-1999; 99US-0162678P.

XX

XX (LEXI-) LEXICON GENETICS INC.

XX

PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;

XX

DR WPI; 2001-291053/30.

DR N-PSDB; AAS03114.

XX

PT Nucleic acids encoding human proteins that share structural similarity with mammalian melastatin proteins, and which function as tumor progression inhibitors, useful for treating cancers.

PS Disclosure; Page 52-54; 129pp; English.

XX

CC The present sequence representing human melastatin-like protein #10 is 1 of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full length cDNA sequence for melastatin-like protein is also described (AAS03147). The melastatin-like proteins are tumour progression inhibitors sharing structural and functional similarity with mammalian melastatin proteins. The novel melastatin-like proteins were found to be expressed in inter alia, human cell lines, adult brain, pituitary, prostate, thymus, thyroid, testis, kidney, and gene trapped human cells. The nucleic acids encoding melastatin-like proteins and the polypeptides themselves may be used for treating cancer by inhibiting tumour growth and metastasis. The melastatin-like polynucleotide and polypeptide sequences can be used in therapeutic, diagnostic and pharmacogenomic applications

XX

SQ Sequence 1109 AA;

Query Match 3.5%; Score 93; DB 4; Length 1109;

Best Local Similarity 25.3%; Pred. No. 1.1e+02;

Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;

QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381

Db 7 FDTKPDLLHLMTKEWQLEPLKLLISVHGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65

QY 382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439

Db 66 FTGGVNTGVIRHVGDALKDHASKRGKI-CTIGIAPWGIVENQED-----LIG 112

QY 440 TEPDMIRDGSTI--PIAKM-FQEIIVHKSVVLIPLGAVDDGGEHSQNEKINR 486

Db 113 R--DVVRPYQTMSPMSKLTVLNSMHSFILADNGTT--GKYGAEVKLR 158

RESULT 548

AAU02402

ID AAU02402 standard; protein; 1124 AA.

XX

AC AAU02402;

XX

DT 29-AUG-2001 (first entry)

XX

DE Human novel melastatin-like protein #16.

XX

KW Human; melastatin-like protein; tumour progression inhibitor; cancer;

KW tumour growth; metastasis.

XX

OS Homo sapiens.

XX

PN WO200132870-A1.

XX

PD 10-MAY-2001.

XX

PF 31-OCT-2000; 2000WO-US029851.

XX

PR 01-NOV-1999; 99US-0162678P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;

XX

DR WPI; 2001-291053/30.

DR N-PSDB; AAS03120.

XX

PT Nucleic acids encoding human proteins that share structural similarity with mammalian melastatin proteins, and which function as tumor progression inhibitors, useful for treating cancers.

PT

XX

PS Disclosure; Page 71-73; 129pp; English.

XX

CC The present sequence representing human melastatin-like protein #16 is 1 of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full length cDNA sequence for melastatin-like protein is also described (AAS03147). The melastatin-like proteins are tumour progression inhibitors sharing structural and functional similarity with mammalian melastatin proteins. The novel melastatin-like proteins were found to be expressed in inter alia, human cell lines, adult brain, pituitary, prostate, thymus, thyroid, testis, kidney, and gene trapped human cells. The nucleic acids encoding melastatin-like proteins and the polypeptides themselves may be used for treating cancer by inhibiting tumour growth and metastasis. The melastatin-like polynucleotide and polypeptide sequences can be used in therapeutic, diagnostic and pharmacogenomic applications

XX

SQ Sequence 1124 AA;

Query Match 3.5%; Score 93; DB 4; Length 1124;

Best Local Similarity 25.3%; Pred. No. 1.1e+02;

Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;

QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381

Db 7 FDTKPDLLHLMTKEWQLEPLKLLISVHGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65

QY 382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439

Db 66 FTGGVNTGVIRHVGDALKDHASKRGKI-CTIGIAPWGIVENQED-----LIG 112

QY 440 TEPDMIRDGSTI--PIAKM-FQEIIVHKSVVLIPLGAVDDGGEHSQNEKINR 486

Db	113 R--DVVRPYQTMSNPMKLTVLNSMHSFILADNGTT--GKYGAEVKLRR	158
RESULT 549		
ADSL17707		
ID	ADSL17707 standard; protein; 1132 AA.	
AC		
XX	ADSL17707;	
DT	16-DEC-2004 (first entry)	
DE	Green fluorescent protein joined to human major vault protein (GL-MVP).	
XX		
KW	vault; carrier molecule; major vault protein; MVP;	
KW	vault poly-ADP ribose polymerase; VPARP; toxin.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO2004081533-A2.	
PD	23-SEP-2004.	
XX		
PF	10-MAR-2004; 2004WO-US007434.	
XX		
PR	10-MAR-2003; 2003US-0453800P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;	
XX		
DR	WPI; 2004-690644/67.	
DR	N-PSDB; ADS17708.	
XX		
PT	Using vaults as carrier molecules to deliver substance(s) to an organism,	
PT	to a specific tissue, to specific cells, or to an environmental medium	
PT	comprises incorporating the substance(s) into the vaults and	
PT	administering them.	
XX		
PS	Disclosure; SEQ ID NO 46; 459pp; English.	
XX		
CC	The invention relates to a novel method of using vaults as carrier	
CC	molecules to deliver one, or more than one, substance to an organism, or	
CC	to a specific tissue or to specific cells, or to an environmental medium.	
CC	The method comprises providing vaults, incorporating the substance into	
CC	the vaults, and administering the vaults comprising the substance to the	
CC	organism, to the specific tissue, to the specific cells, or to the	
CC	environmental medium. The invention further comprises: a vault-like	
CC	particle, comprising a major vault protein (MVP) or modified MVP, and/or	
CC	further comprising a vault poly-ADP ribose polymerase (VPARP) or a	
CC	portion of a VPARP, comprising at least about 150 consecutive residues of	
CC	VPARP; a method of preventing damage by one, or more than one, substance	
CC	to an organism, to a specific tissue, to specific cells, or to an	
CC	environmental medium by sequestering the substance within a vault-like	
CC	particle; a method of delivering one or more than one substance,	
CC	particularly a sensor to an organism, to a specific tissue, to specific	
CC	cells, or to an environmental medium; a method of detecting a signal from	
CC	a sensor within an organism, or a specific tissue or specific cells; a	
CC	method of making vault-like particles; and a method of making vault-like	
CC	particles comprising one, or more than one, substance. The method or the	
CC	vault-like particles are useful for delivering substances to an organism,	
CC	or to a specific tissue or to specific cells, or to an environmental	
CC	medium. The vault-like particles are also useful for preventing damage by	
CC	a substance (e.g., toxin) to an organism, to a specific tissue, to	
CC	specific cells, or to an environmental medium. This sequence represents a	
CC	Green fluorescent protein joined to human major vault protein (GL-MVP) of	
CC	the invention.	
XX		
SQ	Sequence 1132 AA;	
Query Match	3.5%; Score 93; DB 8; Length 1132;	
Best Local Similarity	20.6%; Pred. No. 1.1e+02;	
Matches	52; Conservative 42; Mismatches 80; Indels 78; Gaps 12;	

QY	32	PALLEKVFQYID-----LH-----QDEFVQTLKEWVAIESDSVQVPRFRQ	72
Db	445	PAVFEEVLDLVDVILTEKTAHLRARRNFRDPFGVSRRTGEWLVTVDTEAHVPDVHE	504
QY	73	ELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSD-PTKGTVCFYG	131
Db	505	EVLGVVPITT-----LGPHNYCVILDPVG-PDGKN-----QLGQKRVVKGEKSFF-	548
QY	132	HLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLNVN-	190
Db	549	---LQPGEQLEQGIQDVYVLSEQQLL-----LRALQPLEEGEDEEKVSH	590
QY	191	-----IKFI-----IEGMEEAGSVALEEL-----VEKEKDRFFSGVDYIVISD	228
Db	591	QAGDHWLIRGPLEYVPSAKVEVEERQAIPLDENEGIYVQDVKTGKVRVIGSTYMLTQD	650
QY	229	N-LWISQRKPAI	239
Db	651	EVLWEKELPPGV	662
RESULT 550			
AAU02390			
ID	AAU02390	standard; protein; 1134 AA.	
XX			
AC	AAU02390;		
XX			
DT	29-AUG-2001	(first entry)	
XX			
DE	Human novel melastatin-like protein #4.		
XX			
KW	Human; melastatin-like protein; tumour progression inhibitor; cancer;		
KW	tumour growth; metastasis.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200132870-A1.		
XX			
PD	10-MAY-2001.		
XX			
PF	31-OCT-2000; 2000WO-US029851.		
XX			
PR	01-NOV-1999; 99US-0162678P.		
XX			
PA	(LEXI-) LEXICON GENETICS INC.		
XX			
PI	Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;		
XX			
DR	WPI; 2001-291053/30.		
DR	N-PSDB; AAS03108.		
XX			
PT	Nucleic acids encoding human proteins that share structural similarity		
PT	with mammalian melastatin proteins, and which function as tumor		
PT	progression inhibitors, useful for treating cancers.		
XX			
PS	Disclosure; Page 33-35; 129pp; English.		
XX			
CC	The present sequence representing human melastatin-like protein #4 is 1		
CC	of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full		
CC	length cDNA sequence for melastatin-like protein is also described		
CC	(AAS03147). The melastatin-like proteins are tumour progression		
CC	inhibitors sharing structural and functional similarity with mammalian		
CC	melastatin proteins. The novel melastatin-like proteins with mammalian		
CC	expressed in inter alia, human cell lines, adult brain, pituitary,		
CC	prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.		
CC	The nucleic acids encoding melastatin-like proteins and the polypeptides		
CC	themselves may be used for treating cancer by inhibiting tumour growth		
CC	and metastasis. The melastatin-like polynucleotide and polypeptide		
CC	sequences can be used in therapeutic, diagnostic and pharmacogenomic		
CC	applications		
XX			
SQ	Sequence 1134 AA;		







DR WPI; 2002-519667/55.  
DR N-PSDB; ABZ33729.  
XX  
PT Novel human transporter and ion channel polypeptide, useful in diagnosis,  
PT prevention or treatment of transport, neurological, muscle, immunological  
PT and cell proliferative disorders.  
XX  
PS Claim 58; SEQ ID NO 3; 146pp + Sequence Listing; English.  
XX  
CC The invention relates to human transporter and ion channel polypeptide  
CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-  
CC ABP74127), a naturally occurring polypeptide comprising a sequence having  
CC at least sequence 90 % identity to (I) or a biologically active or  
CC immunogenic fragment of (I). (I) is useful for screening a compound for  
CC effectiveness as an agonist or antagonist, for screening a compound that  
CC specifically binds (I) or modulates the activity of (I) and for preparing  
CC a polyclonal or monoclonal antibody by hybridoma technology.  
CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for  
CC screening a compound altering gene expression. (I) and (II) are useful in  
CC a diagnostic tests for a condition or a disease associated with the  
CC expression of TRICH in a biological sample, especially disorders selected  
CC from a transport disorder such as cystic fibrosis, diabetes mellitus,  
CC Parkinson's disease, cardiac disorders, neurological disorders such as  
CC Alzheimer's disease, Huntington's disease, muscle disorders,  
CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell  
CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and  
CC cancer. (II) is useful for creating knock-in humanised animals or  
CC transgenic animals to model human diseases, in somatic or germline gene  
CC therapy, to generate a transcript image of a tissue or cell type, for  
CC detecting differences in the chromosomal location due to translocation,  
CC inversion among normal, carrier or affected individuals and for mapping  
CC genomic sequences. Note: The sequence data for this patent is not  
CC represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 1172 AA;

Query Match 3.5%; Score 93; DB 5; Length 1172;  
Best Local Similarity 25.3%; Pred. No. 1.1e+02;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;  
  
Qy 331 FDTKEEILMHL----WR--YPSL--SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381  
Db 7 FDTKPDLLLHMTKEWQLPCLLISVHGGQLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65  
  
Qy 382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439  
Db 66 FTGGVNTGVIRHVGDKDASKSRGKI-CTIGIAPWGIVENQED-----LIG 112  
  
Qy 440 TEPDMIRDGSTI--PIAKM-FQEIYVHKSVMVLIPLGAVDDGHSQNEKINR 486  
Db 113 R--DVVRPYQTMSPMSKLTVLNSMHSFILADNGTT--GKYGAEVKLRR 158

RESULT 555  
AAU02403  
ID AAU02403 standard; protein; 1187 AA.  
XX  
AC AAU02403;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human novel melastatin-like protein #17.  
XX  
KW Human; melastatin-like protein; tumour progression inhibitor; cancer;  
KW tumour growth; metastasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200132870-A1.  
XX  
PD 10-MAY-2001.  
XX

PF 31-OCT-2000; 2000WO-US029851.  
XX  
PR 01-NOV-1999; 99US-0162678P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;  
XX  
XX WPI; 2001-291053/30.  
DR N-PSDB; AAS03121.  
XX  
PT Nucleic acids encoding human proteins that share structural similarity  
PT with mammalian melastatin proteins, and which function as tumor  
PT progression inhibitors, useful for treating cancers.  
XX  
PS Disclosure; Page 75-77; 129pp; English.  
XX  
CC The present sequence representing human melastatin-like protein #17 is 1  
CC of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full  
CC length cDNA sequence for melastatin-like protein is also described  
CC (AAS03147). The melastatin-like proteins are tumour progression  
CC inhibitors sharing structural and functional similarity with mammalian  
CC melastatin proteins. The novel melastatin-like proteins were found to be  
CC expressed in inter alia, human cell lines, adult brain, pituitary,  
CC prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.  
CC The nucleic acids encoding melastatin-like proteins and the polypeptides  
CC themselves may be used for treating cancer by inhibiting tumour growth  
CC and metastasis. The melastatin-like polynucleotide and polypeptide  
CC sequences can be used in therapeutic, diagnostic and pharmacogenomic  
CC applications  
XX  
SQ Sequence 1187 AA;

Query Match 3.5%; Score 93; DB 4; Length 1187;  
Best Local Similarity 25.3%; Pred. No. 1.2e+02;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;  
  
Qy 331 FDTKEEILMHL----WR--YPSL--SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381  
Db 7 FDTKPDLLLHMTKEWQLPCLLISVHGGQLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65  
  
Qy 382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439  
Db 66 FTGGVNTGVIRHVGDKDASKSRGKI-CTIGIAPWGIVENQED-----LIG 112  
  
Qy 440 TEPDMIRDGSTI--PIAKM-FQEIYVHKSVMVLIPLGAVDDGHSQNEKINR 486  
Db 113 R--DVVRPYQTMSPMSKLTVLNSMHSFILADNGTT--GKYGAEVKLRR 158

RESULT 556  
AAU02391  
ID AAU02391 standard; protein; 1197 AA.  
XX  
AC AAU02391;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human novel melastatin-like protein #5.  
XX  
KW Human; melastatin-like protein; tumour progression inhibitor; cancer;  
KW tumour growth; metastasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200132870-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 31-OCT-2000; 2000WO-US029851.  
XX  
PR 01-NOV-1999; 99US-0162678P.  
XX







QY 1 MDPKLGMAASLLAVLLLLLLE-RGMFSSPPSPPPALLEKVFQYID---LHQDEFVQTLKEW 56  
Db 173 LDPLNNILASSRSYAMLLFAWEGWHNAVGIPLKPLYQETALSNEAYRQDGFSDTGAYW 232  
QY 57 VAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGA---RVASVDMGPPQLPDGQSLPIPPV 113  
Db 233 -----RSWYDSPTFEEDLERIYHQLEPLYLNHAYVRRVLHRRYGDRI--NLRGPIPAH 285  
QY 114 ILAELGSD-----PTKGTVCIFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGR 161  
Db 286 LLGNMWAQSWESIYDMVVPFPDK-----PNLDVTSTMVQKGW----- 322  
QY 162 GATDNKGPVLAWINAVSAFRALEQD-----LPVNIKFIIEGMEEAGSVALEELVEKEKD 215  
Db 323 -----NATHMFRVAEEFFTSGLLLPMPPEFWAESMLEKPEDGREVVCHASAW 369  
QY 216 RFFSGVDYIVISDNLWISQRPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMAD 275  
Db 370 DFYNRKDF-RIKQCTQVTMDQLSTVHHMGHVQYLYQKQDPVSLRRANPG--FHEAIGD 426  
QY 276 LVALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAHILD-----LEEYR----- 321  
Db 427 VLAL---SVSTPAHLHKIGLLDHTNDTESDINYLKMALEKIAFLPFGYLVQDQWRWGVF 483  
QY 322 -NSSRVEKFLDFTKEEILMHLWRYPSLSIHGI-----EGAFDEPGTKTVIPG-----R 368  
Db 484 SRTFSSRYNFD-----WWYLRTKYQGICPPVVRNETHFD-AGAKFHIPSVTPYIR 533  
QY 369 VIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSNMVVSMTLGL-HPWTIANIDDTQ 426  
Db 534 YFVSFVLQFQFHQALCMEAGHQGLHQCDIYQSTRAGAKLRAVLQAGCSRPPQWQVLKD-- 591  
QY 427 YLAAKRAIRTVEGTEPDMIRDGSI-----PIAKMFOEIVHKSVVLIPLGAVDDGEHSQN 481  
Db 592 -MVASDAL-----DAQPLLDYFQPVTVQWLQE-----QNERN 621  
QY 482 EKINRW-----NYIEGTKLF-----AAFFLE 502  
Db 622 GEVLGWPEYQWRPPLPNPNYPEGIDLVTDAAEASRFVE 658  
RESULT 560  
AAU02410  
ID AAU02410 standard; protein; 1544 AA.  
XX  
AC AAU02410;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human novel melastatin-like protein #24.  
XX  
KW Human; melastatin-like protein; tumour progression inhibitor; cancer;  
KW tumour growth; metastasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200132870-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 31-OCT-2000; 2000WO-US029851.  
XX  
PR 01-NOV-1999; 99US-0162678P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Donoho G, Hilbun E, Turner CA, Abuin A, Zambrowicz B, Sands AT;  
XX  
DR WPI; 2001-291053/30.  
DR N-PSDB; AAS03128.  
XX  
PT Nucleic acids encoding human proteins that share structural similarity  
PT with mammalian melastatin proteins, and which function as tumor

PT progression inhibitors, useful for treating cancers.  
XX Claim 4; Page 97-100; 129pp; English.  
XX

CC The present sequence representing human melastatin-like protein #24 is 1  
CC of 42 novel human melastatin-like proteins (AAU02387-AAU02428). The full  
CC length cDNA sequence for melastatin-like protein is also described  
CC (AAS03147). The melastatin-like proteins are tumour progression  
CC inhibitors sharing structural and functional similarity with mammalian  
CC melastatin proteins. The novel melastatin-like proteins were found to be  
CC expressed in inter alia, human cell lines, adult brain, pituitary,  
CC prostate, thymus, thyroid, testis, kidney, and gene trapped human cells.  
CC The nucleic acids encoding melastatin-like proteins and the polypeptides  
CC themselves may be used for treating cancer by inhibiting tumour growth  
CC and metastasis. The melastatin-like polynucleotide and polypeptide  
CC sequences can be used in therapeutic, diagnostic and pharmacogenomic  
CC applications  
XX  
SQ Sequence 1544 AA;

Query Match 3.5%; Score 93; DB 4; Length 1544;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;

QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAPD-EPGKTIVIPGRVIGKFSIRLVPHM 381  
Db 7 FDTKPDLLHLMTKEWQLELPKLLISVHGGLQNFELQPKLKQVF-GKGLIKAAMTTGAWI 65  
QY 382 NVSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439  
Db 66 FTGGVNTGVIRHVGDAKDHASKSRGKI-CTIGIAPWGIENQED-----LIG 112  
QY 440 TEPDMIRDGSI--PIAKM-FOEIVHKSVVLIPLGAVDDGEHSQNEKINR 486  
Db 113 R--DVVRPYQTMSPNPSKLTVLNSMHSFILADNGTT--GKYGAEVKLRR 158

RESULT 561  
ADC83406

ID ADC83406 standard; protein; 1544 AA.

XX ADC83406;

AC ADC83406;  
XX  
DT 01-JAN-2004 (first entry)

XX Human LTRPC3d SEQ ID 7.

XX Cytostatic; Nephrotropic; Gynecological; Nootropic; Neuroprotective;  
KW Antiinflammatory; Osteopathic; Dermatological; Vasotropic; Endocrine;  
KW Antianaemic; Ophthalmological; Gene therapy; Human;  
KW transient receptor potential channel; renal disorder; calcium regulation;  
KW neural disorder; Alzheimer's disease; cancer; reproductive disorder;  
KW cerebellum disorders; choroid plexus neoplasm; prion disorder;  
KW multiple sclerosis; movement disorder; chromosome 9q21.11-21.31;  
KW amyotrophic lateral sclerosis; early onset pulverulent cataract;  
KW infantile nephronophthisis; hypomagnesemia with secondary hypocalcemia;  
KW osteoporosis; DNA-repair deficiency; xeroderma pigmentosum;  
KW UV sensitivity; gamma irradiation sensitivity;  
KW pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's syndrome;  
KW skin blood vessel dilation; signal transduction; FEN1; calcium channel;  
KW LTRPC3.

XX Homo sapiens.

OS  
XX WO2003012063-A2.

PN  
XX 13-FEB-2003.

XX 01-AUG-2002; 2002WO-US024445.

XX 02-AUG-2001; 2001US-0309544P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.







KW Antianaemic; Ophthalmological; Gene therapy; Human;  
KW transient receptor potential channel; renal disorder; calcium regulation;  
KW neural disorder; Alzheimer's disease; cancer; reproductive disorder;  
KW cerebellum disorders; choroid plexus neoplasm; prion disorder;  
KW multiple sclerosis; movement disorder; chromosome 9q21.11-21.31;  
KW amyotrophic lateral sclerosis; early onset pulverulent cataract;  
KW infantile nephronophthisis; hypomagnesemia with secondary hypocalcemia;  
KW osteoporosis; DNA-repair deficiency; xeroderma pigmentosum;  
KW UV sensitivity; gamma irradiation sensitivity;  
KW pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's syndrome;  
KW skin blood vessel dilation; signal transduction; FEN1; calcium channel;  
KW LTRPC3.  
XX  
OS Homo sapiens.  
XX  
XX WO2003012063-A2.  
PN  
XX 13-FEB-2003.  
PD  
XX 01-AUG-2002; 2002WO-US024445.  
PF  
XX 02-AUG-2001; 2001US-0309544P.  
PR  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA  
XX Lee N, Chen J, Feder JN, Wu S, Lee L, Blonar MA, Bol D;  
PI Levesque PC, Sun L;  
PI  
XX WPI; 2003-278394/27.  
DR N-PSDB; ADC83407.  
DR  
XX New human transient receptor potential channel (LTRPC3) nucleic acid,  
XX useful in preventing, treating or ameliorating a medical condition, such  
XX as renal disorder, neural disorder e.g., Alzheimer's disease, or cancer.  
XX Example.2; Fig 4; 508pp; English.  
XX  
XX The present invention relates to novel proteins and their coding  
XX sequences (ADC83400-ADC83405) encoding human transient receptor potential  
XX channels. The coding sequences are useful for preparing a medicament for  
XX preventing, treating or ameliorating a medical condition, such as renal  
XX disorders; a disorder related to aberrant calcium regulation; neural  
XX disorders e.g., Alzheimer's disease; cancer; a reproductive disorder;  
XX cerebellum disorders; various choroid plexus neoplasms; prion disorders;  
XX multiple sclerosis; movement disorders; a disorder that maps to or is  
XX associated with chromosome locus 9q21.11-21.31; amyotrophic lateral  
XX sclerosis; early onset pulverulent cataract; infantile nephronophthisis;  
XX hypomagnesemia with secondary hypocalcemia; osteoporosis; DNA-repair  
XX deficiencies; xeroderma pigmentosum; UV sensitivity; gamma irradiation  
XX sensitivity; pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's  
XX syndrome; blood vessel dilations in the skin; conditions involving  
XX increased levels of apurinic/aprimidinic/abasic sites; disorders related  
XX to aberrant signal transduction; and disorders related to misregulation  
XX of FEN1 expression or activity. The present sequence is a human transient  
XX receptor potential channel LTRPC3 variant.  
XX  
SQ Sequence 1556 AA;  
  
Query Match 3.5%; Score 93; DB 7; Length 1556;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
Matches 43; Conservative 32; Mismatches 63; Indels 32; Gaps 12;  
  
QY 331 FDTKEEILMHL-----WR--YPSL--SIHGIEGAFD-EPGTKTVIPGRVIGKFSIRLVPHM 381  
| | | | : | | | : | | | | : | | | : | | | | : | | | : | | | :  
Db 7 FDTKPDLLLHLMTKEWQLLPKLLISVHGGLQNFELQPKLKQVF-GKGLIKAAAMTTGAWI 65  
| | | | : | | | : | | | | : | | | : | | | | : | | | : | | | :  
QY 382 NVSAVEKQVTRHLEDVFSKRNSSNKWVSMTLGLHPW--IANIDDTQYLAAKRAIRTVFG 439  
| | | | : | | | : | | | | : | | | : | | | | : | | | : | | | :  
Db 66 FTGGVNTGVIRHVGDALKDHASKSRGKI-CTIGIAPWGIVENQED-----LIG 112  
| | | | : | | | : | | | | : | | | : | | | | : | | | : | | | :  
QY 440 TEPDMIRDGSTI--PIAKM-FQEIYVHKSIVLPLGAVDDGEHSQNEKINR 486  
| | | | : | | | : | | | | : | | | : | | | | : | | | : | | | :  
Db 113 R--DVVRPYQTMSPNMSKLTVLNSMHSFILADNGITT--GKYGAEVKLRR 158  
| | | | : | | | : | | | | : | | | : | | | | : | | | : | | | :

RESULT 566  
ADC83403  
ID ADC83403 standard; protein; 1566 AA.  
XX  
AC ADC83403;  
XX  
DT 01-JAN-2004 (first entry)  
DE Human LTRPC3b SEQ ID 4.  
XX  
KW Cytostatic; Nephrotropic; Gynecological; Nootropic; Neuroprotective;  
KW Antiinflammatory; Osteopathic; Dermatological; Vasotropic; Endocrine;  
KW Antianaemic; Ophthalmological; Gene therapy; Human;  
KW transient receptor potential channel; renal disorder; calcium regulation;  
KW neural disorder; Alzheimer's disease; cancer; reproductive disorder;  
KW cerebellum disorders; choroid plexus neoplasm; prion disorder;  
KW multiple sclerosis; movement disorder; chromosome 9q21.11-21.31;  
KW amyotrophic lateral sclerosis; early onset pulverulent cataract;  
KW infantile nephronophthisis; hypomagnesemia with secondary hypocalcemia;  
KW osteoporosis; DNA-repair deficiency; xeroderma pigmentosum;  
KW UV sensitivity; gamma irradiation sensitivity;  
KW pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's syndrome;  
KW skin blood vessel dilation; signal transduction; FEN1; calcium channel;  
KW LTRPC3.  
XX  
OS Homo sapiens.  
XX  
PN WO2003012063-A2.  
XX  
PD 13-FEB-2003.  
XX  
PF 01-AUG-2002; 2002WO-US024445.  
XX  
PR 02-AUG-2001; 2001US-0309544P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Lee N, Chen J, Feder JN, Wu S, Lee L, Blonar MA, Bol D;  
PI Levesque PC, Sun L;  
PI  
XX WPI; 2003-278394/27.  
DR N-PSDB; ADC83402.  
DR  
XX New human transient receptor potential channel (LTRPC3) nucleic acid,  
XX useful in preventing, treating or ameliorating a medical condition, such  
XX as renal disorder, neural disorder e.g., Alzheimer's disease, or cancer.  
XX Claim 1; Fig 2; 508pp; English.  
XX  
XX The present invention relates to novel proteins and their coding  
XX sequences (ADC83400-ADC83405) encoding human transient receptor potential  
XX channels. The coding sequences are useful for preparing a medicament for  
XX preventing, treating or ameliorating a medical condition, such as renal  
XX disorders; a disorder related to aberrant calcium regulation; neural  
XX disorders e.g., Alzheimer's disease; cancer; a reproductive disorder;  
XX cerebellum disorders; various choroid plexus neoplasms; prion disorders;  
XX multiple sclerosis; movement disorders; a disorder that maps to or is  
XX associated with chromosome locus 9q21.11-21.31; amyotrophic lateral  
XX sclerosis; early onset pulverulent cataract; infantile nephronophthisis;  
XX hypomagnesemia with secondary hypocalcemia; osteoporosis; DNA-repair  
XX deficiencies; xeroderma pigmentosum; UV sensitivity; gamma irradiation  
XX sensitivity; pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's  
XX syndrome; blood vessel dilations in the skin; conditions involving  
XX increased levels of apurinic/aprimidinic/abasic sites; disorders related  
XX to aberrant signal transduction; and disorders related to misregulation  
XX of FEN1 expression or activity. The present sequence is a human transient  
XX receptor potential channel LTRPC3 variant.  
XX  
SQ Sequence 1566 AA;  
  
Query Match 3.5%; Score 93; DB 7; Length 1566;











CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1617 AA;

Query Match 3.5%; Score 93; DB 6; Length 1617;  
Best Local Similarity 17.8%; Pred. No. 1.9e+02;  
Matches 101; Conservative 72; Mismatches 171; Indels 224; Gaps 22;  
  
QY 106 QSLPIPPVILAEGLSDPTKGT-----CFYGHLDV-----QPA 138  
Db 1055 KSIPVSPQVRDALGLDGGGVVTEPPNLIKAILQAPVDLLFNGGIGTYIKAESDSA 1114  
  
QY 139 DRGDGWLTPYVL--TEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL----- 187  
Db 1115 DVGDR-ANDPVRVNGSSVRKVI GEGG--NLG-----VTALGRVEFDLSGGRINTDA 1163  
  
QY 188 -----PVNIKFIIEGMEEAGSVALEE--LVEKEKDRFFSGVDYIVISDN--- 229  
Db 1164 MDSAGVDCSDHEVNIKILIDSLVTAGKVKPQERKPLLESMTDE----VAALVLTDNEDQ 1219  
  
QY 230 -----LWISQRKPAITYGTRGNS----- 247  
Db 1220 NDLIGTSRANAPSLPVPHARQIQLYVDERGLNRELEALPSEKEIQORRAEAGIGLTSPELC 1279  
  
QY 248 -----YFMVEVKCRDQDF-----HSGTFGGILHEPMADLVA--LL 280  
Db 1280 TLMAHVKLDLKBQMLQTELTEQDVFASRLPLYFPTPLRHRFTPEIRAHQLRREIVATMLI 1339  
  
QY 281 GSLVDSSGHILVPGIYDEVVPLTEEEINTYKAI-----HLD 316  
Db 1340 NELVDAAGISYAFRIVEDVGVSADVARTYVATDAIFGVGEIWRRIIRAANLPVALSDRLT 1399  
  
QY 317 LEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIR 376  
Db 1400 LDTRRLIDRAGRLLN-----YRPOPLAV-----GAEINRFAAK 1433  
  
QY 377 ---LVPHM-----NVSAVEKQVTRHLEDVFSKRNSNKMVVSMTGLHPW---IANI 422  
Db 1434 VKALTPRMSEWLRGDDKAIVEKEAAE-----FESQAGPRDLAYLVAAGLYRFSLLDIIDI 1488  
  
QY 423 DDQYLAAKRAIRTVFGTEPDMIRDG-----STPIAKMFQEIHKSV-----VL 467  
Db 1489 GDINDIDAAEVADTYFALMDRLGTDLGLTAVSELPRNDRWHSRLARLAICDDIYASLRSLC 1548  
  
QY 468 IPLGAVDDGEHSQNEKINRWNYIEGTKL 495  
Db 1549 FDLVAVGEPEDESGBEKAIEWEHLSASRV 1576

RESULT 573  
ADN27223  
ID ADN27223 standard; protein; 2773 AA.

XX  
AC ADN27223;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #9876.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
PT  
PS Claim 1; SEQ ID NO 9876; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 2773 AA;

Query Match 3.5%; Score 93; DB 8; Length 2773;  
Best Local Similarity 20.8%; Pred. No. 4.3e+02;  
Matches 87; Conservative 59; Mismatches 143; Indels 130; Gaps 21;

QY 37 KVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTL----QRLGARV 92

Db	27	KVWEDITLG-----KALSAWSETYGDNIALTEADRVQTYRELETAARRMAAGWQRRG--F	79	PR	26-JUL-2000;	2000US-0220963P
				PR	26-JUL-2000;	2000US-0220964P
Qy	93	ASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFYGHLDVQPADRGDWLTDPYVLT	152	PR	14-AUG-2000;	2000US-0224518P
				PR	14-AUG-2000;	2000US-0224519P
Db	80	GRGDKIVQLPNSIEFVVSAPALFKLGVIPVMAL-----PAQR-----KT	119	PR	14-AUG-2000;	2000US-0225213P
				PR	14-AUG-2000;	2000US-0225214P
Qy	153	EVDGKLYGRGATDNKGPVL-----AWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEE	208	PR	14-AUG-2000;	2000US-0225267P
				PR	14-AUG-2000;	2000US-0225268P
Db	120	EIKGIIIEKSGA--KGYVIEKYLGFDYKSLAREIRREIETDLAVIVIGRSD-FIAYED	175	PR	14-AUG-2000;	2000US-0225270P
				PR	14-AUG-2000;	2000US-0225447P
Qy	209	LVE----KEKDRFFSG-VDYIVIS-----DNLWISQRKPAITYGTRGNSY	248	PR	14-AUG-2000;	2000US-0225757P
				PR	14-AUG-2000;	2000US-0225758P
Db	176	LGEGPELRDEPEIGSGEVGLFLLSGGTTGIPKLIPRRHADYLYVAQK-----	222	PR	14-AUG-2000;	2000US-0225759P
				PR	18-AUG-2000;	2000US-0226279P
Qy	249	FMVEVKCR-DQDFHSGTGGIILHEPMADLVALLGSLVDSSGHILVPGIY--DEVVPLTEE	305	PR	22-AUG-2000;	2000US-0226681P
				PR	22-AUG-2000;	2000US-0226686P
Db	223	--TAERCRLDQESVYLAALPVAHNFPLGCPGLLGLTL-SVGRVVICAVASPDIEIPLIEE	279	PR	22-AUG-2000;	2000US-0227182P
				PR	23-AUG-2000;	2000US-0227009P
Qy	306	E-----INTYKAHLD---LEEYRNSSRVEKFLFDT---	333	PR	30-AUG-2000;	2000US-0228924P
				PR	01-SEP-2000;	2000US-0229287P
Db	280	EGVTITGLVPALAHMCIEFLELDGECDISLKVIVQGGAVLDSYL-AARIEKAFACLTQQ	338	PR	01-SEP-2000;	2000US-0229343P
				PR	01-SEP-2000;	2000US-0229344P
Qy	334	-----KEEILMHLWRYPSSLHIGEGAFDEPGTKTVIPGRVIGKFSIR	376	PR	01-SEP-2000;	2000US-0229345P
				PR	05-SEP-2000;	2000US-0229509P
Db	339	IFGIAEGLICCTDLADREEIRYHTQGP-ISAYDEILIVDEKQE--VPEGEYGEHLTVR	394	PR	05-SEP-2000;	2000US-0229513P
				PR	06-SEP-2000;	2000US-0230437P
				PR	06-SEP-2000;	2000US-0230438P
				PR	08-SEP-2000;	2000US-0231242P
				PR	08-SEP-2000;	2000US-0231243P
				PR	08-SEP-2000;	2000US-0231244P
				PR	08-SEP-2000;	2000US-0231413P
				PR	08-SEP-2000;	2000US-0231414P
				PR	08-SEP-2000;	2000US-0232080P
				PR	08-SEP-2000;	2000US-0232081P
				PR	12-SEP-2000;	2000US-0231968P
				PR	14-SEP-2000;	2000US-0232397P
				PR	14-SEP-2000;	2000US-0232398P
				PR	14-SEP-2000;	2000US-0232399P
				PR	14-SEP-2000;	2000US-0232400P
				PR	14-SEP-2000;	2000US-0232401P
				PR	14-SEP-2000;	2000US-0233063P
				PR	14-SEP-2000;	2000US-0233064P
				PR	14-SEP-2000;	2000US-0233065P
				PR	21-SEP-2000;	2000US-0234223P
				PR	21-SEP-2000;	2000US-0234274P
				PR	25-SEP-2000;	2000US-0234997P
				PR	25-SEP-2000;	2000US-0234998P
				PR	26-SEP-2000;	2000US-0235484P
				PR	27-SEP-2000;	2000US-0235834P
				PR	27-SEP-2000;	2000US-0235836P
				PR	29-SEP-2000;	2000US-0236327P
				PR	29-SEP-2000;	2000US-0236367P
				PR	29-SEP-2000;	2000US-0236368P
				PR	29-SEP-2000;	2000US-0236369P
				PR	29-SEP-2000;	2000US-0236370P
				PR	02-OCT-2000;	2000US-0236802P
				PR	02-OCT-2000;	2000US-0237037P
				PR	02-OCT-2000;	2000US-0237038P
				PR	02-OCT-2000;	2000US-0237039P
				PR	02-OCT-2000;	2000US-0237040P
				PR	13-OCT-2000;	2000US-0239935P
				PR	13-OCT-2000;	2000US-0239937P
				PR	20-OCT-2000;	2000US-0240960P
				PR	20-OCT-2000;	2000US-0241221P
				PR	20-OCT-2000;	2000US-0241785P
				PR	20-OCT-2000;	2000US-0241786P
				PR	20-OCT-2000;	2000US-0241787P
				PR	20-OCT-2000;	2000US-0241808P
				PR	20-OCT-2000;	2000US-0241809P
				PR	20-OCT-2000;	2000US-0241826P
				PR	01-NOV-2000;	2000US-0244617P
				PR	08-NOV-2000;	2000US-0246474P















KW combined rod cone dystrophy; human; animal model; transgenic animal;  
KW therapy; diagnosis.  
XX Homo sapiens.  
OS  
XX WO9738004-A1.  
XX PD 16-OCT-1997.  
XX PF 10-APR-1997; 97WO-US005903.  
XX PR 10-APR-1996; 96US-00630592.  
XX PR 22-AUG-1996; 96US-00701380.  
XX PR 04-SEP-1996; 96US-00706292.  
XX PR 17-SEP-1996; 96US-00714991.  
XX (SEQU-) SEQUANA THERAPEUTICS INC.  
PA (JACK-) JACKSON LAB.  
XX  
XX Nishina P, Nobentrauth K, Naggert J, North M;  
XX WPI; 1997-512642/47.  
DR N-PSDB; AAT96643.  
XX  
XX Mammalian TULP protein - used for detecting pre-disposition to neuro-  
PT sensory defects.  
XX  
XX Claim 3; Page 57-58; 89pp; English.  
XX  
XX This protein comprises human TULP2, a member of the mammalian TULP  
CC family. Its amino acid sequence was deduced from a retinal cDNA clone  
CC (see AAT96643). Expression of TULP2 is restricted to the retina and  
CC testis, with retinal expression relatively low in the adult. The TULP2  
CC locus is associated with a predisposition to combined rod cone dystrophy.  
CC TULP2 is a member of the mammalian TULP gene family associated with  
CC various defects in sensory neurons such as cochlear defects, retinitis  
CC pigmentosa and combined rod cone dystrophy. TULP family polypeptides can  
CC be used as immunogens to raise antibodies that specifically identify TULP  
CC expressing cells, in drug screening assays directed at neurosensory  
CC defects, and for therapeutic purposes. (Updated on 25-MAR-2003 to correct  
CC PI field.)  
XX  
SQ Sequence 520 AA;

Query Match 3.5%; Score 92.5; DB 2; Length 520;  
Best Local Similarity 20.5%; Pred. No. 36;  
Matches 85; Conservative 50; Mismatches 142; Indels 137; Gaps 19;  
QY 21 ERGMFSSPPPALLEKVFQYIDLHQDEFVQTLK-----EWVAIESDSVQVPVFRQE 73  
DB 106 ERGL-----PTPRTEAVFRNLGL-QSPFLSWLPDNSDAELEVSVENGSVSP-PFFKQS 157  
QY 74 LFRMVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHL 133  
DB 158 P-RIRKKGWAHQRPQTR-AEGESDSQDMGDAHKSP-----NMGNPNMGMDGDCVYENL 208  
QY 134 DVQ-----PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRA-- 182  
DB 209 AFQKEEDLEKKREASESTGTNSSAAHNEELSKALKGEGGTDSDH---MRHEASLAIRSPC 265  
QY 183 --LEQDLPVNI-----KFIIEGME 200  
DB 266 PGLEEDMEAYVLRPALPGTMMQCYLTRDKHGVKGLFPLYLYLETSDSLQRFLLAGKR 325  
QY 201 AGS-----VALE-ELVEKEKDRFFSGVDYIVISDNLWISQR--KPAITYGTRGNSYFMV 251  
DB 326 RRSKTSNYLISLPTLLSRDGDNFVGKVRNSVFSTKFTIFDNGVNPDPREHLTRNTARIQ 385  
QY 252 EVKCRDQDFHSGTFGILHEPMADLVALLSGLVDSSGHILVPGIYDE-----VVPLTEEE 306  
DB 386 EL-----GAVCYEP-----NVLYGLGRKMTVILPGTNSQNRINVOPLNEQE 428  
QY 307 INTYKAIHLDLEEVNRRSRVEKFLFDTKEEILMHLWRYP-----LSIHG 351

Db 429 -----SLLSRYQRGDKQGLLLHKNKTPSWDKENGVYTLNPHG 465  
RESULT 582  
AAB26906  
ID AAB26906 standard; protein; 520 AA.  
XX  
AC AAB26906;  
XX DT 15-JAN-2001 (first entry)  
XX Human TULP2 protein.  
XX KW Human; TULP; neurosensory defect; retina; retinal dystrophy; testes;  
KW chromosome 19q.  
XX OS Homo sapiens.  
XX PN US6114502-A.  
XX PD 05-SEP-2000.  
XX PF 27-FEB-1998; 98US-00032365.  
XX PR 10-APR-1996; 96US-00630592.  
XX PR 22-AUG-1996; 96US-00701380.  
XX PR 04-SEP-1996; 96US-00706292.  
XX PR 17-SEP-1996; 96US-00714991.  
XX PR 30-APR-1997; 97US-00850218.  
XX PR 01-AUG-1997; 97US-00904699.  
XX PR 17-SEP-1997; 97US-00932306.  
XX (AXYS-) AXYS PHARM INC.  
XX North M, Nishina P, Noben-Trauth K, Naggert J;  
XX WPI; 2000-586483/55.  
DR N-PSDB; AAA94636.  
XX  
XX Mammalian proteins expressed in retina and brain, useful for producing  
PT antibodies and for diagnosing neurosensory defects including cochlear  
PT degeneration, peripheral retinal degeneration and cone-rod retinal  
PT dystrophy.  
XX Claim 1; Col 65-68; 61pp; English.  
PS  
XX  
CC The present sequence is human TULP2. The gene encoding this sequence is a  
CC member of the neurosensory defect associated gene family, and is  
CC expressed in the retina and testes. TULP2 gene is tightly linked to  
CC framework marker WI-9028 on chromosome 19q. The TULP2 gene is useful as  
CC an immunogen to raise antibodies that specifically identify TULP  
CC expressing cells and in drug screening assays directed at neurosensory  
CC defects. The present protein can be used for the treatment of  
CC neurosensory degenerative conditions (retinal dystrophies) e.g. retinitis  
CC pigmentosa, combined cone rod dystrophy, age related macular dystrophy,  
CC Stargardt's macular dystrophy, Best's disease, pigment pattern  
CC dystrophies, central alveolar choroidal dystrophy, dominant drusen,  
CC hereditary haemorrhagic macular dystrophy, North Carolina macular  
CC dystrophy, pericentral choroidal dystrophy, adult foveomacular dystrophy,  
CC benign concentric annular macular dystrophy, central areolar pigment  
CC epithelial dystrophy, congenital macular coloboma, dominantly inherited  
CC cystoid macular oedema, familial foveal retinoschisis, fenestrated sheen  
CC macular dystrophy, progressive foveal dystrophy, slowly progressive  
CC macular dystrophy, Sorsby's pseudoinflammatory dystrophy, progressive  
CC cone dystrophy, Leber's congenital amaurosis and Goldman-Favre syndrome  
XX Sequence 520 AA;  
SQ

Query Match 3.5%; Score 92.5; DB 3; Length 520;  
Best Local Similarity 20.5%; Pred. No. 36;  
Matches 85; Conservative 50; Mismatches 142; Indels 137; Gaps 19;

















Db 555 DSEPRFKRGLKDG-----ELWNKFFVRI-LNANDEAQVS 587

RESULT 592

ABP52140  
ID ABP52140 standard; protein; 1501 AA.

XX AC ABP52140;

XX DT 10-OCT-2002 (first entry)

XX DE Saccharomyces cerevisiae protein Snq2P SEQ ID NO:92.

XX KW ATP-binding cassette transporter; ABC transporter; modulation; D loop;  
KW cancer; bacterial infection; fungal infection; protozoal infection;  
KW antibacterial; fungicide; protozoacide.

XX OS Saccharomyces cerevisiae.

XX PN EP1217066-A1.

XX PD 26-JUN-2002.

XX PF 21-DEC-2000; 2000EP-00870316.

XX PR 21-DEC-2000; 2000EP-00870316.

XX PA (UYGE-) UNIV GENT.

XX WPI; 2002-550404/59.

XX PT Modulating activity of ATP-binding cassette (ABC) transporters by  
PT influencing dimerization of nucleotide binding domains through use of D  
PT loop sequence of an ABC transporter, or its antisense peptide or peptide  
PT mimetic.

XX PS Disclosure; Fig 3; 290pp; English.

XX CC The present invention describes a method (M1) for modulating the activity  
CC of ATP-binding cassette (ABC) transporters by influencing the  
CC dimerisation of the nucleotide binding domains comprising using: (a) a  
CC polypeptide (polyP) consisting of 5-50 amino acids comprising the D loop  
CC sequence of an ABC transporter (ABP52049 to ABP52091); (b) a polyP  
CC consisting of the D loop sequence of an ABC transporter; (c) a peptide  
CC mimetic or antisense peptide of (a) or (b). ABC transporters have  
CC antibacterial, fungicide and protozoacide activities. (M1) is useful for  
CC selectively modulating the activity of ABC transporters belonging to the  
CC group of multidrug transporter/P-glycoproteins. Bacterial, fungal or  
CC protozoal ABC transporters are involved in the infection of a mammal or  
CC in the induction of resistance to antibiotics or drugs in a mammal. (M1)  
CC is useful for preventing, treating or alleviating diseases associated  
CC with functionality of an ABC transporter. ABP52092 to ABP52140 represent  
CC ABC transporter proteins given in the exemplification of the present  
CC invention

XX SQ Sequence 1501 AA;

Query Match 3.5%; Score 92.5; DB 5; Length 1501;  
Best Local Similarity 20.8%; Pred. No. 1.9e+02;  
Matches 59; Conservative 27; Mismatches 84; Indels 113; Gaps 13;

Qy 124 KGTVCFYGHLDVQ-----PADRGDWLTDPVYLTEVD----- 155

Db 236 KADVIYNGELDVHFPYLTVKQTLDFAIACKTPALRVNNSVKKEYIASRRDLYATIFGLRH 295

Qy 156 -----GKLYGRGATDN-----KGPVLAWINA---VSAFRALEQDLPVNIKF 193

Db 296 TYNTKVGNDFVRGVSGGERKRVSAEALAAKGSIIYCDNATRGLDASTALEY----- 347

Qy 194 IIEGMEEAGSVALBELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEV 253

Db 348 -----AKAIRIMTNLLKSTAF--VTIYQASENIYETFDKVTIVLSGK-QIYF---- 391

Qy 254 KCRDQDFHSGTFGGILHE-----PMADLVALLGSLVDSSG-HILVPGIYDEV 299  
Db 392 -----GLIHEAKPYFAKMGYLCPPRQATAEFLTALTDPNGFHLIKPG-YENK 437

Qy 300 VPLTEEEINTY-----KAHLDLEEYRNSRVEKFLFDTKE 335  
Db 438 VPTAAEFETYWLNSPEFAQMKKDIAAYKEKVNTEK-----TKE 476

RESULT 593

ADN18953

ID ADN18953 standard; protein; 1501 AA.

XX AC ADN18953;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #1606.

XX KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 1606; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan



CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 1501 AA;

Query Match 3.5%; Score 92.5; DB 8; Length 1501;  
Best Local Similarity 20.8%; Pred. No. 1.9e+02;  
Matches 59; Conservative 27; Mismatches 84; Indels 113; Gaps 13;  
QY 124 KGTVCYFGHLDVQ-----PADRGDWLTDPYVLTEVD----- 155  
Db 236 KADVIYNGELDVHFPYLTVKQTLDFAIACKTPALRVNNSVKKEYIASRRDLVATIFGLRH 295  
QY 156 -----GKLYGRGATDN-----KGPVLAWINA---VSAFRALEQDLPVNIKF 193  
Db 296 TYNTKVGNDFVRGSGGERKRVSIABALAAKGSYICWDNATRGDLDASTALEY----- 347  
QY 194 IIEGMEAGSVALEELVEKEDRFFSGVDYIVISDNLWISQRPKPAITYGTRGNSYFMVEV 253  
Db 348 -----AKAIRMTNLKSTAF--VTIYQASENIYETFDKVTVLYSGK-QIYF---- 391  
QY 254 KCRDQDFHSGTGGILHE-----PMADLVALLGSLVDSG-HILVPGIYDEV 299  
Db 392 -----GLIHEAKPYFAKMGYLCPPRQATAEFLTALDTPNGFHLIKPG-YENK 437  
QY 300 VPLTEEEINTY-----KATHLDLEEYRNSRRVEKFLDFTKE 335  
Db 438 VPTAEFEFYWLNSPEFAQMKKDIAAYKEKVNTKE-----TKE 476

RESULT 594  
ADM25528  
ID ADM25528 standard; protein; 2042 AA.  
XX  
AC ADM25528;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Hyperthermophile Methanopyrus kandleri protein #134.  
XX  
KW hyperthermophile; protein stability enhancement;  
KW protein activity enhancement.  
XX  
OS Methanopyrus kandleri.  
XX  
PN WO2003076575-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 04-MAR-2003; 2003WO-US006664.  
XX  
PR 04-MAR-2002; 2002US-0361742P.  
PR 14-MAY-2002; 2002US-0380423P.  
PR 16-SEP-2002; 2002US-0410974P.  
XX  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
XX  
PI Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;  
XX  
XX WPI; 2003-748383/70.  
DR N-PSDB; ADM27081.  
XX  
PT New isolated nucleic acids encoding any of about 1700 Methanopyrus  
PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
PT as diagnostic agents.  
XX  
PS Claim 31; SEQ ID NO 134; 1023pp; English.  
XX  
CC The invention comprises the amino acid sequence of proteins from the  
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the

CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
CC proteins of the invention are useful for enhancing the stability and/or  
CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
CC a variety of diagnostic and analytical methods. The present amino acid  
CC sequence represents a Methanopyrus kandleri protein of the invention.  
XX  
SQ Sequence 2042 AA;

Query Match 3.5%; Score 92.5; DB 7; Length 2042;  
Best Local Similarity 19.8%; Pred. No. 3e+02;  
Matches 88; Conservative 54; Mismatches 145; Indels 157; Gaps 21;  
QY 34 LLEKVFQYIDLHQDEFVQTLKENVVAIESDSVQVPFRQELFRMMAVAADTLQRLGARVA 93  
Db 993 IVELLFESARLERTNLFNAL-----SGGYVP-PGFNSSPFKQI---DALP-TGRNAC 1039  
QY 94 SVDMPQQQLPDGQSLPIPPVILAEIGSDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTE 153  
Db 1040 MFD--PRKWPDWISINVAYTVAIPLRT-VTRKVVAF-----DW----- 1074  
QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEAGSVALEELVEKE 213  
Db 1075 -----ATDN-----INT-----RGLPIAVQMLLLGV-----LPHRN 1100  
QY 214 KORFFSGVDYIVISDNLWISQRPKPAITYGTRGNSY-----FMVEVKCRDQDFHSGTFG 266  
Db 1101 ADWVVTGVD-----PSLCMNPSGVSYTRRLGQILVVGRIVRMESLGSQAVR 1146  
QY 267 GILHEPMA-----DLVALIGSLVDSSGHILVPG---IYDEVVPLT 303  
Db 1147 LVLEPPMGQRIEVRCPNVNLPILPLHLDDEVMLVGLTIVSTGGRVEVNVARVLSSEAKRI 1206  
QY 304 EEEINT---YKAHLDLEEYRNSRRVEK-----FLFDTKEEILMHLWRYPSLSIHGIEG 354  
Db 1207 EDEVLTPQTLSAVGRAFGRLPIRGVRVERVEGRIVLTDGCTEVVRVRI-----DEG 1256  
QY 355 AFDEPGTKTIPGRVIGKFSIRLV---PHMNVSAVEKQVTRHLEDVFSKRNSSNKMV--- 408  
Db 1257 RVPEGETVTVIG-----TVTLVGDEPVISASLVLRVPRRLTDVIVTGTSCFRDVF 1310  
QY 409 -----VSMITGLHPWIANI 422  
Db 1311 NILTELFLGRVAAILAAEPYLARL 1334

RESULT 595  
ADJ70287  
ID ADJ70287 standard; protein; 2106 AA.  
XX  
AC ADJ70287;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human heat mitochondrial protein as a therapeutic target SegID2093.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
OS Homo sapiens.

XX WO2003087768-A2.  
PN  
XX 23-OCT-2003.  
PD  
XX  
PF 04-APR-2003; 2003WO-US010870.  
XX  
PR 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.



QY 405 NKMVSVMTLGLHPWIANIDTQYLAAKRAIRTVFGTEPDM--IRDGSTIP----- 452  
Db 142 EDATAGLT-HMIIWHSNLNDTTYQTRALVRT--GMDPRMCSLMQGSTLPRRSAGAAGAAV 198  
QY 453 --IAKMFOEIVHKSVVLIPLGAVD----DGEHSQNEKI 484  
Db 199 KGVGTMMELIR----MIKRGINDRNFWRGNGRRTRI 232

RESULT 597  
ABP28720  
ID ABP28720 standard; protein; 327 AA.  
XX  
AC ABP28720;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 6616.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX

OS Streptococcus agalactiae.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-000005640.  
XX

PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;  
PI Tettelin H;  
XX  
DR WPI; 2002-352536/38.  
DR N-PSDB; ABN69351.

XX New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.

PS Claim 1; Page 3823; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX

SQ Sequence 327 AA;  
Query Match 3.5%; Score 92; DB 5; Length 327;  
Best Local Similarity 20.4%; Pred. No. 20;  
Matches 57; Conservative 38; Mismatches 84; Indels 100; Gaps 14;

QY 21 ERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLK-----EWVAIE-----SDSV-QPVPRF 70  
Db 76 ERKPFIKRMHDKGLIASISVGVKDYEYDFVTSLKEDAPEFITIDIAHGHSNVIEMIQHI 135  
QY 71 ROELFRMMAVAADT-----LQRLGARVASYDMGPPQQL-----PDGQSLPI-- 110  
Db 136 KQELPETFVIAGNVGTPEAVRELENAGADATKVGIGPGKVCITKVKGTGFGWQLAALR 195  
QY 111 -----PPVILAELGSDPTKTGTV-----FYGHLDVQPADRGDGLWTD 148  
Db 196 WCSKAARKPIAD--GGIRTHGDIAKSIRFGASMMVIGSLFAGHLE-----SP 241  
QY 149 YVLTEVDG-----KLYGRGATDNKG-----PVLAWINAVSAFRALEQDLFVNIK 192  
Db 242 GKLEVEGQQKFKEYYGSASEYQKGEHKNVEGKKILLPVKGRLE--DTLTEMQQDLQSSIS 299  
QY 193 FIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLM 231  
Db 300 Y-----AGGKELDSL-----RHVDYIVIVKNSIW 322

RESULT 598  
AAB96331  
ID AAB96331 standard; protein; 423 AA.  
XX  
AC AAB96331;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Putative P. abyssi DNA repair exonuclease.  
XX  
KW Hyperthermophilic archaeon; hyperthermophilic protein.  
XX  
OS Pyrococcus abyssi.

PN FR2792651-A1.  
XX  
PD 27-OCT-2000.  
XX  
PF 21-APR-1999; 99FR-00005034.  
XX  
PR 21-APR-1999; 99FR-00005034.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
XX  
PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;  
PI Querellou J, Weissenbach J, Saurin W, Heilig R;  
XX

DR WPI; 2001-126236/14.  
XX  
PT New nucleotide sequences isolated from Pyrococcus abyssi encode proteins  
PT useful in industry.  
XX  
PS Claim 7; Page 1002-1003; 1657pp; French.  
XX  
CC The present invention relates to the genomic sequence of Pyrococcus  
CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is  
CC a hyperthermophilic archaeon, which is isolated from deep-sea  
CC hydrothermal vents. The present sequence is one such P. abyssi protein.  
CC The proteins of the present invention have various potential industrial  
CC uses, since the proteins are stable at very high temperatures, some up to  
CC 110 degrees centigrade. Note: This patent is in the same patent family as  
CC WO200065062, which contains additional sequences as shown in AAB99132-  
CC AAB99143, AAH75903-AAH75920 and AAG66436  
XX

SQ Sequence 423 AA;  
Query Match 3.5%; Score 92; DB 4; Length 423;  
Best Local Similarity 19.5%; Pred. No. 29;  
Matches 77; Conservative 64; Mismatches 105; Indels 148; Gaps 20;



QY	196	EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC	255
Db	37	KAFEDAIIKICVDE-----KVDFVIAGDLFNSSRP---SPGTIKTAVKILQIP-	81
QY	256	RQQDF-----HSGTFFG--ILHEPMADLVALLGSLVDSSGHILVPGIYDEVWP---	L 302
Db	82	RDNINIPVAIEGNHRTQGPSILH-----LLEDLGLLYVLGVRDEKVENEYL	129
QY	303	TEEEINT-----YKAHLDLEEYRNSSRVE-----KFLFDTKKEILMHLWR-----	343
Db	130	TSEKTKAGLVKGMKYKDVIEHGMKYMSAWFEGNIELFKSMFRPEGDAILVLHQGVREIT	189
QY	344	---YPSLS-----JH-GIEGAFDEPGTKTVIPGRV-----IGKFSIR	376
Db	190	ENNYPNYSSELSDLPKGYLYYALGHTRKFELTYDD--APVVYPGSLERWDFGDYSLK	247
QY	377	LVPHMNVSAVEKQV-----TRHLEDVFSKRNSSNMVVSMTLGLH	416
Db	248	LT--WNGFQKBEVGVDKGYFIVEDFKPRFIRINARDFIDVHIKHSENEIKKAVKLAVP	305
QY	417	-----PWIANIDDTQYLAAKRAIRTVPFGTPEDMIR-----DGSTI	451
Db	306	KIPRNSYVRFNIRWKRPVDVWIKSVINAIFYR-----VNPRIIKEERGPDGKDL	355
QY	452	PIAKMFQEIYVHKSVDLPLGAVDDGGEHSQNEKIN	485
Db	356	DVKKFFTELEWK---IIELEASEKEYEYILNQIID	386
RESULT 599			
AAE20629	ID AAE20629 standard; protein; 511 AA.		
XX	AC	AAE20629;	
XX	DT	01-JUL-2002 (first entry)	
XX	DE	Human gene 2 encoded secreted protein HMWFG79, SEQ ID NO:32.	
KW	Human;	secreted protein; proliferative disorder; cancer; tumour; sepsis;	
KW	foetal	abnormality; developmental abnormality; haematopoietic disorder;	
KW	immune	system; skin; cognitive; neurological; cardiovascular; angiogenic;	
KW	kidney;	gastrointestinal; pregnancy-related; endocrine; gene therapy;	
KW	AIDS;	autoimmune disease; rheumatoid arthritis; inflammation; psoriasis;	
KW	Alzheimer's	disease; Parkinson's disease; schizophrenia; atherosclerosis;	
KW	asthma;	diabetes; infection; wound healing; vulneryary; cell culture;	
KW	chemotaxis;	food additive; allergy.	
XX	OS	Homo sapiens.	
XX	FH	Key	Location/Qualifiers
FT	Peptide	1. .40	
FT	Protein	/label= Signal_peptide	
FT		41. .511	
FT	Misc-difference	/label= Mature_secreted_protein	
FT		171	
FT		/label= Unknown	
FT		/note= "Encoded by TTW"	
FT	Misc-difference	358	
FT		/label= Unknown	
FT		/note= "Encoded by TGN"	
FT	Misc-difference	388	
FT		/label= Unknown	
FT		/note= "Encoded by TTK"	
XX	PN	WO200218411-A1.	
XX	PD	07-MAR-2002.	
XX	17-JAN-2001;	2001WO-US001383.	
PF	28-AUG-2000;	2000US-0228083P.	
XX	05-JAN-2001;	2001US-0259804P.	
PR			

XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;	
XX	Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;	
PI	Fiscella M, Ni J;	
XX	WPI; 2002-281059/32.	
DR	N-PSDB; AAD33049.	
XX	Seven nucleic acid molecules encoding human secreted proteins, useful in	
PT	the prevention, treatment and diagnosis of cancer, immune disorders,	
PT	cardiovascular disorders and neurological diseases.	
XX	Claim 11; Page 395-397; 421pp; English.	
PS		
XX	AAAD33048-AAAD33067 represent cDNAs corresponding to 7 human secreted	
CC	protein genes, and AAE20628-AAE20647 represent the proteins they encode.	
CC	AAE20648-AAE20652 represent human secreted protein fragments or variants.	
CC	The secreted protein and their genes are useful for preventing, treating	
CC	or ameliorating medical conditions, e.g., by protein or gene therapy.	
CC	Pathological conditions can be diagnosed by determining the amount of the	
CC	new protein in a sample or by determining the presence of mutations in	
CC	the new genes. Specific uses are described for each of the 7 genes, based	
CC	on the tissues in which they are most highly expressed, and include	
CC	developing products for the diagnosis or treatment of proliferative	
CC	disorders, cancer, tumours, foetal and developmental abnormalities,	
CC	haematopoietic disorders, diseases of the immune system, AIDS, autoimmune	
CC	diseases (e.g., rheumatoid arthritis), inflammation, allergies,	
CC	neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),	
CC	cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,	
CC	psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,	
CC	angiogenic disorders, kidney disorders, gastrointestinal disorders,	
CC	pregnancy-related disorders, endocrine disorders, and infections. The	
CC	proteins can also be used to aid wound healing and epithelial cell	
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs	
CC	before transplantation, for supporting cell culture of primary tissues,	
CC	to regenerate tissues, to identify their cognate ligands or binding	
CC	partners, and in chemotaxis, and can be used as a food additive or	
CC	preservative to modify storage properties. Antibodies specific for a	
CC	protein of the invention can be used in alleviating symptoms associated	
CC	with the disorders mentioned above, and in diagnostic immunoassays e.g.,	
CC	radioimmunoassay or enzyme linked immunosorbent assay (ELISA). Expression	
CC	of the genes can be driven by a range of promoters active in eukaryotic	
CC	cells. The present sequence is human secreted protein of the invention	
XX	Sequence 511 AA;	
SQ		
Query Match 3.5%; Score 92; DB 5; Length 511;		
Best Local Similarity 18.9%; Pred. No. 39;		
Matches 57; Conservative 59; Mismatches 111; Indels 74; Gaps 13;		
QY	230	LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFG----- 267
Db	52	LWQAE-EGELLPTQGDSEGLEEPSQEQSFSDKLFSGKGLHFQPSVLDFGIQFLGHPVA 110
QY	268	-ILH--EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTBEETINTYKAHLDLEEYRNS 324
Db	111	KILHAYNPSRDSEVVVNSVFAAGHFHVPVPCRVIPAMGK--TSFRIIFLPTEE----- 163
QY	325	RVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 384
Db	164	-----GSISSLXINTSSYGLVSYH-VSGI-----GTR-----RISTEGSAKQLPNA-YF 206
QY	385	AVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVPFGTEPDM 444
Db	207	LLPKVQSIQLSQMAETTTSLLOVQLECSLHNKVC-----QQLKGCYLESDDV 255
QY	445	IRDCSTIPI-----AKMFOE-----IVHKSVDLPLGAVDDGGEHSQNEKINRWNYIEGTK 494
Db	256	LRLQMSIMVTMENFSKEFEENTQHLLDHLISIVYV---ATDESETSDDSAVNMVILHSGNS 312
QY	495	L 495







Db 111 KILHAYNPSRDESEVVNSVFAAAGHFHVPVPCRVIPAMGK--TSFRIIFLPTEE----- 163

Qy 325 RVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 384

Db 164 -----GSISSLXINTSSYGVLSTYH-VSGI-----GTR-----RISTEGSAKQLPNA-YF 206

Qy 385 AVEKQVTRHLEDVFSKRNSSNKMVSMVMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDM 444

Db 207 LLPKVQSLQSQMAETNTSLQVLECSLHNKVC-----QQLKGCYLESDDV 255

Qy 445 IRDGSSTIPI-----AKMFQE-----IVHKSVMVLIPLGAVDDGHSQNEKINRWNYIEGTK 494

Db 256 LRLQMSIMVTMENFSKEFEENTQHLHDLSIVYV---ATDESETSDDSAVNMYILHSGNS 312

Qy 495 L 495

Db 313 L 313

RESULT 603

ABG72985

ID ABG72985 standard; protein; 539 AA.

XX ABG72985;

AC

DT 04-MAR-2003 (first entry)

XX Human RGS9 protein 132 residue deletion mutant.

DE Human; RGS9; human regulator of G-protein signaling protein 9; evectin;

XX RGS9-evectin dimer; G-protein activity; Alzheimer's disease;

KW Parkinson's disease; mutant; mutein.

KW Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Domain 460..539

FT /label= Proline\_rich\_domain

FT /note= "In the wild-type protein this domain extends to

FT amino acid 671"

FT 461..539

FT /label= Evectin\_binding\_domain

FT /note= "In the wild-type protein this domain extends to

FT amino acid 602. This domain is specifically claimed in

FT claim 1 of the specification"

FT Misc-difference 539

FT /note= "Amino acids 540 to 671 have been deleted from the

FT wild-type sequence"

XX

PN WO200279401-A2.

XX

PD 10-OCT-2002.

XX

PF 22-MAR-2002; 2002WO-US009064.

XX

PR 28-MAR-2001; 2001US-0279240P.

XX (AMHP ) WYETH.

PA Jones PG, Young KH;

XX WPI; 2003-103266/09.

XX New human regulator of G-protein signaling protein 9 polypeptide fragment

PT and evectin polypeptide, useful for treating neurological disorders e.g.,

PT Alzheimer's disease or Parkinson's.

XX Example 1; Page; 134pp; English.

PS The invention relates to an isolated human regulator of G-protein

XX signaling protein 9 (RGS9) polypeptide fragment and evectin polypeptide.

CC The invention also discloses methods which are useful for assaying the

CC effects of test compounds on the activity of a RGS9-evectin polypeptide

CC dimer and transgenic animal, producing a transgenic animal, and for

CC modulating G-protein activity in a subject. The methods are also useful

CC for diagnosis of a disease or susceptibility to a disease in a subject

CC related to the activity of a RGS9-evectin dimer. The methods are also

CC useful for the treatment of a subject in need of enhanced RGS9-evectin

CC dimer activity, or inhibiting RGS9-evectin dimer activity. The

CC polypeptide is useful for treating neurological disorders e.g.,

CC Alzheimer's disease or Parkinson's. The present sequence represents the

CC polypeptide sequence of a mutant human RGS9 protein with a 132 residue C

CC terminal deletion. The deletion mutant was used to find which regions of

CC the RGS9 protein bind to evectin protein. Note: The present sequence is

CC not shown in the specification but is derived from the human RGS9

CC sequence given on pages 131 to 133 and from the information given in

CC example 1 of the specification (see ABG72975)

XX

SQ Sequence 539 AA;

Query Match 3.5%; Score 92; DB 6; Length 539;

Best Local Similarity 21.5%; Pred. No. 43;

Matches 53; Conservative 37; Mismatches 81; Indels 76; Gaps 12;

Qy 318 BEYR---NSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374

Db 164 EGYRAGKERNKADRYALDCQEKAYWLVRCPD---GMDNVLDYGLDRVTNPNE----- 213

Qy 375 IRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNKMVSMVMTLGLHPW 418

Db 214 ---VKKQTVAVKKEIMYQQALMRSTVSSVSLGGIVKYSEQFSSNDAIMSGCLPSNPW 270

Qy 419 IANIDDTQY--LAAK-----RAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVMVLI 468

Db 271 IT--DDTQFWDNLNAKLVEIPTKMRVERWAFNFS-ELIRDPKG---RQSEQYFLKKEFSGE 324

Qy 469 PLG---AVDDGEHSQNEKI-----NRWNYIEGTKLFAA-----PF 500

Db 325 NLGFWEACEDLKYGDQSKVKEKAEIYKLFAPGARRWINIDGKTMIDITVKGLKHPHYV 384

Qy 501 LEMAAQLH 507

Db 385 LDDAAQTH 391

RESULT 604

ABG72984

ID ABG72984 standard; protein; 571 AA.

XX ABG72984;

AC

DT 04-MAR-2003 (first entry)

XX Human RGS9 protein 100 residue deletion mutant.

DE Human; RGS9; human regulator of G-protein signaling protein 9; evectin;

KW RGS9-evectin dimer; G-protein activity; Alzheimer's disease;

KW Parkinson's disease; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Domain 460..571

FT /label= Proline\_rich\_domain

FT /note= "In the wild-type protein this domain extends to

FT amino acid 671"

FT 461..571

FT /label= Evectin\_binding\_domain

FT /note= "In the wild-type protein this domain extends to

FT amino acid 602. This domain is specifically claimed in

FT claim 1 of the specification"

FT Misc-difference 571

FT /note= "Amino acids 572 to 671 have been deleted from the

FT wild-type sequence"

XX	WO200279401-A2.	XX	14-FEB-2002 (first entry)
PN		DE	Haemophilus influenzae cellular proliferation protein #53.
XX	10-OCT-2002.	XX	
PD		KW	Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX		KW	antibacterial; drug design.
PF	22-MAR-2002; 2002WO-US009064.	XX	
XX		OS	Haemophilus influenzae.
PR	28-MAR-2001; 2001US-0279240P.	XX	
XX		PN	WO200170955-A2.
PA	(AMHP ) WYETH.	XX	
XX		PD	27-SEP-2001.
PI	Jones PG, Young KH;	XX	
XX		PF	21-MAR-2001; 2001WO-US009180.
DR	WPI; 2003-103266/09.	XX	
XX		PR	21-MAR-2000; 2000US-0191078P.
PT	New human regulator of G-protein signaling protein 9 polypeptide fragment	PR	23-MAY-2000; 2000US-0206848P.
PT	and eVectin polypeptide, useful for treating neurological disorders e.g.,	PR	26-MAY-2000; 2000US-0207727P.
PT	Alzheimer's disease or Parkinson's.	PR	23-OCT-2000; 2000US-0242578P.
XX		PR	27-NOV-2000; 2000US-0253625P.
PS	Example 1; Page; 134pp; English.	PR	22-DEC-2000; 2000US-0257931P.
XX		PR	16-FEB-2001; 2001US-0269308P.
CC	The invention relates to an isolated human regulator of G-protein	XX	(ELIT-) ELITRA PHARM INC.
CC	signaling protein 9 (RGS9) polypeptide fragment and eVectin polypeptide.	PA	
CC	The invention also discloses methods which are useful for assaying the	XX	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
CC	effects of test compounds on the activity of a RGS9-eVectin polypeptide	PI	Yamamoto RT, Xu HH;
CC	dimer and transgenic animal, producing a transgenic animal, and for	XX	
CC	modulating G-protein activity in a subject. The methods are also useful	DR	WPI; 2001-611495/70.
CC	for diagnosis of a disease or susceptibility to a disease in a subject	DR	N-PSDB; AAS53271.
CC	related to the activity of a RGS9-eVectin dimer. The methods are also	XX	
CC	useful for the treatment of a subject in need of enhanced RGS9-eVectin	PT	New polynucleotides for the identification and development of
CC	dimer activity, or inhibiting RGS9-eVectin dimer activity. The	PT	antibiotics, comprise sequences of antisense nucleic acids.
CC	polypeptide is useful for treating neurological disorders e.g.,	XX	
CC	Alzheimer's disease or Parkinson's. The present sequence represents the	PS	Example 3; SEQ ID NO 11005; 511pp; English.
CC	polypeptide sequence of a mutant human RGS9 protein with a 100 residue C	XX	
CC	terminal deletion. The deletion mutant was used to find which regions of	CC	The invention relates to antisense inhibitors of genes essential to
CC	the RGS9 protein bind to eVectin protein. Note: The present sequence is	CC	prokaryotic cellular proliferation, their use in identifying the genes,
CC	not shown in the specification but is derived from the human RGS9	CC	their use in the discovery of novel antibiotics, the essential genes
CC	sequence given on pages 131 to 133 and from the information given in	CC	themselves and the encoded proteins. The prokaryotes used are Escherichia
CC	example 1 of the specification (see ABG72975)	CC	coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX		CC	Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
SQ	Sequence 571 AA;	CC	useful for the identification of potential new targets for antibiotic
		CC	development. The antisense nucleic acids can also be used to identify
		CC	proteins used in proliferation, to express these proteins, and to obtain
		CC	antibodies capable of binding to the expressed proteins. The proteins can
		CC	be used to screen compounds in rational drug discovery programmes. The
		CC	antisense nucleic acid sequence is also useful to screen for homologous
		CC	nucleic acids which are required for cell proliferation in a wide variety
		CC	of organisms. The present sequence represents an essential prokaryotic
		CC	cellular proliferation protein. Note: The sequence data for this patent
		CC	did not form part of the printed specification, but was obtained in
		CC	electronic format directly from WIPO at
		CC	ftp.wipo.int/pub/published_pct_sequences
		XX	
		SQ	Sequence 588 AA;
			Query Match 3.5%; Score 92; DB 4; Length 588;
			Best Local Similarity 21.8%; Pred. No. 49;
			Matches 89; Conservative 62; Mismatches 146; Indels 112; Gaps 22;
QY	318 EEYR---NSSRVEKFLFDTKKEILMLHWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFS 374	QY	39 FQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMVAADTLQRLGARVASVDMG 98
Db	164 EQRAGKERNKADRYALDCQEKAYWLVRCP--GMDNVLDYGLDRVTNPNE----- 213	Db	125 YRYDLRRPEMAQRLKTRAKITSF----VRRFMD--NGFLDIETPMLTKATPEGARDYLV 179
QY	375 IRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNKQVVSMTLGLHPW 418	QY	99 PQLPDPGQ--SLPIPPVILAE-----GSDPTKGTV-CFYG---HLDVQP-----ADRGDW 144
Db	214 ---VKKQTVVAVKKEIMYYQQALMRSTVKSSVSLGGIVKYSEQFSSNDAIMSGCLPSNPW 270	Db	180 PSRVHKGKFYALPQSPQLFKLLMMSGFDRIYQIVKCFRDEDLRADRQPEFTQIDVETSF 239
QY	419 IANIDDTQY--LAAK-----RAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSUVLI 468	QY	145 LTDPYVLTVEVDGKLYGR-----GATDNKGPVLAWINAVSAFRALEQDL-----PVNIKFI 194
Db	271 IT--DDTQFWDLNAKLVEIPTKMRVERWAFNFS-ELIRDPKG---RQSFQYFLKKEFSGE 324	Db	240 LTAPEVREIMERMVHGLWLDITIGVDLGLKFPVMTWQEAAMRRFGSDKPDLRNPLEMVDVADI 299
QY	469 PLG---AVDGEHSQNEKI-----NRWNYIEGTXLFAA-----FF 500		
Db	325 NLGFWEACEDLKYGDQSKVKEKAEIYKFLAPGARRWINIDGKTMDITVKGLKHPHYV 384		
QY	501 LEMAOHLH 507		
Db	385 LDAAQTH 391		
			RESULT 605
			AAU35412
ID	AAU35412 standard; protein; 588 AA.		
XX			
AC	AAU35412;		
XX			







```
Query Match      3.5%; Score 92; DB 6; Length 624;
Best Local Similarity 21.5%; Pred. No. 53;
Matches 53; Conservative 37; Mismatches 81; Indels 76; Gaps 12;

QY 318 EYR---NSSRVEKFLDTEKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374
   |||  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 164 EYRAGKERNKADRYALDCQEKAYWLVRHCPP-----GMDNVLDYGLDRVTTNPE----- 213

QY 375 IRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNMVVSMTLGLHPW 418
   |||  ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 214 ---VKKQTVVAVKKEIMYYQQALMRSTVKSSVSLGGIVKYSEQFSSNDAINSGCLPSNPW 270

QY 419 IANIDDTQY--LAAK-----RAIRTVFGTEPDMIRDGSTIPIAKMFQEIYHKS VWLI 468
   |||  ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 271 IT--DDTQFWDLNAKLVEIPTKMRVERWAFNFS-ELIRDPKG---RQSFQYFLKKEFSGE 324

QY 469 PLG---AVDDGEHSQNEKI-----NRWNYIEGTKLFAA-----FF 500
   |||  ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 325 NLGFEACEDLKYGDQSKVKEKAEIYKFLAPGARRWINIDGKTMDITVKGLKHPHYV 384

QY 501 LEMAOQLH 507
   |||  |||
Db 385 LDAAQTH 391
```

```
RESULT 609
ABG72981
ID ABG72981 standard; protein; 643 AA.
XX
AC ABG72981;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human RGS9 protein 28 residue deletion mutant.
XX
KW Human; RGS9; human regulator of G-protein signaling protein 9; evectin;
KW RGS9-evectin dimer; G-protein activity; Alzheimer's disease;
KW Parkinson's disease; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 460..643
FT /label= Proline_rich_domain
FT Domain 461..602
FT /label= Evectin_binding_domain
FT /note= "This domain is specifically claimed in claim 1
FT of the specification"
FT Misc-difference 643
FT /note= "Amino acids 644 to 671 have been deleted from the
FT wild-type sequence"
XX
PN WO200279401-A2.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-US009064.
XX
PR 28-MAR-2001; 2001US-0279240P.
XX
PA (AMHP ) WYETH.
XX
PI Jones PG, Young KH;
XX
XX WPI; 2003-103266/09.
XX
XX New human regulator of G-protein signaling protein 9 polypeptide fragment
PT and evectin polypeptide, useful for treating neurological disorders e.g.,
PT Alzheimer's disease or Parkinson's.
XX
PS Example 1; Page; 134pp; English.
XX
```

```
CC The invention relates to an isolated human regulator of G-protein
CC signaling protein 9 (RGS9) polypeptide fragment and evectin polypeptide.
CC The invention also discloses methods which are useful for assaying the
CC effects of test compounds on the activity of a RGS9-evectin polypeptide
CC dimer and transgenic animal, producing a transgenic animal, and for
CC modulating G-protein activity in a subject. The methods are also useful
CC for diagnosis of a disease or susceptibility to a disease in a subject
CC related to the activity of a RGS9-evectin dimer. The methods are also
CC useful for the treatment of a subject in need of enhanced RGS9-evectin
CC dimer activity, or inhibiting RGS9-evectin dimer activity. The
CC polypeptide is useful for treating neurological disorders e.g.,
CC Alzheimer's disease or Parkinson's. The present sequence represents the
CC polypeptide sequence of a mutant human RGS9 protein with a 28 residue C
CC terminal deletion. The deletion mutant was used to find which regions of
CC the RGS9 protein bind to evectin protein. Note: The present sequence is
CC not shown in the specification but is derived from the human RGS9
CC sequence given on pages 131 to 133 and from the information given in
CC example 1 of the specification (see ABG72975)
XX
SQ Sequence 643 AA;

Query Match      3.5%; Score 92; DB 6; Length 643;
Best Local Similarity 21.5%; Pred. No. 56;
Matches 53; Conservative 37; Mismatches 81; Indels 76; Gaps 12;

QY 318 EYR---NSSRVEKFLDTEKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374
   |||  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 164 EYRAGKERNKADRYALDCQEKAYWLVRHCPP-----GMDNVLDYGLDRVTTNPE----- 213

QY 375 IRLVPHMNVSAVEKQVTRHLEDV-----FSKRNSSNMVVSMTLGLHPW 418
   |||  ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 214 ---VKKQTVVAVKKEIMYYQQALMRSTVKSSVSLGGIVKYSEQFSSNDAINSGCLPSNPW 270

QY 419 IANIDDTQY--LAAK-----RAIRTVFGTEPDMIRDGSTIPIAKMFQEIYHKS VWLI 468
   |||  ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 271 IT--DDTQFWDLNAKLVEIPTKMRVERWAFNFS-ELIRDPKG---RQSFQYFLKKEFSGE 324

QY 469 PLG---AVDDGEHSQNEKI-----NRWNYIEGTKLFAA-----FF 500
   |||  ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 325 NLGFEACEDLKYGDQSKVKEKAEIYKFLAPGARRWINIDGKTMDITVKGLKHPHYV 384

QY 501 LEMAOQLH 507
   |||  |||
Db 385 LDAAQTH 391

RESULT 610
ABG72975
ID ABG72975 standard; protein; 671 AA.
XX
AC ABG72975;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human regulator of G-protein signaling 9 (RGS9) protein.
XX
KW Human; RGS9; human regulator of G-protein signaling protein 9; evectin;
KW RGS9-evectin dimer; G-protein activity; Alzheimer's disease;
KW Parkinson's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 460..671
FT /label= Proline_rich_domain
FT Domain 461..602
FT /label= Evectin_binding_domain
FT /note= "This domain is specifically claimed in claim 1
FT of the specification"
XX
PN WO200279401-A2.
XX
PD 10-OCT-2002.
```







identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://wipo.int/pub/published/pct/sequences)





CC chimeric DNA construct capable of altering sucrose phosphate synthase  
CC (SPS) activity. The method is useful for increased yield of a cotton  
CC plant, quality of cotton fiber such as increased strength, increased  
CC length, and increased micronaire, as compared to a cotton plant lacking  
CC the transgene, and for regulating the ratio of cellulose to other dry  
CC weight components to exceed 40% in xylem or phloem cells of a plant such  
CC as sugarcane, sugar beets, forest trees, forage crops, fiber producing  
CC plants, and seed producing plants. The method is also useful for  
CC increasing tolerance of photosynthetic efficiency to cool night  
CC temperatures and regulating the thickness of cell walls in fiber  
CC producing plants. The method is further useful for increasing the  
CC harvestable yield of fiber from a fiber containing plant, the yield of  
CC seed from a plant, and altering the quality of fiber isolated from a  
CC fiber producing plant. The fiber has an altered quality such as increased  
CC or decreased strength, length, weight/unit length, as compared to a plant  
CC lacking the transgene. This is the amino acid sequence of fava bean  
CC sucrose phosphate synthase (SPS) that can be used to control cellulose  
CC synthesis in plants to optimise the level of production and quality of  
CC plant products.

XX  
SQ Sequence 1059 AA;

Query Match 3.5%; Score 92; DB 7; Length 1059;  
Best Local Similarity 20.6%; Pred. No. 1.2e+02;  
Matches 97; Conservative 51; Mismatches 149; Indels 174; Gaps 23;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX Bacteria.  
OS  
XX US2003233675-A1.  
PN 18-DEC-2003.  
PD  
XX 20-FEB-2003; 2003US-00369493.  
PF  
XX 21-FEB-2002; 2002US-0360039P.  
PR  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 16162; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transforming plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved lignin production or improved galactomannan  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX  
SQ Sequence 1160 AA;

Query Match 3.5%; Score 92; DB 8; Length 1160;  
Best Local Similarity 19.1%; Pred. No. 1.4e+02;  
Matches 73; Conservative 67; Mismatches 141; Indels 102; Gaps 16;

RESULT 617  
ADS27129  
ID ADS27129 standard; protein; 1160 AA.  
XX  
AC ADS27129;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #16162.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;

Qy 146 TDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVA 205  
Db 22 TCPTNMTGIVGP-NGCGKSNIDPV-RWVMAQSSASRLRGDSLTDVIFSGSSARKPVSA 79  
Qy 206 LEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTF 265  
Db 80 TVELIFDNSDHTISG-EFASFNE---ISVKRLVSRDGT--SAYILINGTKCRRRD----- 127  
Qy 266 GGILHEPMADLVALLGS-LVDSSGHILVPGIYDEVVPLTTEEEINTYKAHLDLEEYR--- 321  
Db 128 -----ITDL--FLGTGLGPRSYSIIEQGMISQIIIEARPEDLRVYLEEAAGISKYKERR 178

QY 322 --NSSRVEKF-----LFDTKKEI---LMHLWR-----YPSLSI 349  
Db 179 KETETRIRHTRENLDRLGDLREEITKQLAHLQRAQAEQYQALQAEERIKDAEWKALEY 238  
QY 350 HGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVV 409  
Db 239 RGLDGRLOGLREK-----LNQETRLQQLIAEQRDAAEARI-- 273  
QY 410 SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLLIP 469  
Db 274 -----ETGRVRRREAAEAAVAKAQADVVYQVGGA--LARIEQQIQHQRELSHR 317  
QY 470 LGAVDDGEHSQNEKINRWNYIEG 492  
Db 318 LHKARDEAQSQQLQELTQ--HISG 338

RESULT 618  
ADS26746  
ID : ADS26746 standard; protein; 1160 AA.  
XX  
AC  
XX  
XX  
DT 02-DEC-2004 (first entry)  
DE  
XX  
XX

Bacterial polypeptide #15779.

Recombinant DNA construct; transformed plant; improved plant property;  
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
pathogen tolerance; pest tolerance; plant disease resistance;  
cell cycle pathway modification; plant growth regulator;  
homologous recombination; seed oil yield; protein yield; carbohydrate;  
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
bacterial polypeptide.

Bacteria.

US2003233675-A1.

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0360039P.

(CAOY/) CAO Y.  
(HINK/) HINKLE G J.  
(SLAT/) SLATER S C.  
(CHEN/) CHEN X.  
(GOLD/) GOLDMAN B S.

Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide  
for expression of a polynucleotide encoding a polypeptide from a  
microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 15779; 122pp; English.

The invention relates to a recombinant DNA construct comprising a  
promoter functional in a plant cell, where the promoter is positioned to  
provide for expression of a polynucleotide encoding a polypeptide from a  
microbial source. The invention also relates to a transformed plant  
comprising the recombinant DNA construct and a method of producing a  
transformed plant having an improved property. The plant is a crop plant  
such as maize or soybean. The method of producing a transformed plant  
having an improved property comprises transforming a plant with the  
recombinant DNA construct and growing the transformed plant, where the  
polynucleotide or polypeptide is useful for improving plant properties.  
The recombinant DNA construct is useful for producing plants with  
improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 1160 AA;

Query Match 3.5%; Score 92; DB 8; Length 1160;  
Best Local Similarity 19.1%; Pred. No. 1.4e+02;  
Matches 73; Conservative 67; Mismatches 141; Indels 102; Gaps 16;

QY 146 TDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEERAGSVA 205  
Db 22 TCPTNMTGIVGP-NGCGKSNIIDPV-RWVMAQSSASRLRGDSLTDVIFSGSSARKPVSQL 79  
QY 206 LEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITVYTRGNSYFMVEVKCRDQDFHSGTF 265  
Db 80 TVELIFDNDHTISG-EFASFNE---ISVKRLVSRDGT--SAYYLNKTKRRRD----- 127  
QY 266 GGILHEPMADLVALLGS-LVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYR--- 321  
Db 128 -----ITDL--FLGTGLGPRSYSIIEQGMISQIEARPEDLRVYLEAAAGISKYKERR 178  
QY 322 --NSSRVEKF-----LFDTKKEI---LMHLWR-----YPSLSI 349  
Db 179 KETETRIRHTRENLDRLGDLREEITKQLAHLQRAQAEQYQALQAEERIKDAEWKALEY 238  
QY 350 HGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVV 409  
Db 239 RGLDGRLOGLREK-----LNQETRLQQLIAEQRDAAEARI-- 273  
QY 410 SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLLIP 469  
Db 274 -----ETGRVRRREAAEAAVAKAQADVVYQVGGA--LARIEQQIQHQRELSHR 317  
QY 470 LGAVDDGEHSQNEKINRWNYIEG 492  
Db 318 LHKARDEAQSQQLQELTQ--HISG 338

RESULT 619  
ADS26378

ID : ADS26378 standard; protein; 1167 AA.

XX

AC

XX

DT 02-DEC-2004 (first entry)

XX

DE

XX

KW

KW

KW

KW

KW

KW

XX

OS

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PN

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PD

XX

PF

20-FEB-2003; 2003US-00369493.





Db 1620 -CKEGKVDGPHGHRVRVANRVFTGPSEIEDENGQRKPTDEHVALSALRHWDIPRVG 1678

QY 302 --LTEEEINTYKAHLD---LEEYRNSSRVEKFLFD-----TKEEILMHL 341

Db 1679 CRLVPEHVETRPLLPDPKPGIEQGRLELWDMFPMMPAPGTPDLDISPRKPKKYELRVIV 1738

QY 342 WRYPSLSIHGIEGAFDEPGTKVIPGRVIGK-----FSIR-LVPHM 381

Db 1739 WNTDEVVLEDDDDFTGEKSSDIFVRGWLKQQEDKQTDVHYHSLTGEGNFWRYLFPFD 1798

QY 382 NVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA---NIDDTQYLAA----- 430

Db 1799 YLAABEKIVMSKKESMFSDTEYKIPARLTLOI--WDADHFSADD--FLGAIELDLNRF 1854

QY 431 KRAIRTVFGTEPDMIRDSGTIPAKMFQE 459

Db 1855 PRGAKTAKQCTMEMATGEVDVPLVSIFKQ 1883

RESULT 621

AAU70669

ID AAU70669 standard; protein; 2298 AA.

XX

AC AAU70669;

DT 14-FEB-2002 (first entry)

XX

DE Murine cochlea otoferlin.

XX

KW Human; mouse; otoferlin; OTOF; brain; auditory function;

KW autosomal nonsyndromic prelingual deafness; DFNB9.

XX

OS Mus sp.

XX

PN WO200170972-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-IB000578.

XX

PR 24-MAR-2000; 2000US-0191738P.

XX

PA (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;

PI Weil D;

XX

DR WPI; 2001-611499/70.

DR N-PSDB; AAS95022.

XX

PT Novel human gene Otoferlin, underlying an autosomal recessive

PT nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the

XX

XX gene, implicated in deafness.

PS Claim 19; Fig 13A; 99pp; English.

XX

CC The invention relates to a purified polynucleotide (I) encoding a protein

CC sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long

CC human otoferlin isoform in brain. (I) was identified as underlying an

CC autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for

CC detecting deafness disease in humans and for characterising the functions

CC of proteins and genes encoding them in auditory function. AAU70669-

CC AAU70676 represent human and mouse otoferlin amino acid sequences of the

CC invention

XX

SQ Sequence 2298 AA;

Query Match 3.5%; Score 92; DB 4; Length 2298;

Best Local Similarity 19.8%; Pred. No. 4e+02;

Matches 89; Conservative 67; Mismatches 169; Indels 124; Gaps 23;

QY 108 LPIPPVILAEGLSDPTKGRVCFYG-----HLDVQPADRGDWLTDPYV 150

Db 1491 VPLPEDVSREAGYDPTYG--MFQGIPSNDPINLVRIYVVRATDLHPADING--KADPVI 1546

QY 151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGM-----EEAGSVA 205

Db 1547 AI----KLGKTDIRDKENYISKQLNPV-----FGKSPDIEASFPMESMLTJAVYDWDLVG 1597

QY 206 LEELVEKEK---DRFES-----GV--DYIVISDNLWISQRKPAITYGTRGNSYFVMEV 253

Db 1598 TDDLIGETKIDLENRFYSKERATCGIAQYTSIHGYNWRDPMKP-----SQILTRL 1648

QY 254 KCRDQDFHSGTFFGGILHEPMDLVALLS-LVDSSG-----HILVPGI-YDEVVP--- 301

Db 1649 -CKEGKVDGPHGHRVRVANRVFTGPSEIEDENGQRKPTDEHVALSALRHWDIPRVG 1707

QY 302 --LTEEEINTYKAHLD---LEEYRNSSRVEKFLFD-----TKEEILMHL 341

Db 1708 CRLVPEHVETRPLLPDPKPGIEQGRLELWDMFPMMPAPGTPDLDISPRKPKKYELRVIV 1767

QY 342 WRYPSLSIHGIEGAFDEPGTKVIPGRVIGK-----FSIR-LVPHM 381

Db 1768 WNTDEVVLEDDDDFTGEKSSDIFVRGWLKQQEDKQTDVHYHSLTGEGNFWRYLFPFD 1827

QY 382 NVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA---NIDDTQYLAA----- 430

Db 1828 YLAABEKIVMSKKESMFSDTEYKIPARLTLOI--WDADHFSADD--FLGAIELDLNRF 1883

QY 431 KRAIRTVFGTEPDMIRDSGTIPAKMFQE 459

Db 1884 PRGAKTAKQCTMEMATGEVDVPLVSIFKQ 1912

RESULT 622

AAU70670

ID AAU70670 standard; protein; 2371 AA.

XX

AC AAU70670;

XX

DT 14-FEB-2002 (first entry)

XX

DE Murine brain otoferlin.

XX

KW Human; mouse; otoferlin; OTOF; brain; auditory function;

KW autosomal nonsyndromic prelingual deafness; DFNB9.

XX

OS Mus sp.

XX

PN WO200170972-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-IB000578.

XX

PR 24-MAR-2000; 2000US-0191738P.

XX

PA (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;

PI Weil D;

XX

DR WPI; 2001-611499/70.

DR N-PSDB; AAS95023.

XX

PT Novel human gene Otoferlin, underlying an autosomal recessive

PT nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the

XX

XX gene, implicated in deafness.

PS Claim 19; Fig 13B; 99pp; English.

XX

CC The invention relates to a purified polynucleotide (I) encoding a protein

CC sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long

CC human otoferlin isoform in brain. (I) was identified as underlying an

CC autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for

CC detecting deafness disease in humans and for characterising the functions

CC of proteins and genes encoding them in auditory function. AAU70669-

CC AAU70676 represent human and mouse otoferlin amino acid sequences of the

CC invention

XX









CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 496 AA;

Query Match 3.5%; Score 91.5; DB 6; Length 496;  
Best Local Similarity 19.4%; Pred. No. 42;  
Matches 81; Conservative 63; Mismatches 145; Indels 129; Gaps 18;

QY 170 VLAWINAVS-----AFRALEQDLPV-----NIKFIEGMEEAGS-----VA 205  
Db 5 ILAVEAVSNEKSLPREKIFEALESALATATKKYQEIDVRVEIDRKSGDFDTRRWVI 64  
QY 206 LLELVEKEK-----DRPFGVDYI-----VISDNLWISQRKPAITYGTRGNSYF 249  
Db 65 VEEVTQPTKEITLEAARFEDESINVGDYVEDQIESVTFDRITTQTAKQVIVQVREARA 124  
QY 250 MVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINT 309  
Db 125 LVVDQFRDQGEIIT--GVVKVNRDNISL---EIKSEG---LPGNAEAVI-LRED---- 171  
QY 310 YKAHLDLEEYRNSRV-----EKFLFDTKBEILMHLWR--YPSL--SIHG 351  
Db 172 ----MLPRENFRPGDRIRGVLYAVRPEARGAQLFVTRSKPEMLVELFRIEVPEIGEEVIE 227  
QY 352 IEGAFDEPGTKTVIP-----GRVIG-----K 372  
Db 228 IKAARDPGSRAKIAVKTNDKRIDPVGACVGNRGARVQAVSTELGGERIDIVLWDDNPAQ 287  
QY 373 FSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSNKMVVSMTLGLHPWIANID 423  
Db 288 FVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQIGRNQONVRLASQLSGWELNVMTVD 347  
QY 424 DTQ--YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVV----LPIGAVDD 475  
Db 348 DLQAKHQAEAAHAAIDTFTKYLDIDEDFATVLVEEGFSTLELAYVPMKELLEIDGLDE 405

RESULT 628  
ADS27419  
ID ADS27419 standard; protein; 504 AA.

XX ADS27419;  
AC  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE  
XX  
XX Bacterial polypeptide #16452.  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

OS Bacteria.  
XX  
XX US2003233675-A1.  
PN  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA

PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 16452; 122pp; English.  
XX

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 504 AA;

Query Match 3.5%; Score 91.5; DB 8; Length 504;  
Best Local Similarity 20.7%; Pred. No. 43;  
Matches 69; Conservative 48; Mismatches 126; Indels 91; Gaps 16;

QY 125 GTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKL-----YGRGATDN-KGPVL 171  
Db 60 GDFTYYDHY-----LDTAYMLGFIPSRFSEFTSYLDVYFAMARGSKDHVASEMT 108  
QY 172 AWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEE-----LVEKEKDRFFSGVDYIVI 226  
Db 109 KWFN-----TNYHIYVPEYEEGLQISLKDNRPLRLYEEAKQEL--GVD---- 149  
QY 227 SDNLWISQRKPAITYGTRGNSYEMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS 286  
Db 150 -----GKPVIL---GPTYFLKLAKGYTQE---QFPNLIKQLVAPYVQLJSELHAA 193  
QY 287 SGHILVPGIYDEVV--PLTEEEINTYKAHLDL-EEYRNSRVEKFLFDTKEEILMHLWR 343  
Db 194 GAQAIQ---VDEPIFASLTKEVQQAKEIYEAIRKEVPNATLLQLTYFDSVEENYEEIIT 250  
QY 344 YPSLS-----IHGIEG-----AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 251 FVSGIGLDFTHGKEGNLNAISKYGFPPADKTLAVGCIDGR-----NIWRADLDEVL 301  
QY 393 HLEDVFSKRNSNKMVWSMTLG-LHPWIANIDDT 425  
Db 302 ELFTTLQKQVQTKDIIVQPSCSLLHTPIDKTEET 335

RESULT 629  
ADN26350  
ID ADN26350 standard; protein; 514 AA.

XX AC ADN26350;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #9003.

XX KW Recombinant DNA construct; transformed plant; improved plant property;

XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

XX KW pathogen tolerance; pest tolerance; plant disease resistance;

XX KW cell cycle pathway modification; plant growth regulator;

XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;

XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

XX PA (HINK/) HINKLE G J.

XX PA (SLAT/) SLATER S C.

XX PA (CHEN/) CHEN X.

XX PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide

XX PT for expression of a polynucleotide encoding a polypeptide from a

XX PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 9003; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a

XX CC promoter functional in a plant cell, where the promoter is positioned to

XX CC provide for expression of a polynucleotide encoding a polypeptide from a

XX CC microbial source. The invention also relates to a transformed plant

XX CC comprising the recombinant DNA construct and a method of producing a

XX CC transformed plant having an improved property. The plant is a crop plant

XX CC such as maize or soybean. The method of producing a transformed plant

XX CC having an improved property comprises transforming a plant with the

XX CC recombinant DNA construct and growing the transformed plant, where the

XX CC polynucleotide or polypeptide is useful for improving plant properties.

XX CC The recombinant DNA construct is useful for producing plants with

XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,

XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

XX CC increased resistance to plant disease, better growth rate by modification

XX CC of the cell cycle pathway with plant growth regulators, increased rate of

XX CC homologous recombination, modified seed oil or protein yield and/or

XX CC content, improved yield by modification of carbohydrate, nitrogen or

XX CC phosphorus use and/or uptake, by modification of photosynthesis or by

XX CC providing improved plant growth and development under at least one stress

XX CC condition, improved lignin production or improved galactomannan

XX CC production. This sequence represents a bacterial polypeptide used in the

XX CC scope of the invention. Note: The sequence data for this patent did not

XX CC form part of the printed specification but was obtained in electronic

XX CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 514 AA;

Query Match 3.5%; Score 91.5; DB 8; Length 514;

Best Local Similarity 21.5%; Pred. No. 44;

Matches 100; Conservative 63; Mismatches 159; Indels 143; Gaps 25;

Qy 13 LAVLLLLLRCGMFSSPPPP-----ALLE-----KVFOYIDLHQDEFVQTLKEWV 57

Db 25 LSGLLSLPRRVLRAAPPPLGSAARLREALIELGPTFVKLGQALSTRPDLLPADVVAEL 84

Qy 58 AIESDSVQVP-----RFRQEL-----FRMMAVAADTLQRLGARVASVDMGPOQ 101

Db 85 SKLQDTPVFPFGDQAVALLIATFNRPDLQLFIAFDROPFAAASLGQVHAHV----- 135

Qy 102 LPDGQSLPI----PPV-----ILAEIGSDPTKTVCFYGHLDVQPADRGDGLTDP 148

Db 136 LPDGTQVVVKVQRPDIASRIQTDLAILADLAT-LAQERLAFAAQYNLSEI-----VWEFSA 190

Qy 149 YVLTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRALEQDLPVNIKF-IIEG 197

Db 191 MLRAELDYVREGRNAERFQMFCTNPHIYIPRVYV--EYTGSRILTTTERIVGVKLNDMAG 248

Qy 198 MEEAG-----SVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGN 246

Db 249 LRAAGVMSRLARASLDITLEE-----IFTHGFFHSDPHPGNFFVLDDGD 292

Qy 247 SYEMVEVKCRDQDFHSGTSGTILHEPMDLVALLGSLVDSGSHILVPGIYD-EVVPLTEE 305

Db 293 VLGVV-----DF--GOVGTLDHATMQGLLWLMGALVNHDSQGLLSLERLEVIPRRAA 343

Qy 306 EINTYKAIHLDLEEYRNSRVEKF-----LFDTKEEI--LMHLWRYPYSLSIHGIEGAFD 357

Db 344 NL-----ALRRDLERF-----VEGFVDRPLGLISARETFDGLTTLRRHRLTI----- 386

Qy 358 EPG-----TKTVIPGRVIGKFSIRLVPHMNV-SAVEKQVTRHLED 396

Db 387 -PGPLATLLKTIIVMMEGLG---MQLDPNLNVFAAARPYIQRALRE 427

RESULT 630

AAG89901

ID AAG89901 standard; protein; 553 AA.

XX AC AAG89901;

XX DT 26-SEP-2001 (first entry)

XX DE C glutamicum protein fragment SEQ ID NO: 3655.

XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

XX KW organic acid synthesis.

XX OS Corynebacterium glutamicum.

XX PN EP1108790-A2.

XX PD 20-JUN-2001.

XX PF 18-DEC-2000; 2000EP-00127688.

XX PR 16-DEC-1999; 99JP-00377484.

XX PR 07-APR-2000; 2000JP-00159162.

XX PR 03-AUG-2000; 2000JP-00280988.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX DR WPI; 2001-376931/40.

XX DR N-PSDB; AAH65120.

XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying

XX PT mutation point of a gene, measuring expression of a gene, analyzing

XX PT expression profile or pattern of a gene and identifying homologous gene.

XX PS Claim 17; SEQ ID NO 3655; 246pp + Sequence Listing; English.

XX CC The present invention provides a number of nucleotide and protein

XX CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These







	Query Match	3.5%;	Score 91.5;	DB 3;	Length 839;
	Best Local Similarity	18.7%;	Pred. No. 94;		
	Matches 69;	Conservative 43;	Mismatches 98;	Indels 159;	Gaps 15;
QY	87	RLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYFYLHVQPADRGDWLT	146		
Db	436	KLGSRQAQVNLTVVDKP-----DPPAGTPC--ASDIRSSSLTLSWY-	474		
QY	147	DPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-----QDL-----	187		
Db	475	-----GSSYDGGSAVQSYSIEIWDSSANKTWKELATCRSTSFNVQDLLPDHEYKFRV	525		
QY	188	-PVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN	246		
Db	526	RAINVYGTSEPSQSESLTVGEKPEEPKDE-----VEVSDD---DEKEPEVDYRT---	572		
QY	247	SYFMVEVKCRDQDFH-----SGTFGGI-----	268		
Db	573	--VTINTEQKVSDFYDIEERLGSCKFGQVRLVEKKTRKVWAGKFFKAYSACEKENIRQE	630		
QY	269	-----LHEP-----MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE-----	306		
Db	631	ISIMNCLHHPKLVQCVDAAFEKANIWMVLEIV---SGGELFERIIDDFELTEREXIKYM	687		
QY	307	-----INTYKAHLHLDLE-----EYRNSSRVE-----KFLFDTKX	335		
Db	688	QRISEGEVYIHKQGIHVHLDLKPENIMCVNKTGTRIKLIDFGLARRLENAGSLKVLFGTPE	747		
QY	336	EILMHLWRY	344		
Db	748	FVAPEVINY	756		

RESULT 634  
ABU49828  
ID ABU49828 standard; protein; 959 AA.  
XX AC  
XX ABU49828;  
DT 19-JUN-2003 (first entry)  
XX DE  
XX Protein encoded by Prokaryotic essential gene #35355.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Yersinia pestis.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA53698.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 77752; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)







Db 271 WPLMIDPQDQANRWI-----RNKESKSGLKIIKLTDSNFLRILENSIRLG 315  
QY 191 IKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGT--RGNSY 248  
Db 316 LPVLLEELKETLDPALEPILLKQ--IFISGRRLLIRLGDSDIDYDKNFRFYMTTKMPNPH 373  
QY 249 FMVEV--KCRDQDFHSGTGGILHEPNMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306  
Db 374 YLPEVCIKVTIINF-TVTKSGLEDQLLSDVVR-----EKPRLEEQR 414  
QY 307 INTYKAIHLDLEEYRN-SSRVEKFLFDTKBEIL 338  
Db 415 IKLIVRINTDKNQLKTIIEKILRMLFTSEGNIL 447

RESULT 638  
ADRI8229  
ID ADR18229 standard; protein; 1416 AA.

XX ADR18229;

AC ADR18229;

XX 18-NOV-2004 (first entry)

XX Rat GOBLIN protein SEQ ID NO:10.

XX cancer; GOBLIN; micrometastasis; metastasis; cytostatic; gene therapy;  
KW squamous cell carcinoma; hepatocellular carcinoma; melanoma;  
KW head and neck cancer; adenocarcinoma; gastrointestinal cancer;  
KW renal cell cancer; bladder cancer; prostate cancer;  
KW non-squamous carcinoma; glioblastoma; medullablastoma; ovarian cancer;  
KW basal cell carcinoma; clear cell carcinoma; endometrioid ovarian cancer;  
KW mucinous ovarian cancer; breast cancer; lobular lesion; stromal lesion;  
KW ductal carcinoma; ductal adenocarcinoma;  
KW proliferative fibrocystic change; epitheliosis; intraductal papilloma;  
KW atypical ductal hyperplasia; hyperproliferative disease; rat.

XX Rattus sp.

OS WO2004072285-A1.

XX 26-AUG-2004.

PD 12-FEB-2004; 2004WO-AU000169.

XX 14-FEB-2003; 2003US-0447697P.

PR (GARV-) GARVAN INST MEDICAL RES.

XX Stanford P, Harris J, Ormandy C;

XX WPI; 2004-625877/60.

DR N-PSDB; ADR18228.

XX Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises

PT determining the level of expression of a GOBLIN gene in a sample.

XX Claim 39; SEQ ID NO 10; 217pp; English.

XX The present invention describes a method for detecting a cancer cell in a  
CC subject. The method comprises determining the level of expression of a  
CC GOBLIN gene in a sample of the subject where elevated expression of the  
CC gene is indicative of a primary cancer or its micrometastasis or  
CC metastasis. Also described: (1) an isolated GOBLIN nucleic acid molecule;  
CC (2) a vector comprising the isolated nucleic acid of (1); (3) a  
CC monoclonal or polyclonal antibody that binds specifically to a GOBLIN  
CC polypeptide; (4) an isolated GOBLIN polypeptide, or its immunogenic  
CC epitope; (5) a fusion protein comprising the isolated polypeptide of (4);  
CC (6) a method of identifying a compound that reduces or antagonises  
CC expression of a GOBLIN gene; (7) a process for identifying or determining  
CC and producing a compound; (8) an isolated nucleic acid that antagonises  
CC expression of a GOBLIN gene, where the nucleic acid comprises a  
CC nucleotide sequence comprising any of the 21 bp sequences of SEQ ID

CC NOS:46-353; (9) an isolated antisense nucleic acid that antagonises  
CC expression of a GOBLIN gene, where the nucleic acid comprises a  
CC nucleotide sequence capable of selectively hybridising to mRNA encoded by  
CC the isolated nucleic acid of (1); and (10) a process for monitoring the  
CC efficacy of treatment of a cancer in a subject. GOBLIN sequences have  
CC cytostatic activity, and can be used in gene therapy. An isolated GOBLIN  
CC nucleic acid molecule can be used for detecting a cancer cell. An  
CC isolated GOBLIN polypeptide can be used for producing an antibody. The  
CC method, nucleic acid molecules and the encoded polypeptides, and  
CC antibodies can be used for detecting a cancer, e.g. squamous cell  
CC carcinoma, hepatocellular carcinoma, melanoma, head and neck cancer,  
CC adenocarcinoma, gastrointestinal cancer (e.g. gastric, colon, or  
CC pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer,  
CC non-squamous carcinoma, glioblastoma, medullablastoma, ovarian cancer  
CC (e.g. basal cell carcinoma, clear cell carcinoma, endometrioid ovarian  
CC cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular  
CC lesion, stromal lesion, ductal carcinoma, ductal adenocarcinoma,  
CC proliferative fibrocystic change, epitheliosis, intraductal papilloma, or  
CC atypical ductal hyperplasia) in a subject. The antagonist of GOBLIN  
CC function, method, and compound are useful for treating hyperproliferative  
CC disease, like cancer. The present sequence represents a rat GOBLIN  
CC protein which is used in the exemplification of the present invention.

XX Sequence 1416 AA;

Query Match 3.5%; Score 91.5; DB 8; Length 1416;  
Best Local Similarity 21.6%; Pred. No. 2.1e+02;  
Matches 58; Conservative 36; Mismatches 117; Indels 57; Gaps 10;

QY 19 LLERGMFSSPSPP-----PALLEKVF-QYIDLHQDEFVQTLKEWVAIESDSVQPVPRF 70  
Db 743 LSPRSSLSPPSPCPLIADPLLAGDAFLTPLEFEDTELSPTLCE-LSLGTDGAR--ERF 799  
QY 71 RQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPP-----VILAELGSDPT 123  
Db 800 RLE-----EPGPEGKPLGQAASVAPGCGLKVACVSAAVSDSV 837  
QY 124 KGTVCFY----GHLDVQPADRGDGLTDPYVLTEVDCKLYGRGATDNKGPVLAWINAVSA 179  
Db 838 AGDSGVYEASMQRLGTSEAAAFDSDESEAVGTVQVIALKYDEKSKQFAILYQLSNLSA 897  
QY 180 FRALEQDLPVNIKFIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAI 239  
Db 898 L-LLQQDQKVNIRVAILPCSESSTCLF-----RTRPLDSADSLVFNEAFWVSMSPAL 949  
QY 240 TYGTRGNSYFMVEVKCRDQDFHSGTFFG 267  
Db 950 HQKT-----LRVDVCTTDRSHTTECLGG 972

RESULT 639

ADQ39529

ID ADQ39529 standard; protein; 1654 AA.

XX ADQ39529;

XX 18-NOV-2004 (first entry)

XX Human myocardial infarction-associated gene derived protein, SEQ ID 1192.  
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
KW cardiant; gene therapy; human.

OS Homo sapiens.

XX WO2004058052-A2.

PN 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.





Db 1063 PVPPEQTKGPLGIDPQKGVTAYEGHVRIKPKPAGVKQWQALAVVCDFKFLYD----- 1117

Qy 166 NKGpVLAWINAVSAFRALEQDLpVNIKFIIEGMEEAAGSVALEELVEKEKDRFFSGVDYIV 225

Db 1118 -----IAEGKASQPSSVISQVIDMRDEEF--SVSSVL 1147

Qy 226 ISDNLWISQRKPAITYGTRGNSYFMVEVKC-----RDQDFHSGTGGILHEPMADLVALL 280

Db 1148 ASDVIHASRKDIPICIFRVITASQLSAPSDKCSILMLADSETERSKWVGVLSE----LHKVL 1203

Qy 281 GSLVDSSGHILVP-GIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFD-TKEEIL 338

Db 1204 KKNKFRDRSVYVPKEAYDSTLPLIK---TTQAAAIIHERVALGNEEGLFVVHVTKDEII 1260

Qy 339 -----MHLWRYPSLSIHGIEGAF---DEPGTKTVIPG 367

Db 1261 RVGDNKKIHQIELIPSDQLVAVISGRNRHVRVLFPMsALDGRETFYKLAETKGCQTIAAG 1320

Qy 368 RV-IGKFSIRLVPHMNVSAVEKQV-----TRH 393

Db 1321 KVRHGALSCLCV-----AMKRQVLCYELFQSKTRH 1350

RESULT 641

ADF89992

ID ADF89992 standard; protein; 1732 AA.

XX

AC ADF89992;

XX

DT 26-FEB-2004 (first entry)

XX

DE Rat serine/threonine kinase homologue polypeptide.

XX

KW Serine/threonine kinase; neuroprotective; cardiovascular; muscular;

KW antiinflammatory; uropathic; respiratory; antidiabetic; cytosstatic;

KW antiasthmatic; nootropic; antiparkinsonian; tranquiliser; cardiant;

KW antianginal; antiarrhythmic; hypotensive; antiarteriosclerotic;

KW osteopathic; antirheumatic; antiarthritic; vasotropic; chromosome lq42;

KW enzyme; rat.

XX

OS Rattus norvegicus.

XX

PN WO2003097822-A1.

XX

PD 27-NOV-2003.

XX

PF 15-MAY-2003; 2003WO-EP005092.

XX

PR 15-MAY-2002; 2002US-0380294P.

PR 10-JUN-2002; 2002US-0386734P.

PR 12-DEC-2002; 2002US-0432628P.

XX

PA (FARB ) BAYER AG.

XX

PI Liou J;

XX

DR WPI; 2004-022873/02.

DR EMBL; AF021935.

XX

PT New human serine/threonine kinase polypeptide and polynucleotide, useful

PT in preventing, ameliorating, or treating diseases associated with human

PT serine/threonine kinase dysfunction, e.g. neurological or respiratory

PT disorder.

XX

PS Disclosure; SEQ ID NO 3; 150pp; English.

XX

PS

CC The invention relates to a novel human serine/threonine kinase

CC polypeptide and polynucleotide. The serine/threonine kinase can be

CC expressed by standard recombinant methodology. An expression vector

CC comprising the polynucleotide or a reagent that modulates the activity of

CC the polypeptide are useful in preparing a medicament for modulating the

CC activity of a serine/threonine kinase in a disease, e.g. a neurological

CC disorder, a cardiovascular disorder, a musculo-skeletal disorder, an

CC inflammatory disorder, a genitourological disorder, a respiratory

CC disorder, diabetes or cancer. The human serine/threonine kinase

CC polypeptide and polynucleotide are useful in preventing, ameliorating, or

CC treating diseases associated with human serine/threonine kinase

CC dysfunction such as chronic obstructive pulmonary disease, asthma,

CC Alzheimer's disease, Parkinson's disease, anxiety disorders, myocardial

CC infarction, angina, arrhythmias, hypertensive vascular disease,

CC atherosclerosis, osteoporosis, multiple myeloma, Paget's disease,

CC rheumatoid arthritis, urinary incontinence, benign prostatic hyperplasia,

CC or erectile dysfunction. Fusion proteins comprising the polypeptide are

CC useful for generating antibodies against serine/threonine kinase

CC polypeptide and for use in various assay systems. The human

CC serine/threonine kinase can be used to identify test compounds that may

CC act as activators or inhibitors at the enzyme's active site. The present

CC sequence represents a serine/threonine kinase polypeptide homologous

CC sequence from rat.

XX

SQ Sequence 1732 AA;

Query Match 3.5%; Score 91.5; DB 8; Length 1732;

Best Local Similarity 20.2%; Pred. No. 2.9e+02;

Matches 68; Conservative 43; Mismatches 126; Indels 99; Gaps 15;

Qy 109 PIPP-VILAEIGSDPTKGT-VCFYGHLDV-QPADRGDWLTDPPYVLTEVDGKLYGRGATD 165

Db 1063 PVPPEQTKGPLGIDPQKGVTAYEGHVRIKPKPAGVKQWQALAVVCDFKFLYD----- 1117

Qy 166 NKGpVLAWINAVSAFRALEQDLpVNIKFIIEGMEEAAGSVALEELVEKEKDRFFSGVDYIV 225

Db 1118 -----IAEGKASQPSSVISQVIDMRDEEF--SVSSVL 1147

Qy 226 ISDNLWISQRKPAITYGTRGNSYFMVEVKC-----RDQDFHSGTGGILHEPMADLVALL 280

Db 1148 ASDVIHASRKDIPICIFRVITASQLSAPSDKCSILMLADSETERSKWVGVLSE----LHKVL 1203

Qy 281 GSLVDSSGHILVP-GIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFD-TKEEIL 338

Db 1204 KKNKFRDRSVYVPKEAYDSTLPLIK---TTQAAAIIHERVALGNEEGLFVVHVTKDEII 1260

Qy 339 -----MHLWRYPSLSIHGIEGAF---DEPGTKTVIPG 367

Db 1261 RVGDNKKIHQIELIPSDQLVAVISGRNRHVRVLFPMsALDGRETFYKLAETKGCQTIAAG 1320

Qy 368 RV-IGKFSIRLVPHMNVSAVEKQV-----TRH 393

Db 1321 KVRHGALSCLCV-----AMKRQVLCYELFQSKTRH 1350

RESULT 642

ADJ68907

ID ADJ68907 standard; protein; 2294 AA.

XX

AC ADJ68907;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human heat mitochondrial protein as a therapeutic target SeqID713.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2003087768-A2.

XX

PD 23-OCT-2003.

XX





QY 355 AFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLG 414  
Db 406 A-----QMEKIPLLIHSSCDQNISE--KDLLDTENKRKKDFLTSENS 445  
QY 415 LHPWIANI-----DDTQY-----LAAKRAIRTVFGTEPDMIRDGST 450  
Db 446 L-PRISSLPKSEKPLNEETVNVNKRDEEQHLESHTDCILAVKQAI-----SGT 491  
QY 451 IPIAKMFQEIIVHKSVVLI 468  
Db 492 SPVASSFQGI-KKSIFRI 508  
RESULT 644  
AAW19211  
ID AAW19211 standard; protein; 3418 AA.  
AC AAW19211;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAR-1998 (first entry)  
XX  
DE Human breast cancer susceptibility gene BRCA2 product.  
XX  
KW Human; breast cancer; susceptibility; gene; BRCA2; diagnosis; screening;  
KW treatment; gene therapy.  
XX  
OS Homo sapiens.  
XX WO9722689-A1.  
XX  
PD 26-JUN-1997.  
XX  
PF 17-DEC-1996; 96WO-US019598.  
XX  
PR 18-DEC-1995; 95US-00573779.  
PR 20-DEC-1995; 95US-00575359.  
PR 21-DEC-1995; 95US-00576559.  
PR 11-JAN-1996; 96US-00585391.  
PR 29-APR-1996; 96US-00639501.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (UYPE-) UNIV PENNSYLVANIA.  
PA (HSCR-) HSC RES & DEV LP.  
PA (ENDO-) ENDO RECH INC.  
XX  
PI Tavtigian SV, Kamb A, Simard J, Couch F, Rommens JM, Weber BL;  
XX WPI; 1997-341680/31.  
DR N-PSDB; AAT69707.  
XX  
PT Human breast cancer susceptibility gene BRCA2 - useful for diagnosing  
PT breast cancer and screening for compounds to treat breast cancer.  
XX  
PS Claim 1; Page 90-106; 189pp; English.  
XX  
CC The present sequence is the human breast cancer susceptibility gene BRCA2  
CC product, which can be used to diagnose breast cancer and screen for  
CC compounds to treat breast cancer. BRCA2 can also be used in gene therapy  
CC to restore wild type BRCA2 gene function to a cell, which has lost its or  
CC has altered (i.e. by virtue of a mutation in BRCA2) BRCA2 gene function.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 3418 AA;  
Query Match 3.5%; Score 91.5; DB 2; Length 3418;  
Best Local Similarity 17.9%; Pred. No. 8.3e+02;  
Matches 100; Conservative 74; Mismatches 167; Indels 217; Gaps 26;  
QY 21 ERGMFSSPSPPP-----ALLEKFQYIDLHODEFVQTLKEWVAIESDSVQVPVPRFRQELF 75  
Db 58 EPNLFKTPQRKPSYNQLASTPIIFKEQGLTPLYQSPVKELDKFKLDLGRNVNPSRHKSL 117

QY 76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPI-----PPVIL--AELGSDPTKGT 126  
Db 118 RTVTKMDQ-----ADDVSCPLLNSCLSESPVVLQCTHVTPPQRDKSV 159  
QY 127 VCFYGHLDVQPADRGDWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-- 184  
Db 160 VC-----GSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSS 207  
QY 185 -----QDLPVNIKFIIEGMEEAAGSVALEELVEKEKDRFFSGVDYIVISDN 229  
Db 208 VLIVRNEEASETVFPHDTTANVKSYSFNHDES-----LKNDRFIASV---TDSN 255  
QY 230 LWTISQRKPAITYG---TRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDS 286  
Db 256 ---TNQREAAASHGFGKTSGNS-FKVN-SCKD---HIG-----KS 286  
QY 287 SCHILVPGIYDEVVPLTEEE-----INT-----YKAHLDLEEYRN 322  
Db 287 MPNVLEDEVYETVVDTSSEDSFSLCFSKCRCTKNLQKVRTSKTRKKIFHEANADECEKSKN 346  
QY 323 SSRVEKFLF-----DT-----KEEILMHLWRYPSSLIHGIEG 354  
Db 347 QVK-EKYSFVSEVEPNDDPLDSNVAHQKPFESSGDKISKVVPSLACEWSQLTSLGLNG 405  
QY 355 AFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLG 414  
Db 406 A-----QMEKIPLLIHSSCDQNISE--KDLLDTENKRKKDFLTSENS 445  
QY 415 LHPWIANI-----DDTQY-----LAAKRAIRTVFGTEPDMIRDGST 450  
Db 446 L-PRISSLPKSEKPLNEETVNVNKRDEEQHLESHTDCILAVKQAI-----SGT 491  
QY 451 IPIAKMFQEIIVHKSVVLI 468  
Db 492 SPVASSFQGI-KKSIFRI 508  
RESULT 645  
AAW04357  
ID AAY04357 standard; protein; 3418 AA.  
XX  
AC AAY04357;  
XX  
DT 21-JUN-1999 (first entry)  
XX  
DE Human BRCA2 (omi4) protein.  
XX  
KW Human; BRCA2; genetic testing; protein therapy; haplotype; detection;  
KW gene therapy; breast cancer; ovarian cancer.  
XX  
OS Homo sapiens.  
XX WO9909164-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 14-AUG-1998; 98WO-US016905.  
XX  
PR 15-AUG-1997; 97US-0055784P.  
PR 07-NOV-1997; 97US-0064926P.  
PR 12-NOV-1997; 97US-0065367P.  
PR 01-MAY-1998; 98US-00071715.  
PR 22-MAY-1998; 98US-00084471.  
XX  
PA (ONCO-) ONCORMED INC.  
XX  
PI Murphy PD, White MB, Rabin MB, Olson SJ, Yoshikawa M, Jackson GM;  
PI Eskandari T, Schryer B, Park M;  
XX  
DR WPI; 1999-190163/16.  
DR N-PSDB; AAX30258.  
XX









Reducing the proliferation of a cancer cell involves inhibiting ligand binding to an integrin receptor on the cancer cell, where the integrin receptor comprises an integrin.  
 Disclosure; SEQ ID NO 42; 161pp; English.  
 The present invention relates to compositions and methods for reducing the proliferation of cancer cells through interaction with integrins. The invention is useful for reducing the proliferation of cancer cells e.g. melanoma, adenoma, lymphoma, myeloma, carcinoma, glioma, plasmocytoma, sarcoma, thymoma, leukaemia, skin cancer, retinal cancer, breast cancer, prostate cancer, colon cancer, esophageal cancer, stomach cancer, pancreas cancer, brain tumours, lung cancer, ovarian cancer, cervical cancer, hepatic cancer, gastrointestinal cancer, and head and neck cancer cells. The invention is also useful for identifying a therapeutic target which involves assaying potential reagent for activity. The present sequence is human BRAC protein.  
 Sequence 3418 AA;

Db 256 --TNQREAAASHGFGKTSNGS-FKVN-SCKD---HIG-----KS 286  
Qy 287 SGHILVPGIYDEVVPLTEEE-----INT-----YKAHLDLEEYRN 322  
Db 287 MPNVLEDEVYETVVDTSEEDSFLCFKSCRTKNLQKVRTSKTRKKIFHEANADECEKSKN 346  
Qy 323 SSRVEKFLF-----DT-----KKEILMHLWRYPSSLHIGIEG 354  
Db 347 QVK-EKYSFVSEVEPNDDPLDSNVAHQKPFESGSDKISKEVVPSSLACEWSQLTSLGLNG 405  
Qy 355 AFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLG 414  
Db 406 A-----QMEKIPLLHISSCDQNISE--KDLLDTENKRRKKDFLTSENS 445  
Qy 415 LHPWIANI-----DDTQY-----LAAKRAIRTVFGTEPDMIRDGST 450  
Db 446 L-PRISLPKSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAI-----SGT 491  
Qy 451 IPIAKMFQEIHKSVVLI 468  
Db 492 SPVASSFQGI-KKSIFRI 508

RESULT 651

ADL32565  
ID ADL32565 standard; protein; 3418 AA.

XX AC ADL32565;

DT 03-JUN-2004 (first entry)

XX DE Human BRCA2 protein SEQ ID NO:23.

XX KW detection; cancer; 8q22.3; chromosome 8; human; EDD; tumour suppressor;  
KW cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein;  
KW progesterone receptor; cytostatic; gene therapy; squamous cell carcinoma;  
KW hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma;  
KW head and neck cancer; adenocarcinoma; squamous lung cancer;  
KW gastrointestinal cancer; renal cell cancer; bladder cancer;  
KW prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma;  
KW BRCA2.

XX OS Homo sapiens.

XX PN WO2004022750-A1.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-AU001164.

XX PR 05-SEP-2002; 2002AU-00951346.

XX PR 07-NOV-2002; 2002US-0425218P.

XX PA (GARV-) GARVAN INST MEDICAL RES.

XX PI Watts C, Saunders D, Henderson M, Clancy J, Henshall S;

XX PI Sutherland R, O'brien P;

XX DR WPI; 2004-248472/23.

XX DR N-PSDB; ADL32564.

XX PT Detecting a cancer cell in a subject sample, also related to cancer  
PT treatments, comprises determining the level of nucleic acid that is  
PT linked to map position 8q22.3 of the human genome or its expression  
PT product.

XX PS Claim 29; SEQ ID NO 23; 331pp; English.

XX CC The present invention describes a method for detecting a cancer cell in a  
CC subject, which comprises determining the level of nucleic acid that is  
CC linked to map position 8q22.3 of the human genome or its expression  
CC product in a sample of the subject, where an elevated level of the

CC nucleic acid or polypeptide is indicative of cancer in the subject. Also  
CC described: (1) a method for diagnosing a cancer or predicting recurrence  
CC of a cancer in a subject comprising determining the level of mRNA or  
CC protein encoded by a nucleic acid as described above; (2) the isolated  
CC nucleic acid molecule for detecting cancer cell; (3) an isolated or  
CC recombinant protein complex; (4) an antibody that binds to the protein  
CC complex; (5) a kit for detecting or producing a protein complex,  
CC comprising an EDD polypeptide or a portion of an EDD polypeptide and a  
CC second polypeptides selected from a protein having tumour suppressor  
CC activity, a protein having cell cycle modulatory activity, a protein  
CC associated with DNA repair or damage, a nuclear targeting protein, and a  
CC progesterone receptor protein or its portion, where the portion of the  
CC second polypeptide is sufficient to bind to the EDD polypeptide or the  
CC portion of an EDD polypeptide; (6) methods for isolating the protein  
CC complex; (7) a method for determining a predisposition for disease, or  
CC disease state; (8) a method for determining a modulator of the activity,  
CC formation or stability of an isolated or recombinant protein complex; (9)  
CC a method for determining a modulator of the level of protein complex  
CC formation; (10) a method for treating a condition associated with  
CC elevated expression of EDD protein in a cell; (11) an antisense nucleic  
CC acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and  
CC (12) a pharmaceutical composition comprising the antisense nucleic acid,  
CC ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and  
CC can be used in gene therapy. The methods and modulator are useful for  
CC treating a condition associated with EDD over expression such as cancer,  
CC e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer,  
CC breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous  
CC lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic  
CC cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous  
CC carcinoma, glioblastoma and medullablastoma. The components and  
CC composition are useful for reducing the expression of EDD in a cell to  
CC inhibit cellular proliferation. The present sequence represents human  
CC BRCA2 protein, which is used in the exemplification of the present  
CC invention.

XX SQ Sequence 3418 AA;

Query Match 3.5%; Score 91.5; DB 8; Length 3418;

Best Local Similarity 17.9%; Pred. No. 8.3e+02;

Matches 100; Conservative 74; Mismatches 167; Indels 217; Gaps 26;

Qy 21 ERGMFSSPPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELF 75  
Db 58 EPNLFKTPQRKPSYNQLASTPIIFKEQGLTPLYQSPVKELDKFLDLGRNVPSNRHKS 117

Qy 76 RMMVAADTLQRLGARVASVDMGPQQLPDGQSLPI-----PPVIL--AELGSDPTKGT 126

Db 118 RTVTKMDQ-----ADDVSCPLNLSCLSESPVVLQCTHTVTPQRDKSV 159

Qy 127 VCFYGHLDVQPADRGDGLWLTDPVVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-- 184

Db 160 VC-----GSLFHTPKFVKGRQTPKHISELSLGAEVDPMDSWSSSLATPTLSST 207

Qy 185 -----QDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDN 229

Db 208 VLIVRNEEASETVFPDHTTANVKSYPFSNHDES-----LKKNDRFTASV---TDSEN 255

Qy 230 LWISQRKPAITYG---TRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS 286

Db 256 ---TNQREAAASHGFGKTSNGS-FKVN-SCKD---HIG-----KS 286

Qy 287 SGHILVPGIYDEVVPLTEEE-----INT-----YKAHLDLEEYRN 322

Db 287 MPNVLEDEVYETVVDTSEEDSFLCFKSCRTKNLQKVRTSKTRKKIFHEANADECEKSKN 346

Qy 323 SSRVEKFLF-----DT-----KKEILMHLWRYPSSLHIGIEG 354

Db 347 QVK-EKYSFVSEVEPNDDPLDSNVAHQKPFESGSDKISKEVVPSSLACEWSQLTSLGLNG 405

Qy 355 AFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTLG 414

Db 406 A-----QMEKIPLLHISSCDQNISE--KDLLDTENKRRKKDFLTSENS 445



Qy 415 LHPWIANI-----DDTOY-----LAAKRAIRTVFGTEPDMIRDGST 450  
| | | | |  
Db 446 L-PRISLPKSEKPLNEETVVKRDEEQHLESHTDCILAVKQAI-----SGT 491  
| | | | |  
Qy 451 IPIAKMFQEIIVHKSUVLI 468  
| | | | |  
Db 492 SPVASSFQGI-KKSIFRI 508  
| | | | |  
RESULT 652  
ABG23417  
ID ABG23417 standard; protein; 3423 AA.  
XX AC ABG23417;  
XX DT 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #23408.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS87604.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 53776; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 3423 AA;

Query Match 3.5%; Score 91.5; DB 4; Length 3423;  
Best Local Similarity 17.9%; Pred. No. 8.3e+02;

Matches 100; Conservative 74; Mismatches 167; Indels 217; Gaps 26;  
Qy 21 ERGMFSSPPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 75  
| | | | |  
Db 60 EPNLFKTPQRKPSYNQLASTPIIFKEQGLTLPLYQSPVKELDKFKLDLGRNVNPSRHKSL 119  
| | | | |  
Qy 76 RMMAVAADTLQRLGARVASVDMGPPQLPDGQSLPI-----PPVIL--AELGSDPTKGT 126  
| | | | |  
Db 120 RTVKTMDQ-----ADDVSCPLLNSCLSESPVVLQCTHTVTPQRDKSV 161  
| | | | |  
Qy 127 VCFYGHLDVQPADRGDWLTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-- 184  
| | | | |  
Db 162 VC-----GSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSST 209  
| | | | |  
Qy 185 -----QDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDN 229  
| | | | |  
Db 210 VLIVRNEEASETVPFPHDTTANVKSIFYSNHDES-----LKNDRFIASV---TDSN 257  
| | | | |  
Qy 230 LWSQRKPAITYG---TRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS 286  
| | | | |  
Db 258 ---TNQREAAASHGFGKTSGNS-FKVN-SCKD---HIG-----KS 288  
| | | | |  
Qy 287 SGHILVPGIYDEVVPLTEEE-----INT-----YKAHLDLEEVRN 322  
| | | | |  
Db 289 MPNVLEDEVYETVVDTSEEDSFSLCFKCRTKNQLQVRTSKTRKKIFHEANADECEKSKN 348  
| | | | |  
Qy 323 SSRVEKFLF-----DT-----KEEILMHLWRYPPSLSIHGIEG 354  
| | | | |  
Db 349 QVK-EKYSFVSEVEPNDDPLDSNVAHQKPFESGSKISKEWVPSLACEWSQLTSLGNG 407  
| | | | |  
Qy 355 AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLG 414  
| | | | |  
Db 408 A-----QMEKIPLLHISSCDQNISE--KDLLDTENKRKKDFTLSNS 447  
| | | | |  
Qy 415 LHPWIANI-----DDTOY-----LAAKRAIRTVFGTEPDMIRDGST 450  
| | | | |  
Db 448 L-PRISLPKSEKPLNEETVVKRDEEQHLESHTDCILAVKQAI-----SGT 493  
| | | | |  
Qy 451 IPIAKMFQEIIVHKSUVLI 468  
| | | | |  
Db 494 SPVASSFQGI-KKSIFRI 510  
| | | | |  
RESULT 653  
ABB58592  
ID ABB58592 standard; protein; 4820 AA.  
XX AC ABB58592;  
XX DT 26-MAR-2002 (first entry)  
XX DE Drosophila melanogaster polypeptide SEQ ID NO 2568.  
XX KW Drosophila; developmental biology; cell signalling; insecticide;  
XX KW pharmaceutical.  
XX OS Drosophila melanogaster.  
XX PN WO200171042-A2.  
XX PD 27-SEP-2001.  
XX PF 23-MAR-2001; 2001WO-US009231.  
XX PR 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
DR N-PSDB; ABL02695.



KW homologous recombination; seed oil yield; protein yield; carbohydrate; KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan; KW bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

DR

XX New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

PT

XX Claim 1; SEQ ID NO 20150; 122pp; English.

PS

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 289 AA;

Query Match . 3.5%; Score 91; DB 8; Length 289;

Best Local Similarity 24.6%; Pred. No. 20;

Matches 57; Conservative 37; Mismatches 92; Indels 46; Gaps 12;

QY 140 RGDGWLTPDY--VLTEVDGKLYGRGATD-----NKGPPVLAWINAVSAFRALEQDLPV 189

Db 75 KGDSGHTQPVETVAISSDGKLIASGSDDYTIKLWDLHTLKLDDTITTHSGFVSKVAFSPD 134

QY 190 NIKFIITEGMEEAGSVALEELVEKEKDRFF----SGVDYIVISDNLWISQRPKAITYGTRG 245

Db 135 MQTLVSAGGDDNTIRLIDLQTKTRHILKGHTGVDAIAITPD-----SKKLVT-GSFG 188

QY 246 NSYFMVEVKCRDQDFHSGTF-----GGIILHEPMADLVALLGSLVDS-SGHILVPGIYDEV 299

Db 189 -----QLVSRNRAISTLKLWNLTQTKLJHE-FADNFSSVESLVSPNGKILICGNYDGT 241

QY 300 VPLTEEEINTYKAIHLDLEEYRNSRV-----EKFLFDTKKEILMHLWR 343

Db 242 IKMW--SLETLKLHLHTRSD---GSSSVLGLALSLDGKTLVSSNEDSIHHWQ 288

RESULT 656

ABU28121

ID ABU28121 standard; protein; 315 AA.

XX AC ABU28121;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #13648.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Enterobacter cloacae.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

PI WPI; 2003-029926/02.

DR N-PSDB; ACA31991.

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

PT Claim 25; SEQ ID NO 56045; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this



CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 315 AA;

Query Match 3.5%; Score 91; DB 6; Length 315;  
Best Local Similarity 20.6%; Pred. No. 23;  
Matches 52; Conservative 51; Mismatches 94; Indels 56; Gaps 12;

QY 276 LVALLGSLVDS-----SGHILVPGIYDE-----VVPLTEEEINTYKAHLDLEE 319  
Db 64 VVAIIIVSRDLSLSENLAQTMLPAFYEQGYDPIMMESQFSVLVEE-----HLGMLQ 115  
QY 320 YRNSSRVEKFLFDTKHEILMLWRYPSLSI-----HGIEG-AFDEPGTKVIPGRVIGK- 372  
Db 116 RNNIDGVVLFGTGKDEMILKPWQ-PSLVLLARDAHGFPASVCYDDEGAIITLMQRLFDEG 174  
QY 373 ---FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGL---HPWIANI---- 422  
Db 175 HRHISFLGVPHADVTTCRRHEAYL--AFCKKHLNSAVASLPLGKMGQYEQVASVLTPO 232  
QY 423 -----DDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDD 475  
Db 233 TTALVCATDTLALGASKYLQEQRIDNLQVASVGST-PLMK----FLHPEIITVDPGYAES 287  
QY 476 GEHSQNEKINRW 488  
Db 288 GRQAAAQLIEQIN 300

RESULT 657  
ABB69816  
ID ABB69816 standard; protein; 478 AA.  
XX  
AC ABB69816;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 36240.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
DR N-PSDB; ABL13919.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 36240; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 478 AA;

Query Match 3.5%; Score 91; DB 4; Length 478;  
Best Local Similarity 20.2%; Pred. No. 44;  
Matches 67; Conservative 53; Mismatches 128; Indels 84; Gaps 15;

QY 190 NIKFIIIEGMEBAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI----- 239  
Db 11 DIEIVFDGAEHKTAEVKGEDGKVEKMLLF--YDGETVSGKVNVTLLKPGSKLJHQGIKIE 68  
QY 240 -----TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVP 293  
Db 69 FIGQIELYYDRGNHH---EFKC-----LAKALARPGDLIQNNS----- 103  
QY 294 GIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLDFTKE-EILMH-LWRYPSLSIH- 350  
Db 104 --YPDFPKVEKQFEVYAGSNVRLRYFLRATIVRRISDITKEVDIAVHTLCSYPENNNPI 161  
QY 351 ---GIEGA----FDEPGTKTVIPGRVIGKFSIRLV---PHMNVSAVEKQVTRHLEDVF 398  
Db 162 KMEVGIEDCLHIEFEYNKSKYHLRDTIIGKIYFLLVRIKIKHMEIAI IKKESTGTGPTMF 221  
QY 399 SKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTV---FGTEPDMIRDGSTIPIAK 455  
Db 222 NENETIAKYEI-----MDGAPVKGESIPIRVFLAGYNLTPTM-RD-----INK 263  
QY 456 MFEQIVHKSVVLIPLGAVDDGEHSQNEKINRW 487  
Db 264 KFSVKYFLNLVJLMD---TEDRRYFKQOEITLW 292

RESULT 658  
ABU18380  
ID ABU18380 standard; protein; 505 AA.  
XX  
AC ABU18380;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #3907.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Bacillus anthracis.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA22250.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to







Query Match	3.5%;	Score 91;	DB 7;	Length 737;	
Best Local Similarity	20.7%;	Pred. No. 86;			
Matches	90;	Conservative	52;	Mismatches 172; Indels 120; Gaps 23;	
QY	63	SVQPVPRFQELRMMVAADTLQRLGARVASV----	DMGPOQLP-DGQSLPIPPVILAE	118	
Db	258	SMYETPTLEQDLERLFOELQPLYLNLHAYVGRALHRHYGAQHINLEG----	PIPAHLGNM	314	
QY	119	GSD-----	PTKGTVCYGHLDVQPADRGDGLTDPVYLTEVDGKLYGRGATDN	166	
Db	315	WAQTSNIYDLVAPFPSAST-----	MDATEAMIKQGW-TPRRMFEEADKFFISLGL---	364	
QY	167	KGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVI		226	
Db	365	-----	LPVPPPEFNKSMLEKPTDGREVVCHASAWDFYNGKDF-RI	403	
QY	227	SDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMDLVALLGS----		282	
Db	404	KQCTTVNMEDLVVVHHEMGHIQYFMQYKDLPVALREGANPG-FHEAIGDVLALSVPKX		462	
QY	283	-----	LVDSSGHILVPGIYDEVVPLTEEBEINTYKAHLD-----	LEEYRNSSRVE 327	
Db	463	LHSINLSSEG-----	GGY-----	EHDINFLMKMALDKIAIPFSYLVDEWRW----	506
QY	328	KFLFD---TKEEILMHLWRYPSLSIHGI-----	EGAFDEPGTKTVIPG-----	RVIGK 372	
Db	507	--VFDSITKENYNQEWWSL-RLKYQGLCPPAPRSQGFED-PCA	PHIPSSVPYIRYFVS	562	
QY	373	FSIRLVPHMV-SAVEKQVTRHLEDVFSKRNSNMVVSMTLGL-HPWIANIDDTQYLAA		430	
Db	563	FIIQFQFHEALCKAAGHTGPLHTCDITYQSKEAGKRLADAMKLGYSKPW-----		610	
QY	431	KRAIRTVFGTEPDM	444		
Db	611	PEAMKVITG-QPNM	623		
RESULT 662					
ABU23674					
ID	ABU23674	standard; protein; 871 AA.			
XX	AC	ABU23674;			
XX	DT	19-JUN-2003 (first entry)			
XX	DE	Protein encoded by Prokaryotic essential gene #9201.			
XX	XW	Antisense; prokaryotic essential gene; cell proliferation; drug design.			
XX	OS	Clostridium acetobutylicum.			
XX	PN	WO200277183-A2.			
XX	PD	03-OCT-2002.			
XX	PF	21-MAR-2002; 2002WO-US009107.			
XX	PR	21-MAR-2001; 2001US-00815242.			
PR	06-SEP-2001; 2001US-00948993.				
PR	25-OCT-2001; 2001US-0342923P.				
PR	08-FEB-2002; 2002US-00072851.				
PR	06-MAR-2002; 2002US-0362699P.				
XX	PA	(ELIT-) ELITRA PHARM INC.			
XX	PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;			
PI	Wali D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;				
XX	WPI; 2003-029926/02.				
DR	N-PSDB; ACA27544.				
XX	PT	New antisense nucleic acids, useful for identifying proteins or screening			

PT	for homologous nucleic acids required for cellular proliferation to				
PT	isolate candidate molecules for rational drug discovery programs.				
XX					
PS	Claim 25; SEQ ID NO 51598; 1766pp; English.				
XX					
CC	The invention relates to an isolated nucleic acid comprising any one of				
CC	the 6213 antisense sequences given in the specification where expression				
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:				
CC	(1) a vector comprising a promoter operably linked to the nucleic acid				
CC	encoding a polypeptide whose expression is inhibited by the antisense				
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated				
CC	polypeptide or its fragment whose expression is inhibited by the				
CC	antisense nucleic acid; (4) an antibody capable of specifically binding				
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular				
CC	proliferation or the activity of a gene in an operon required for				
CC	proliferation; (7) identifying a compound that influences the activity of				
CC	the gene product or that has an activity against a biological pathway				
CC	required for proliferation, or that inhibits cellular proliferation; (8)				
CC	identifying a gene required for cellular proliferation or the biological				
CC	pathway in which a proliferation-required gene or its gene product lies				
CC	or a gene on which the test compound that inhibits proliferation of an				
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a				
CC	compound's activity; (11) a culture comprising strains in which the gene				
CC	product is overexpressed or underexpressed; (12) determining the extent				
CC	to which each of the strains is present in a culture or collection of				
CC	strains; or (13) identifying the target of a compound that inhibits the				
CC	proliferation of an organism. The antisense nucleic acids are useful for				
CC	identifying proteins or screening for homologous nucleic acids required				
CC	for cellular proliferation to isolate candidate molecules for rational				
CC	drug discovery programs, or for screening homologous nucleic acids				
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,				
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of				
CC	the target prokaryotic essential genes. Note: The sequence data for this				
CC	patent did not form part of the printed specification, but was obtained				
CC	in electronic format directly from WIPO at				
CC	ftp.wipo.int/pub/published_pct_sequences				
XX					
SQ	Sequence 871 AA;				
	Query Match	3.5%;	Score 91;	DB 6;	Length 871;
	Best Local Similarity	23.0%;	Pred. No. 1.1e+02;		
	Matches	99;	Conservative	53;	Mismatches 157; Indels 122; Gaps 26;
Qy	104	DGQSL-----	PIPPVILAE	157	
Db	8	DGNSLMNRAFYALPELTNAE--GLHTNG--	YGFMTMLIKMRDE--IKPDYIVTTFDRK	60	
Qy	158	L-----	YGRG-----	ATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEA	201
Db	61	APTFRHKEYEDYKAGRKMPPELSEQFPVL-----	KELLEKLAINI-FEIDGFEAD	110	
Qy	202	GSVALEELVEKEKDRFFSGVD-YIVISDN--	LWISQKPAITYGTRGNSYFMVEVKCRDQ	258	
Db	111	DLIGTLACFAKEK-----	GIEVYIVTGDKDALQADNNVKVINKKG---MTEKEIYDK	161	
Qy	259	DFHSGTGGILHEPMDLVALLGSLVDSSGHIL-VPGI-----	YDEVVPLTEEE	306	
Db	162	NRMIEEF-GVTPVQFIDVKGLMG--	DNSDNI PGVPGIGPKTAFKLIQEYGSVENVDNI	217	
Qy	307	INTY-KAHLHDLEEYRNSSRVEKFLPDTKEEILMHLWRYP-SLSIHGIEG--	AFDEPGTK	362	
Db	218	QNIKGKKIKENLENY-----	AEQAVFSKKLATIM--TNVPFIEDIEIRSKESFDFEGAR	270	
Qy	363	TVIPGRVIGKFSIRLVPHMNVSAVEKQ--	VTRHLEDVFSKRNSNMVVSMTLGLHPWIA	420	
Db	271	HLI-RRLQFKSIIIEKIPSLNVAEAKSDFVVEYNLIDEPFK-----	FHELFS	315	
Qy	421	NIDDTQY-----	LAAKRAIRTVF-----	GTEPDMIRDGSTIPI	453
Db	316	AIKDTIYMSYSIGNGELYSKIYIDTIFMKVVEKTYIVDLKKIIEQNREDVLKDLKEFFE	375		
Qy	454	AKMFQEIHKVS	464		

Db 376 NKKIAKIIDS 386

RESULT 663

AAR36821

ID AAR36821 standard; protein; 917 AA.

XX AC AAR36821;

XX 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 25-AUG-1993 (first entry)

XX PE binding/translocation domains-influenza A virus nucleoprotein.

DE Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; NP;

XX anti-viral agent; Pseudomonas exotoxin; fusion construct.

KW Pseudomonas aeruginosa.

KW Influenza A virus.

XX Chimeric.

OS

OS

XX

FH Key Location/Qualifiers

FT Region 2. .414

FT /note= "amino acids 2-414 of PE domains I and II"

FT 415. .912

FT /note= "influenza A virus Nucleoprotein"

FT 913. .917

FT /note= "last 5 amino acids of PE"

XX

PN EP541335-A1.

XX

PD 12-MAY-1993.

XX

PF 04-NOV-1992; 92EP-00310067.

XX

PR 08-NOV-1991; 91US-00792507.

XX

PA (MERI ) MERCK & CO INC.

XX

PI Donnelly JJ, Liu MA, Friedman A, Marshall MS, Hawe LA;

PI Montgomery DL, Oliff AA, Shi X, Ulmer J;

XX

DR WPI; 1993-154266/19.

DR N-PSDB; AAQ41728.

XX

PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful

PT as vaccines against viral infections, tumours and parasites.

XX

PS Example 25; Page 63-67; 81pp; English.

XX

CC Plasmid pApr501 was constructed from the influenza A virus nucleoprotein

CC gene (NP) cloned into the EcoRI site of pBR322. A fragment containing the

CC NP gene was obtained from the plasmid by PCR with primers that added a

CC SacII site adjacent the ATG codon of NP, and the last 5 amino acids of PE

CC followed by a termination codon and an EcoRI site to the 3' end of NP.

CC The PCR fragment was digested with SacII and EcoRI and ligated to

CC SacII/EcoRI-digested plasmid pVC-PEMI-2 (encoding a Pseudomonas exotoxin-

CC influenza A virus MI matrix protein fusion). In the resulting plasmid,

CC pVC-PENPC5aa, the binding and translocation domains of PE are fused to

CC the Influenza A nucleoprotein. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 917 AA;

Query Match 3.5%; Score 91; DB 2; Length 917;

Best Local Similarity 20.1%; Pred. No. 1.2e+02;

Matches 62; Conservative 56; Mismatches 111; Indels 80; Gaps 17;

QY 197 GMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFWVEVKCR 256

Db 382 GPADSGDALLER-----NYPTGAFLGDDVSFSTRGMA-SQGTK-RSYEQMETDGE 432

QY 257 DQDFHSGTGGILHEPMADLVALLGSLVDSSCHILVPGIYDEVVPLTEEEINTYKAHLD 316

Db 433 RQN-----ATEIRASVGKMIGGIGRFYIQ-----MCTELKLSDEG----- 468

QY 317 LEEYRNSSRVEKFL---FDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKF 373

Db 469 -RLIQNSLTIERMVLSAFDERRN--KYLEEHPS-----AGKDPKKTGGPIYRRVNGKW 518

QY 374 SIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMVMTLGLHPWIANIDDTQYLAAKRA 433

Db 519 MRELILY-----DKEEIRR---IWRQANNGDDATAGLT-HMMIWHSNLNDATYQTRAL 568

QY 434 IRTVFGTEPDM--IRDGSTIP-----IAKMFQEIHKSVVLIPLGAVD-----D 475

Db 569 VRT--GMDPRMCSLMQGSTLPRRSGAAGAAGVGVGTMMVMELV-----MIKRGINDRNFWR 622

QY 476 GEHSQNEKI 484

Db 623 GENGKTRI 631

RESULT 664

AAR32469

ID AAR32469 standard; protein; 917 AA.

XX AAR32469;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 20-JUL-1993 (first entry)

XX

DE PE binding and translocation domains - Influenza A nucleoprotein fusion

DE protein.

XX

KW PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion;

KW hybrid; pVC-PENPC5aa; pApr501; pBR322; pVC-PEMI-2; nucleoprotein; NP;

KW PCR; amplification; translocation; binding; domain.

XX

OS Unidentified.

XX

PN EP532090-A2.

XX 17-MAR-1993.

XX

PF 02-SEP-1992; 92EP-00202660.

XX

PR 09-SEP-1991; 91US-00756249.

XX (MERI ) MERCK & CO INC.

XX

PI Donnelly JJ, Liu MA, Friedman A, Montgomery DL, Hawe LA;

PI Oliff AI, Shi X, Ulmer J, Marshall MS;

XX

DR WPI; 1993-087107/11.

DR N-PSDB; AAQ38411.

XX

PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-

PT lymphocyte immune response, used for preventing viral infections, e.g. by

XX influenza virus, HIV and human papilloma:virus.

PS Disclosure; Page 66-70; 85pp; English.

XX

CC Example 25 describes the construction of pVC-PENPC5aa. A fragment contg.

CC the nucleoprotein (NP) of Influenza A virus was obtained from plasmid

CC pApr501. pApr501 is the nucleoprotein gene cloned into the EcoRI site of

CC pBR322, by PCR with oligonucleotide primers which added a SacII site

CC adjacent to the ATG codon of NP to give the sequence of AAQ38409, and the

CC last 5 amino acids of PE followed by a termination codon and an EcoRI

CC site to the 3' end of NP to give the sequence shown in AAQ38410. The PCR

CC fragment was digested with SacII and EcoRI and ligated to the plasmid pVC

CC -PEMI-2 digested with SacII and EcoRI. The resulting plasmid is named pVC

CC -PENPC5aa. The 5' and 3' ends of the PENPC5aa insert (AAQ38411) were

CC verified by sequencing. This construction fuses the binding and







XX	PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;	
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;	
XX	WPI; 2003-450961/43.	
DR	N-PSDB; ADB62814.	
XX	New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.	
PT	Claim 1; Page; 222pp; English.	
XX	The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the encoded protein. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.	
XX	SQ	Sequence 1054 AA;
Query Match 3.5%; Score 91; DB 7; Length 1054;		
Best Local Similarity 18.9%; Pred. No. 1.5e+02;		
Matches 57; Conservative 59; Mismatches 111; Indels 74; Gaps 13;		
QY	230	LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGG----- 267
Db	52	LWQAE-EGELLPTQGDSEEGLEEPSQEQSFSDKLFSGKGLHFQPSVLDFGIQLGHPVA 110
QY	268	-ILH--EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNS 324
Db	111	KILHAYNPSRDSEVVVNSVFAAGHFHVPVPCRVIPAMGK--TSFRIIFLPTEE----- 163
QY	325	RVEKFLDFTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 384
Db	164	-----GSISSLINTSSYGVLSYH-VSGI-----GTR-----RISTEGSAKQLPNA-YF 206
QY	385	AVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPWTIANIDDTQYLAAKRAIRTVFGTEPDM 444
Db	207	LIPKVQSIQLSQMQAETNTSLLOVQLECSLHNKVC-----QQLKGCYLESDDV 255
QY	445	IRDGSTIPI-----AKMFQE-----IVHKSIVVLIPLGAVDDGESHQNEKINRWNYIEGTK 494
Db	256	LRLQMSIMVTMENFSKEFEENTQHLLDHLISIVYV---ATDESETSDSDSAVNMVILHSGNS 312
QY	495	L 495
Db	313	L 313
RESULT 669		
ADN23806		
ID	ADN23806	standard; protein; 1071 AA.

XX ADN23806;  
AC  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #6459.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 6459; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 1071 AA;  
XX  
XX Query Match 3.5%; Score 91; DB 8; Length 1071;  
XX Best Local Similarity 21.1%; Pred. No. 1.5e+02;  
XX Matches 88; Conservative 59; Mismatches 126; Indels 144; Gaps 23;  
XX 173 WIN-AVSFAF---RALEQDLPVNIKFIIEGMEEAGSVALVELVEKEK-----DRFFS 219

Db 515 WLNEALPRFLEVALEKILDIN-----SDDLWTYEMEKILERDATATSQPLRVKNVFS 567  
Qy 220 GVDYIVISDNLWISQRKPAI---TYGTRGNSYFMVEVKCRDQDFHS----- 262  
Db 568 SADIAEI-DHEFIGKKGAAVLRMIQKSGVGNVFENKAIRSFVSSYRSAYPYDDGLWKSFEK 626  
Qy 263 ---GTFGGILHEPMADLVALLGSLVDSSGH--ILVPGIYDEVVPLTETEEINTYKAIHLDL 317  
Db 627 ALGGKLGWNNEL-DVAKFVNTWVDQIGFPLVSVVEKLDDETVELSQER---FKNDHKTK 682  
Qy 318 EYRNSRVRVEKFLFDTKKEILMHLWRYPYSLSIHGIEGAF---DEPGTKTV-----I 365  
Db 683 EQFK--FRNAKYWFN-----WEVPLPLNTSDSIYLNDSNGVYRVNVEEKRWNDI 731  
Qy 366 PGRV---IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMVLGLHPWIANI 422  
Db 732 AKQLEKSHGKLS-----ERTRARLISDVFFALANS-----GALPFETAL 769  
Qy 423 DDTQYLAAKRAIRTVFGTEPDMIR-----DGSTI-----PIAKMFQEIIV 461  
Db 770 NVTSYLPMETA-----TVPWLIATRIFFKKLTERLEGAPIQDKLNSFIYQKIHKKFEEIS 823  
Qy 462 HKS-----VVLIPLGAVDGGEHSQNEKINRWNYIEGTKLFAAFPLEMAQ 505  
Db 824 SSPGEASSNYLKNRLYANLLDLMAIVKPEKS-NEKLN-----ELFVEGFLAPCQ 871  
RESULT 670  
AAB07497  
ID AAB07497 standard; protein; 1077 AA.  
XX  
AC AAB07497;  
XX  
DT 20-OCT-2000 (first entry)  
XX  
DE A T-cell lymphoma invasion and metastasis 2 (TIAM2) protein.  
XX  
KW T-cell lymphoma invasion and metastasis protein 2; TIAM2; metastasis;  
KW tumour suppression; neural development; chromosome 6q25; ovarian cancer;  
KW cancer; cancer cell growth.  
XX  
OS Homo sapiens.  
XX  
PN WO200040607-A2.  
XX  
PD 13-JUL-2000.  
XX  
PF 06-JAN-2000; 2000WO-US0000459.  
XX  
PR 06-JAN-1999; 99US-00227278.  
XX (CHIR ) CHIRON CORP.  
PA Duhl D;  
XX  
PI WPI; 2000-465952/40.  
XX N-PSDB; AAA58867.  
DR  
XX New isolated nucleic acid molecules encoding T-cell lymphoma invasion and  
PT metastasis 2 protein for diagnosis of cancerous cells.  
XX  
PS Claim 11; Page 79-80; 80pp; English.  
XX  
CC The present sequence represents a human T-cell lymphoma invasion and  
CC metastasis 2 (TIAM2) protein. The TIAM2 transcript is present in long and  
CC short forms. The TIAM2 protein may play a role in metastasis or tumour  
CC suppression, and in neural development. The TIAM2 gene is mapped to a 4-  
CC cm region of chromosome 6q25 that is frequently deleted in ovarian  
CC cancer. The TIAM2 polynucleotides and polypeptides are used for the  
CC diagnosis of cancerous cells. TIAM2 antisense oligonucleotides may also  
CC be used to inhibit cancer cell growth  
XX



SQ    Sequence 1077 AA;  
       Query Match            3.5%;    Score 91;    DB 3;    Length 1077;  
       Best Local Similarity    21.2%;    Pred. No. 1.5e+02;  
       Matches    106;    Conservative    55;    Mismatches    164;    Indels    174;    Gaps    27;

QY	1	MDPKLGRMAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60
Db	1	MDSKMKMAELQLSVV-----SDPKNRKAIEHQI-----QQW-----	32
QY	61	SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEIGS	120
Db	33	---EQNLEKFMHDLFRMRCYLA-SLQ-----GGELPNPKSLLA-AAS	69
QY	121	DPTKGTVCVFGHLDVQP-----ADRGDWLTDPYV-LTE-----VDGKLYGRGATDNK	167
Db	70	RPSKPALGRGLGILSVSFFHALVCSRDSALRKRTLSTQGRNKKGIFSSLKGLDTLARK	129
QY	168	G-----PVLAWINAVSAFRALE-QDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVD	222
Db	130	GKEKRPSTQIFDSSGSHGFGSTQLPN-----SSNSSEVDELLH---IYGSTVD	176
QY	223	YIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVAL---	279
Db	177	G-VPRDNTWEIQ-----TY-----VHFQDNHGVTVGIKPEHRVEDILTACK	217
QY	280	-----LGSVDSSGHILVPG-----IYD--EVVPLTEEEINTYK-----	311
Db	218	MRQLEPSHYGLQRLKLVDDNVEYCIAPAYEQQVYDEIEVFPNVDVQLTKTGSVCD	277
QY	312	---AIHLDLEEYRNSRVEKFLFDT-----KEEILMHLWRYPSLSIHGIEG	354
Db	278	FGFAVTAQVDERQHLRSRI--FISDVLDPDGLAYGEGLRKNGEIMTLNGEAVSDLDLKQMEA	335
QY	355	AFDE-----PGTKTVI-----PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFV	398
Db	336	LFSEKSVGLTLIARPPDTKATLCTSDSDLSFRDQKSLPPPN---QSQLEEFLLDNF	391
QY	399	SKRNSSNKM--VVSMTLGL	415
Db	392	-KKNTANDFSNVPDITTL	409

RESULT 671  
 ADJ70147  
 ID    ADJ70147 standard; protein; 1098 AA.  
 XX  
 AC    ADJ70147;  
 XX  
 DT    06-MAY-2004 (first entry)  
 XX  
 DE    Human heat mitochondrial protein as a therapeutic target SeqID1953.  
 XX  
 KW    mitochondrial; human; screening assay; diabetes mellitus;  
 KW    Huntington's disease; osteoarthritis;  
 KW    Leber's hereditary optic neuropathy; LHON;  
 KW    mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW    myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW    neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW    osteopathic; ophthalmological; cytostatic.  
 XX  
 OS    Homo sapiens.  
 XX  
 PN    WO2003087768-A2.  
 XX  
 PD    23-OCT-2003.  
 XX  
 PF    04-APR-2003; 2003WO-US010870.  
 XX  
 PR    12-APR-2002; 2002US-0372843P.  
 PR    17-JUN-2002; 2002US-0389987P.  
 PR    20-SEP-2002; 2002US-0412418P.  
 XX

XX DE Novel human protein sequence #1133.  
XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
KW KW gene therapy; diagnostic marker; morbid state; osteoporosis;  
KW KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
KW KW cancer.  
XX OS Homo sapiens.  
XX PN EP1440981-A2.  
XX PD 28-JUL-2004.  
XX XX 21-JAN-2004; 2004EP-00001196.  
XX PF 21-JAN-2003; 2003JP-00102206.  
XX PR 09-MAY-2003; 2003JP-00131392.  
XX XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Nagai K, Irie R;  
PI XX WPI; 2004-535376/52.  
DR N-PSDB; ADQ63972.  
XX XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
PT XX Claim 1; SEQ ID NO 3321; 2449pp; English.  
PS XX The invention relates to 2495 novel polynucleotides (I) and their encoded  
XX CC polypeptides, sequences hybridizing to these nucleotides, sequences  
CC CC encoding partial polypeptides and sequences having 70% or 90% identity to  
CC CC the nucleotide and protein sequences. The nucleotides and polypeptides  
CC CC are useful as diagnostic markers or therapeutic target for the diseases  
CC CC or morbid states. They are also useful for treating osteoporosis,  
CC CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
CC CC dementia and various cancers. This sequence corresponds to a protein  
CC CC sequence of the invention.  
XX XX Sequence 1268 AA;  
SQ

Query Match 3.5%; Score 91; DB 8; Length 1268;  
Best Local Similarity 19.4%; Pred. No. 2e+02;  
Matches 97; Conservative 67; Mismatches 137; Indels 198; Gaps 26;  
QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
DB 187 MDSKMKMAELQLSVV-----SDPKNRKAIEHQI-----QQW----- 218  
QY 61 SDSVQVPVFRQELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120  
DB 219 ---EQNLEKFHMDLFRMRCYLA-SLQ-----GGELPNPKSLLA-AAS 255  
QY 121 DPTKGTVCFYGHLDVQPADRGDGLWTDYPVLTVDGKLYGRGATDNKGPVLAWINAVSAF 180  
DB 256 RPSKLAL-----GRL-----GILSVSSF 273  
QY 181 RAL--EQDLPVNIKFIIEGMEAGSVALEELVEKEKDRFFS--GVDYIVISDNLWISQRK 236  
DB 274 HALVCSRD-----DSALRKRTLSTQGRNKKGIFSSLKGLDTLARKG---KEKR 320  
QY 237 PAIT-----YGT-----RGSYFMVEVKCRDQDFHSGTGFGILHEPMADLVAL--- 279  
DB 321 PSITQVDELLHIYGSTVDGVPDRNAW-EIQTYVHFQDNHGVTVGKPEHREVDILTACK 379  
QY 280 -----LGS LVDSSGCHILVPG-----IYD--EVVPLTEEEINTYK----- 311  
DB 380 MRQLEPSHYGLQRLKLDNDNVEYCIAPAYEYMQQVYDEIEVFPLNVYDVQLTKTGSVCD 439  
QY 312 ---AIHLDLEEYRNSSRVEKFLFDT-----KEEILMHLWRYPSLSIHGIEG 354

Db 440 FGFAVTAQVDERQHLSRI--FISDVLPGGLAYGEGRLKRGNEIMTLNGEAVSDLDLKQMEA 497  
QY 355 AFDE-----PGTKTVI-----PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFV 398  
Db 498 LFSEKSVGLTLIARPPDTKATLCTSWSDSLFSRDQKSLPPPN---QSQLLLEFLDNF 553  
QY 399 SKRNSSNKM--VVSMTLGL 415  
Db 554 -KKNTANDFSNVDPDITGL 571  
RESULT 673  
AAB47329  
ID AAB47329 standard; protein; 1274 AA.  
XX AAB47329;  
XX 29-AUG-2001 (first entry)  
XX FCTR6.  
KW FCTR6; energy metabolism; adipose storage; muscle mass;  
KW insulin secretion; glucose utilization; serum lipid level; triglyceride;  
KW cholesterol; human; diabetes; metabolic disturbance; obesity;  
KW metabolic syndrome X; anorexia; infectious disease;  
KW cancer-associated cachexia; cancer; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidemia.  
XX OS Homo sapiens.  
XX XX  
FH Key Location/Qualifiers  
FT Peptide 1. .27  
FT Protein /label= Signal peptide  
FT 28. .1274  
FT /label= Mature protein  
XX WO200146231-A2.  
XX 28-JUN-2001.  
XX 21-DEC-2000; 2000WO-US034898.  
XX 21-DEC-1999; 99US-0171329P.  
XX 20-DEC-2000; 2000US-00171329.  
XX (CURA-) CURAGEN CORP.  
XX Burgess CE;  
XX WPI; 2001-418026/44.  
XX N-PSDB; AAC86158.  
PT Novel FCTR6 polypeptides useful for treating, diagnosing and preventing  
PT diabetes, anorexia, obesity, cancer, neurodegenerative disorders, immune  
PT disorders and various lipidemias.  
XX Claim 1; Page 19-20; 116pp; English.  
XX This sequence shows a FCTR6 protein. The DNA sequence originates in  
CC chromosome 20 at map location q13.2-13.33. The FCTR6 protein is a novel  
CC transmembrane protein and has a high probability of sorting into the  
CC plasma membrane. The FCTR6 nucleic acid sequence has 225 of 381 bases  
CC (59%) identical to human cadherin-13 coding sequence. FCTR6 polypeptides  
CC and associated nucleic acids are useful for treating or preventing a  
CC FCTR6-associated disorder related to energy metabolism in an organism  
CC that affects adipose stored, muscle mass, insulin secretion, glucose  
CC utilization and serum lipid levels including, triglycerides and  
CC cholesterol in human. These disorders include diabetes, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X, anorexia,  
CC wasting disorders associated with chronic diseases, metabolic disorders,  
CC obesity, infectious disease, cancer-associated cachexia, cancer,





Db 1019 GMIEGKTPTPLSSFRSLPTTIEICM-----VSIPEPINVAPP--- 1055  
QY 422 IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFOEIVHK-SVVLIPLGAVDDGEHSQ 480  
Db 1056 -----TGFTVLPFSIRYASEVEKTNLPENLLYDVSQVAIPFDNVDD---EQ 1098  
QY 481 NEKINRW 488  
Db 1099 IQKPQRWN 1106

RESULT 675  
ABG25994  
ID ABG25994 standard; protein; 1286 AA.

XX AC ABG25994;  
XX 18-FEB-2002 (first entry)  
DE Novel human diagnostic protein #25985.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.  
XX WO200175067-A2.  
PD 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
PF 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
PI WPI; 2001-639362/73.  
DR N-PSDB; AAS90181.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX PS Claim 20; SEQ ID NO 56353; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 1286 AA;

Query Match 3.5%; Score 91; DB 4; Length 1286;  
Best Local Similarity 19.2%; Pred. No. 2e+02;  
Matches 105; Conservative 65; Mismatches 160; Indels 218; Gaps 26;  
QY 78 MAAVADTLQRLGARVASVDMGPQLP-----DGQSLP-----IPP- 112  
Db 640 LAVLADT---GATV-----LGPKHVPCPNRRRDEENMPGSRREVKNAREEGVEFKENVQPL 691  
QY 113 -----VILAELGSDPTKG---TVCFYGHLDVQPAD-----RGDGWL 145  
Db 692 GIEVNGKVGVMVTEMGEPAKGRRAEIVAGSEHIVPADAVIMAFGRPHNMEWL 751  
QY 146 TDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKF-----IIEGMEE 200  
Db 752 AKHSVELDSQGRITAPESDN-----AFQT-----SNPKIFAGGDIVRGSDL 793  
QY 201 AGSVALEELVEKE---KDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFVMEVKCRD 257  
Db 794 VVTAIAEGQLEQQGTGDTATSYADRLTMSTDNSIYQLLPDAVVFPRSTADVALIARLAA 853  
QY 258 QDFHS-----GTFGGILHEPMA DLVALLGSLVDSSGHI----- 290  
Db 854 QERYSSLIFTPRGGTGTNGQALNQ-----GIIVMSRHMNRRIIEINPEEGCMTAA 904  
QY 291 -----LVP--GIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKKEIL- 338  
Db 905 CVKPSVSQSMAPRQGLFED-LPSSQCRLLALKHVLNLLRDRYDDR-QSALFTTNPALA 962  
QY 339 -----MHLWRYPSLSIHGIEG-----AFDEPGTKTVIP 366  
Db 963 ADDRISLEGETREITSYFPMQFVRY-SLLIHAAAGISLIHAILIHRVMAFWVKG S---IK 1018  
QY 367 GRVIGK-----FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSVMTLGLHPWIAN 421  
Db 1019 GMIEGKTPTPLSSFRSLPTTIEICM-----VSIPEPINVAPP--- 1055  
QY 422 IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFOEIVHK-SVVLIPLGAVDDGEHSQ 480  
Db 1056 -----TGFTVLPFSIRYASEVEKTNLPENLLYDVSQVAIPFDNVDD---EQ 1098  
QY 481 NEKINRW 488  
Db 1099 IQKPQRWN 1106

RESULT 676  
ABG25086  
ID ABG25086 standard; protein; 1286 AA.  
XX AC ABG25086;  
XX 18-FEB-2002 (first entry)  
DE Novel human diagnostic protein #25077.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX







OS Unidentified.  
XX WO2003106654-A2.  
XX  
XX  
XX 24-DEC-2003.  
XX  
XX 16-JUN-2003; 2003WO-US019153.  
XX  
XX 14-JUN-2002; 2002US-0389299P.  
XX  
XX (DIVE-) DIVERSA CORP.  
XX  
XX Steer B, Callen W, Healey S, Hazlewood G, Wu.D, Blum D;  
XX Esteghlalian A;  
XX  
XX WPI; 2004-099016/10.  
XX N-PSDB; ADJ35145.  
XX  
XX Novel xylanase recombinant polypeptide useful for improving textile  
XX texture, treating paper, eliminating microorganisms.  
XX  
XX Claim 60; SEQ ID NO 362; 570pp; English.  
XX  
XX The invention describes an isolated or recombinant polypeptide (I),  
XX having 50% or more identity to 190 300-1200 residue amino acid sequences  
XX (S1), given in the specification, over a region of 100 or more residues  
XX and the polypeptide as thermostable xylanase activity. (I) is useful for:  
XX dough conditioning; beverage production; as a nutritional supplement in  
XX animal feed; reducing lignin in a wood or a wood product; and for  
XX eliminating and protecting animals from a microorganism comprising xylan.  
XX The polynucleotide (II) encoding (I) is useful for amplifying nucleic  
XX acid encoding a polypeptide having a xylanase activity which involves  
XX amplification of a template nucleic acid with a primer pair capable of  
XX amplifying (II) or its subsequence. (I) is useful for treating and  
XX preventing bacterial infection and fungal infection e.g. coccidiosis.  
XX This is the amino acid sequence of a xylanase protein isolated from an  
XX environmental sample.  
XX  
XX Sequence 1680 AA;  
SQ  
Query Match 3.5%; Score 91; DB 8; Length 1680;  
Best Local Similarity 20.1%; Pred. No. 3.le+02;  
Matches 66; Conservative 57; Mismatches 126; Indels 80; Gaps 16;  
QY 170 VLAWINAVSAFRALEQDLP-----VNIKFIIEGMEEAGSVALEELVEKE 213  
Db 7 VLAWI--MSSVLLISMAMPFASGDSSQVPRVIFETGFETGLDGFKGRGSATLRTTDET 64  
QY 214 KDRFFSGVDYIVISDNL--WISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTGGILH 270  
Db 65 QAGDYS----VLVSNRLEHWNGASLPLTGCVLPNGTYEFVGYIKAKADVADNYVMSGEYN 120  
QY 271 EPMAD-----LVALLGSLVDSSGHILVPGIYDEVVPLTTEEBINTYKAHLDLEEVR 321  
Db 121 EGISGNQYWPWISNRLLTVDQDGFVEFRGELTI-----LEDMTSFNLN-FEHQNAEVEFYL 173  
QY 322 NSSRVEKFLPDTKKEILMHLWRYPSLSI-----HGIEGAFDEPGTKTVIPGRVI 370  
Db 174 DSVQVILIEEGQVNDLPMNVRRAP-LTLAETPLHEIWADHFTIGNIYTPGFRTDIRGEV- 231  
QY 371 GKFSIRLVPHMNVSAVEK-QVTRHLE-----DVFSKRNSNKMVVSMTLGLH- 416  
Db 232 -----LAHFNVTAEINIMKPDHLQREQGIFTFSASNDMMEFARANNQEVIGHTLVVHS 285  
QY 417 ---PWIANIDDT--QYLAAKRA-IRTVFG 439  
Db 286 QSFPPWFELNPTRDEAIAIMHAHETVMG 314  
RESULT 680  
ABB08024  
ID ABB08024 standard; protein; 1701 AA.  
XX

AC ABB08024;  
XX  
XX 27-AUG-2002 (first entry)  
XX  
XX Human Rho GEF member, 33521 polypeptide.  
XX  
XX Guanine nucleotide exchange; GEF; 33521; cytosolic; immunomodulator;  
KW antiinflammatory; cardiac; antiarthritic; antidiabetic; antipsoriatic;  
KW antirheumatic; antiarrhythmic; immunosuppressive; gene therapy; human;  
KW Rho.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200226817-A2.  
XX  
XX 04-APR-2002.  
XX  
XX 25-SEP-2001; 2001WO-US029962.  
XX  
XX 25-SEP-2000; 2000US-0235033P.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Meyers RA;  
XX  
XX WPI; 2002-405045/43.  
XX N-PSDB; ABL60582, ABL60583.  
XX  
XX New nucleic acid and polypeptide molecules or the human guanine  
XX nucleotide exchange, designated 33521, useful for diagnosing, preventing  
XX or treating cancer (e.g. sarcoma or leukemia), autoimmune disease or  
XX cardiovascular diseases.  
XX  
XX Claim 5; Page 109-110; 129pp; English.  
XX  
XX The invention relates to a novel human Rho guanine nucleotide exchange  
XX family (GEF) member, designated 33521 and encoding polynucleotides.  
XX Modulators of the 33521 nucleic acid is useful for treating or preventing  
XX a disorder characterized by aberrant activity of a 33521-expressing cell,  
XX specifically for reducing or inhibiting the aberrant activity of the  
XX 33521-expressing cancer cell. In particular, the 33521 nucleic acid and  
XX polypeptide are useful for diagnosing, preventing or treating cancer  
XX (e.g. carcinoma, sarcoma, metastatic or haematopoietic disorders (e.g.  
XX leukemia), or cancers of the lung, breast, thyroid, head neck, prostate  
XX or genito-urinary tract), immune disorders (e.g. inflammatory (e.g.  
XX respiratory inflammation or arthritis), autoimmune disease (e.g. diabetes  
XX mellitus, psoriasis, Wegener's granulomatosis, Crohn's disease or Grave's  
XX disease)), or cardiovascular diseases (e.g. arterial inflammation,  
XX rheumatic heart disease, arrhythmia or aneurysm). The present sequence  
XX represents the novel human 33521 polypeptide  
XX  
XX Sequence 1701 AA;  
SQ  
Query Match 3.5%; Score 91; DB 5; Length 1701;  
Best Local Similarity 19.4%; Pred. No. 3.le+02;  
Matches 97; Conservative 67; Mismatches 137; Indels 198; Gaps 26;  
QY 1 MDPKLGSRMAASLLAVLLLLLGERGMFSSPPSPALLLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 649 MDSKMKMAELQLSVV-----SDPKNRKAIENQI-----QQW---- 680  
QY 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS 120  
Db 681 ---EQNLEKFHMDLFRMRCYLA-SLQ-----GGELPNPKSLLA-AAS 717  
QY 121 DPTKGTVCIFYGHLVDVQPADRGDGLWLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 718 RPSKLAL-----GRL-----GILSVSSF 735  
QY 181 RAL--EQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFS--GVDYIVISDNLWISQRK 236  
Db 736 HALVCSRD-----DSALRKRTLSTLQGRNKKGIFSSLKGLDTLARKG----KEKR 782



PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.



PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 3.5%; Score 90.5; DB 3; Length 178;

Best Local Similarity 23.4%; Pred. No. 11;

Matches 37; Conservative 32; Mismatches 64; Indels 25; Gaps 7;

QY 33 ALLEKVFQYIDLH-----QDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQ 86  
Db 2 SLRLLLVVVWLHLSAVAGDDAIVSRFQEYLRI--NTVQPNPEYKAVDFIIS----- 52  
QY 87 RLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLT 146  
Db 53 --QAKPLSLESQTIEFVKGK----PLLLKKWVGSDPTLPFAFLNLSHTDVVPFE-DSKWT 105  
QY 147 DPVYLTEVD--GKLYGRGATDNKGPVLAWINAVSAFRA 182  
Db 106 HP-LQAHMDHHGDIYARGSQDMKCVGMQYLEAIRKLOA 142

RESULT 683

ABU18525  
ID ABU18525 standard; protein; 224 AA.

XX AC ABU18525;

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #4052.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Bacillus anthracis.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA22395.

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 46449; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 224 AA;

Query Match

Best Local Similarity 3.5%; Score 90.5; DB 6; Length 224;

Matches 66; Conservative 46; Mismatches 83; Indels 95; Gaps 16;

QY 195 IEGMEEAGSV--ALEELVEKEKDRFFSGVDYIVISDN-----LWISQKPAITYGTRG 245  
Db 5 VEIIGEADCVDALEELMKNKPDIVF--LDIQLSDDNNGFEIANILKMKNPFAIVFATAY 62

QY 246 NSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEE 305  
Db 63 DQY-----ALQAFEDDALDYILKP--FDE-----ER 86

QY 306 EINTYKAHLDLEEYRNSSRVEKFLFDTKBEIL-----MHLWRYP---SLSIHGIEGA 355  
Db 87 IVQT-----LKKYKQKQSQ---IEMKQEIKGADVTAEMHKLALPIESIVLVNIE-- 134

QY 356 FDEPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGL 415  
Db 135 -----DIVYVGLVDGKVTVKTVR-----ETYVTHDTLVILEK-----KLPTSKFMRV 176



CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 500 AA;

Query Match 3.5%; Score 90.5; DB 6; Length 500;  
Best Local Similarity 17.9%; Pred. No. 52;  
Matches 76; Conservative 65; Mismatches 142; Indels 141; Gaps 14;

QY 170 VLAWINAVSAFRALEQDLPVNIKFIEGMEAGSVALBELVEKE----- 213  
Db 5 ILAVVEAVSNEKALPREK-----IFEALESALATATKXKYEQIEDVRVEIDRKSGDFT 58  
QY 214 -----KDRFFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 59 FRRWLIVEVTPTKEITLEARFEDESINVG DYVEDQIESVTFDRITTQTAKQVIVQKV 118  
QY 244 RGN SYFMVEVKCRDQDFHSGTGILHEPMDLVALGSLVDSSGHILVPGYDEVVPLT 303  
Db 119 REABRAMVVDQFRDQGEIIVT--GVVKVNRDNI SLEIKSEG MAGNA-----EAVILR 169  
QY 304 EEINTYKAIHLDLEEYRNSRV-----EKFLFDTKEEILMHLWR--YPSL 347  
Db 170 ED-----MLPRENFRPGDRIRGVLVAVRPEARGAQLFVTRSKPEMLIELFRIEVPEI 221  
QY 348 --SIHGIEGAFDEPGTKTIVP-----GRVIG----- 371  
Db 222 GEEVIEIKAAARDPGSRAKIAVKTNDRIDPVGACVGMRGARVQAVSTELGGERIDIVLW 281  
QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGLHP 417  
Db 282 DDNPAQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAIGRNQONVHLASQLSGWEL 341  
QY 418 WIANIDDTQ--YLAAKRAIRTVFGTEPDMIRDGSTIPTAKMFQEI VHKSVV-----LIPLG 471  
Db 342 NVMTVDDLQAKGQAEAAHAIETFTKYLDIDEEFATVLVEEGFSTLEELAYVPMKELLEID 401  
QY 472 AVDD 475  
Db 402 GLDE 405

RESULT 686  
ADJ48678  
ID ADJ48678 standard; protein; 641 AA.

XX ADJ48678;  
AC  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Oil-associated gene related protein #178.  
XX  
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.  
XX  
OS Unidentified.  
XX  
PN US2004025202-A1.  
XX  
PD 05-FEB-2004.  
XX  
PF 14-MAR-2003; 2003US-00389566.  
XX  
PR 15-MAR-2002; 2002US-0365301P.  
PR 26-JUN-2002; 2002US-0391786P.  
PR 26-JUN-2002; 2002US-0392018P.  
XX  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
XX  
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;  
XX  
DR WPI; 2004-142683/14.  
XX  
PT Novel recombinant DNA construct comprising a promoter functional in  
PT plants operably linked to an oil-associated gene for producing transgenic  
PT plant seed.  
XX  
PS Example 3; SEQ ID NO 682; 22pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in plants operably linked to an oil-associated gene.  
CC The construct is useful for transgenic plant seed which has in its genome  
CC the construct, that is functional in the plant to transcribe the oil-  
CC associated gene. The transgenic plant seed grows into a plant having  
CC enhanced seed oil as compared to wild type. The construct is useful for  
CC producing hybrid maize seed. The transgenic plant seed is useful for  
CC producing vegetable oil. The present sequence represents the amino acid  
CC sequence of an oil-associated gene related protein.  
XX  
SQ Sequence 641 AA;

Query Match 3.5%; Score 90.5; DB 8; Length 641;  
Best Local Similarity 23.2%; Pred. No. 77;  
Matches 66; Conservative 41; Mismatches 90; Indels 87; Gaps 17;

QY 171 LAWINAVSAFRALEQDLPVNIKFIEG-----MEEAGSVALEELVEKED-RFFS 219  
Db 149 VAFIRTVSSQQDTNRNCYVRIIFNVPGTFPSPHDANSKMFPGSIYLKEASFRSKDSRHIS 208  
QY 220 GV-----DYIVISDN-----LWISQRKPAITYGT 243  
Db 209 EVVQSIKTLRRQVVARESEARAERATLVTOEKLQLANNRKPIRLSDLWI---RPA--FGG 263  
QY 244 RGN SY-----FMVEVKCRDQDFHSGTGILH---EPMA-DLVALGSLVDSSGH 289  
Db 264 RGRKIPGTLEAHVNGFRYSTTRQDERVDI-MFENIKHAFFQPAENEMITLLHLHDN--H 320  
QY 290 ILVPG-----YDEVVPLTEEEI-----NTYKAIHLDLEEYRNSRVEKF--LFDTK 335  
Db 321 IMVGNKTKDVQFYVEVMDMVQXNVGGKRSYDPPDELE-EEQERQRKNKINVEFQTFV 379  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTIVPGRVIGKFSIRLVP 379  
Db 380 NRVNDLWGQP--QFNGLDLEFDQPLRELGFPG-VPHKSSVFIVP 420





PT protecting humans and other mammals against colonisation and infection by  
PT beta-haemolytic streptococci.

XX Example 1; Fig 2; 76pp; English.

XX This polypeptide comprises the streptococcal C5a peptidase (SCP) of beta-  
CC haemolytic group A Streptococcus M type 12 strain. A claimed vaccine  
CC comprises an immunogenic amount of an SCP (see also AAW22469 and  
CC AAW22471), or its fragment or a mutant, sufficient to immunise a mammal  
CC against beta-haemolytic Streptococcus (beta HS), plus a non-toxic  
CC vehicle. The vaccine is used to protect humans (especially), dogs,  
CC cattle, pigs and horses against colonisation and infection by beta HS of  
CC Streptococcus groups B, C, G or especially A (claimed). SCP, which  
CC converts C5a complement to an inactive form, promotes colonisation of  
CC beta HS by inhibiting the influx of phagocytes to the site of infection  
CC and also retards clearance of bacteria from the host. Only a single  
CC protein, SCP, is required for an effective vaccine, and it generates a  
CC response which is not serotype dependent. (Updated on 17-OCT-2003 to  
CC standardise OS field)

XX Sequence 1167 AA;

Query Match 3.5%; Score 90.5; DB 2; Length 1167;

Best Local Similarity 19.3%; Pred. No. 1.9e+02;

Matches 100; Conservative 82; Mismatches 170; Indels 167; Gaps 28;

QY 47 DEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDG- 105  
Db 604 DKFEVT---VTVHNKSDKP-----QELYQQATVQTDKVD--GKHFA--LAPKLYEAS 649  
QY 106 -QSLPIP-----PV-----ILAELGS-----DPTKGTVCFYGHLDV 135  
Db 650 WQKITIPANSSKQVTPIDASRFSKDLAQMKNGYFLEGVRFKQDPTKEELMSIPYIGF 709  
QY 136 QPADRGDGLWTDPPVLTVEVDGKLYGRGATDN-----KGPVLAWINAVSAFRAL--EQDLP 188  
Db 710 R-GDFGNLSAVEKPIYDSKDGSSYYHEANSDAKDQLDGDGLQFYALKNNFTALTTSNPW 768  
QY 189 VNIKFIIEGMEEAGSVALEELVE-----KEKD-----RFFSGVDYIVISDNLWIS 233  
Db 769 TIILKAVKEGVENIEDIESSEITETIFAGTFAKQDDDDSHYYIHRHANGEPYAAISP----- 824  
QY 234 QRKPAITYGTRGNSYFMVVEVKCRDQDFHSGTGGILHEPMAADLVALLSGLVDSSGHILVP 293  
Db 825 -----GDGN-----RDYVQFGTF-----LRNAKNLVAEVLCKEGNVVWT 859  
QY 294 GIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLDPTKEEILMHLWRYPSLSIHGIE 353  
Db 860 S-----EVTEQVVKNY---NNDLASTLSTGSTRFEKTRWDGKDK-----D 894  
QY 354 GAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVS--- 410  
Db 895 GKVVANGTYT-----YRVRYTP---ISSGAKE--QHTDFDVIVDNTTPEVATSATF 940  
QY 411 -----MTLGLHPWIA-----NIDDTQYLAAKRAIRTVFGTEPDMIRDGS 449  
Db 941 STEDRRLTLASKPKTSQPVYRERIAYTYMDEDLPTTEYISPNEDGTFTLPEEAETM--EGA 999  
QY 450 TIPIAKM--FQEIYVK---SVVLPLGAVDDGEHSQNEK 483  
Db 1000 TVPL-KMSDFTYVVEDMAGNITYTPVTVKLLEGHNSKPEQ 1037

RESULT 689

AAB01264

ID AAB01264 standard; protein; 1167 AA.

XX AAB01264;

AC AAB01264;

XX 25-SEP-2000 (first entry)

DT 25-SEP-2000 (first entry)

XX 25-SEP-2000 (first entry)

DE SCPA12 peptidase (wild type sequence).

XX

KW SCP; beta haemolytic streptococci; peptidase; vaccine; vaccination;  
KW immunise; strep throat; impetigo; rheumatic fever; sepsis;  
KW acute glomerulonephritis, sepsis, toxic shock; necrotising fasciitis.

XX Streptococcus pyogenes.

XX WO200034487-A1.

XX 15-JUN-2000.

XX 03-DEC-1999; 99WO-US028826.

XX 07-DEC-1998; 98US-00206898.

XX (MINU ) UNIV MINNESOTA.

XX Cleary PP, Stafslieen DK;

XX WPI; 2000-423430/36.

XX Vaccine for streptococcal infection comprises immunogenic amount of  
PT variant streptococcal C5a peptidase.

XX Example 1; Page 75-79; 94pp; English.

CC A vaccine for protecting against infection by beta-haemolytic  
CC streptococci comprises a streptococcal C5a peptidase (SCP), which is a  
CC variant of wild-type SCP, in an amount to immunise a susceptible mammal.  
CC The variant peptidase is generally a deletion mutant of the wild type  
CC SCP. The vaccine is useful for protecting a susceptible mammal,  
CC preferably a human, dog, cow, pig, or horse, against beta-hemolytic  
CC Streptococcus, preferably group A, B, C or G Streptococcus, colonisation  
CC or infection. The application of SCP for vaccination reduces the  
CC incidence of strep throat and impetigo, and will also eliminate sequelae  
CC such as rheumatic fever, acute glomerulonephritis, sepsis, toxic shock  
CC and necrotizing fasciitis

XX Sequence 1167 AA;

Query Match 3.5%; Score 90.5; DB 3; Length 1167;

Best Local Similarity 19.3%; Pred. No. 1.9e+02;

Matches 100; Conservative 82; Mismatches 170; Indels 167; Gaps 28;

QY 47 DEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDG- 105  
Db 604 DKFEVT---VTVHNKSDKP-----QELYQQATVQTDKVD--GKHFA--LAPKLYEAS 649  
QY 106 -QSLPIP-----PV-----ILAELGS-----DPTKGTVCFYGHLDV 135  
Db 650 WQKITIPANSSKQVTPIDASRFSKDLAQMKNGYFLEGVRFKQDPTKEELMSIPYIGF 709  
QY 136 QPADRGDGLWTDPPVLTVEVDGKLYGRGATDN-----KGPVLAWINAVSAFRAL--EQDLP 188  
Db 710 R-GDFGNLSAVEKPIYDSKDGSSYYHEANSDAKDQLDGDGLQFYALKNNFTALTTSNPW 768  
QY 189 VNIKFIIEGMEEAGSVALEELVE-----KEKD-----RFFSGVDYIVISDNLWIS 233  
Db 769 TIILKAVKEGVENIEDIESSEITETIFAGTFAKQDDDDSHYYIHRHANGEPYAAISP----- 824  
QY 234 QRKPAITYGTRGNSYFMVVEVKCRDQDFHSGTGGILHEPMAADLVALLSGLVDSSGHILVP 293  
Db 825 -----GDGN-----RDYVQFGTF-----LRNAKNLVAEVLCKEGNVVWT 859  
QY 294 GIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLDPTKEEILMHLWRYPSLSIHGIE 353  
Db 860 S-----EVTEQVVKNY---NNDLASTLSTGSTRFEKTRWDGKDK-----D 894  
QY 354 GAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVS--- 410  
Db 895 GKVVANGTYT-----YRVRYTP---ISSGAKE--QHTDFDVIVDNTTPEVATSATF 940  
QY 411 -----MTLGLHPWIA-----NIDDTQYLAAKRAIRTVFGTEPDMIRDGS 449





Best Local Similarity 19.4%; Pred. No. 2.9e+02;  
Matches 94; Conservative 68; Mismatches 157; Indels 165; Gaps 23;  
QY 42 IDLHODEFVQTLKEWVAIESDSVQVPRFRQ--ELFRMMAVAADTLQRLGARVASVDMGP 99  
Db 562 IDLH-----NPSMPEVSTVQTPELFK-----GTLKEYQMK-----GL 594  
QY 100 QQLPDGQSLPIPPVILAEELGSDPTKGTVCYFGLHDVQPADRGWLTDPPYVLTEVDGKLY 159  
Db 595 QWLNVCEYQGLNGILADEMGLGKTIQAMAFLAHL-----AEENKIW----- 635  
QY 160 GRGATDNKGPVLA-----WINAVSAFRALEQDLPVNFKFIEEGMEEAGSVALEELV 210  
Db 636 -----GPFLVAPASVNLNWADEISRFCPDLKTL-----YWGGLQER-TILRKIN 681  
QY 211 EKEKDRFSGVDYIVISDNLWISQKPAITYGTRGNSYFMV----- 251  
Db 682 PKRMYRRDAGFHILITSYQLLVTDK-----YFRRVKWQYMVLDQAIAKSSSIRWKTLL 737  
QY 252 EVKCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYD----- 297  
Db 738 SFNCRNRLLTGT---PIQNNMAELWALL-----HFIMPMLFDNHDQFNWFSKGTE 786  
QY 298 -----EVVPLTEEEINTYKAIHLDLEEYRNSRVEKFL---PDTKEILMHLWRYPSLSIH 350  
Db 787 NHAHGGTINEHQLN---RLHAILKPFM-LRRVKKDVVSELTXTKTEVTVH-----CKLS 836  
QY 351 GIEGAFDEPGTKTVIPGRVI-----GKFSIRLVPH-MNVSAVEKQVTRHLEDVFSKRNSSN 405  
Db 837 SRQAFYQAIAKNKISLAELFDSNRGQFTDKKVLNLMNIVILQRKVCNHPE-LFERNEGSS 895  
QY 406 KM---VVSMTLGLHPWIANIDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQETVH 462  
Db 896 YLYFGVTSNSLLPH-----FGELEDVHYSGGONPIIYKIPKLLH 935  
QY 463 KSVV 466  
Db 936 QEVL 939

RESULT 692  
ABU36934  
ID ABU36934 standard; protein; 1513 AA.  
XX AC ABU36934;  
XX 19-JUN-2003 (first entry)  
DE Protein encoded by Prokaryotic essential gene #22461.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Mycobacterium tuberculosis.  
OS WO200277183-A2.  
XX PN 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX PF 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA40804.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 64858; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1513 AA;

Query Match 3.5%; Score 90.5; DB 6; Length 1513;  
Best Local Similarity 22.5%; Pred. No. 2.9e+02;  
Matches 73; Conservative 34; Mismatches 99; Indels 119; Gaps 16;  
QY 59 IESDSVQVPVPRFRQEL--FRM-----MAVAADTLQRLGARVASVDMGPFQ 101  
Db 659 VPTDSTLLVERFRDELGDMRWVILHSPYGLRVHGPLALAVGRRRLDRYG-----IDKPTA 713  
QY 102 LPDQGSPLPIPPVILAEELGSDPTKGTVCYFGLHDVQPADRGDWLTDPPYVLTEVDGK--- 157  
Db 714 SDNGIVVRLPDTVSA--GEDSPPGAELF-----VFDAD-----IDPIVTEVAGSALFA 761  
QY 158 -----LYGRGATDNKGPVLAWINAVSAFRALE-----QDLPVNKFIEEGMEEA 201  
Db 762 SRFRESAARALLPRHPGRRSPL--WQQRQRAARLLEVARKYPDFPIVLETVRECLQDV 819  
QY 202 GSV-ALEELVEKEKDR-----FFSGVDYIVISDNLWISQKPAITY 241  
Db 820 YDVPILVELMARIQRRVRVAEAEATAKPSPPFAASLLFGYVGAFFMEGDTPLAERRAALA 879  
QY 242 --GTRGNSYFMVEVKCR-----DQDFHSGTGGILH-----EPMADLVALLGS 282  
Db 880 LDGT-----LLAELLGRVELRELLDPDVIATSRQLQHLAADRVARDAEGVADLLRLLG- 933  
QY 283 LVDSSGHILVPGIYDEVVPLTEEEI 307  
Db 934 -----PLTEDEI 940  
RESULT 693  
ABR52863  
ID ABR52863 standard; protein; 1679 AA.



Db 1437 SIWRMLTDLT-WPVTSTYTTGH-----EFNRGIWKTFGDTRIEDFWIQYCNSTNITDSVQE 1491  
Qy 337 I--LMLWRY--PSLSIHGIEGAFDEPGTKTIPGRVIGKFSI-----RLVPHMNV 384  
Db 1492 IHSFGYAWRYIRASMSLAGLLPPEENGs-MLLDGGYVDNLPVTEMRRARGCQTIFAVDVG 1550  
Qy 385 AVEKQVTRHLED-----VFSKRNSNKMVSMITGLHPWIANIDDTQ---YLAAKRA 433  
Db 1551 SADRTPMEYGDLSNGFWIIFNRWNPFS-----HNIPNMAEIQVRLGYVASVNA 1601  
Qy 434 IRTVGTPEPDM-----IRDSIPIAKMFOEIVHKSV---VLIPLGAVDDGEHSQNEKI 484  
Db 1602 LEKAKNT-PGVVYVRPPIEEYATLDFSK-FEEIYHVGVVDYGRIFLQGLIDD----- 1650  
Qy 485 NRWNYIEGTK 494  
Db 1651 DKMPYIPGSQ 1660  
RESULT 695  
ABB93446  
ID ABB93446 standard; protein; 1963 AA.  
XX  
AC ABB93446;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 2657.  
XX  
KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX  
PR 28-AUG-2001; 2001WO-EP009892.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;  
XX  
DR WPI; 2002-269010/31.  
XX  
PT Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
PS Claim 5; SEQ ID NO 2657; 26lpp + Sequence Listing; English.  
XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 1963 AA;  
Query Match 3.5%; Score 90.5; DB 5; Length 1963;  
Best Local Similarity 20.4%; Pred. No. 4.3e+02;  
Matches 70; Conservative 47; Mismatches 105; Indels 121; Gaps 14;  
Qy 175 NAVSAFRALEQDLP-----VNIKFIEG-----MEEAGSVALEELVEK 212  
: ||| |::| ||::: ||| |

Db 1133 DGVSILFYLQKIFFPGDCSYAVNVAYILESRLEPDLSPDEWNNFLERVKCLSEEL--K 1190  
Qy 213 EKDRFFSGVDYIVISDNLMISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEP 272  
Db 1191 ESDELEEL-----RLWASYRGQTLTRTVRGMVYRKALE----- 1225  
Qy 273 MADLVALLGSLVSDSCHILVPGIYDEVVPLTTEEEINTYKAHLDLEEYRNSSRVEKPLF- 331  
Db 1226 -----LQAFLDMAH-----EDLMGYKAVELNSE---NNSRGERSLWA 1261  
Qy 332 -----DTK-----EEILMHLWRYPSSLIHGIEGAFDEPGTKTV 364  
Db 1262 QCQAVADMKFTYVVSQOYGIHKRSGDPRAQDILRLMTRYPSLRVAYID-EVEEPVKDKS 1320  
Qy 365 IPGRVIGKFSIRL-VPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVV 409  
Db 1321 KKGQKQVYVSVLVKVPK---STDHSTLAQNLDQVIYRIRLPGPAILGEGKPENQHAIF 1377  
Qy 410 SMTLGLHPWIANIDDTQYLAAK-RAIRTVFGTEPDMIRDGSI 451  
Db 1378 SRGEGLOTIDMNQDNMEEALKMRNLLQEFLLTKHDGVRHPSIL 1420  
RESULT 696  
AAY77819  
ID AAY77819 standard; protein; 3418 AA.  
XX  
AC AAY77819;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE BRCA2 protein sequence.  
XX  
KW BRCA2; tumour; prostate cancer; cytostatic; antiproliferative;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 122 /note= "encoded by ACT"  
FT Domain 3334..3344  
FT /note= "granin box domain"  
XX  
CA2218197-A1.  
XX  
PD 05-JUN-1999.  
XX  
PF 12-DEC-1997; 97CA-02218197.  
XX  
PR 05-DEC-1997; 97US-00986106.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
PA (UYVA-) UNIV VANDERBILT.  
XX  
PI Robinson-Benion CL, Thompson ME, Holt JT, Jensen RA, Steiner MS;  
PI King M;  
XX  
DR WPI; 2000-238071/21.  
DR N-PSDB; AAZ87996.  
XX  
PT New method of treatment and suppression of prostate cancer comprises  
PT using the BRCA family of genes to decrease the growth rate of the tumor.  
XX  
PS Claim 9; Page 110-122; 166pp; English.  
XX  
CC The invention relates to a method for suppressing the growth of a  
CC prostate tumour in a mammal that comprises introducing to the tumour a  
CC vector comprising a nucleic acid sequence encoding a BRCA family gene  
CC product operatively linked to a promoter, where production of the BRCA  
CC family gene product results in a decrease in the growth rate of the  
CC tumour. The methods are used to suppress the growth of and also to treat  
CC prostate tumour in a mammal where the tumour is gene-linked hereditary











[illegible]

Db	177	ENGACPPLELKNKHIEDGMMEIGFGAANFK-----EINASKSDPLDIIQNEIC	222
QY	193	---FIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYF	249
Db	226	LYPDYLKMAEDAAGNSMFFARKEQ-----VYVRHIW-----TRGGS--	262
QY	250	MVEVKCRDQDFHSGTFGG--ILHEPMDLVALLGSLVDSSGHI-----	290
Db	263	--EKEAPTDFYLNKNGKDATLKIPSVHFGSPGSLVSTDNQIFNRPYWLFRAGQMNNGI	320
QY	291	-----LVPGIYDEVVPLTEEEINTYKAIHLDLEEEYRNSRRVEKFLFD	332
Db	321	AWNLLFLTVDNTRGTNLTISVASDGTPLTEYDSSKFNVYHRHMEEYKLAFILELCSVE	380
QY	333	TKEEILMHL-----WRY-----PSLSIHGIEGAF---DEPGTK---TWIPGR	368
Db	381	ITAQTVSHLQGLMPSVLENWEIGVQPPTSSI--LEDTRYIESPATKCSANVIPAK	434
RESULT 702			
ID	ADG67846	ADG67846 standard; protein; 496 AA.	
XX	AC	ADG67846;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Human TRP-PLIK2 protein partial sequence SeqID98.	
KW		TRP-PLIK2; transient receptor potential channel; antiinflammatory;	
KW		gynaecological; immunomodulatory; cardiant; cytostatic; neuroprotective;	
KW		antiviral; anti-HIV; gene therapy; immune disorder;	
KW		haematopoietic disorder; inflammatory disorder; renal disorder;	
KW		reproductive disorder; hepatic disorder;	
KW		hyper transient receptor potential activity; prostate cancer;	
KW		testicular cancer; chromosome 9q21 aberration;	
KW		amyotrophic lateral sclerosis; frontotemporal dementia;	
KW		early-onset pulverulent cataract; infantile nephronophthisis;	
KW		hypomagnesaemia;	
KW		secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis;	
KW		neuron degeneration; neurogenic inflammation; allergy; immunodeficiency;	
KW		excessive immune activation; visual defect; hearing disorder; pain;	
KW		cancer; hypertension; cardiovascular disease; Calcium homeostasis;	
KW		osteoporosis; hypercalcaemic stone disease; chronic renal failure;	
KW		proliferative disorder; ischaemia-reperfusion injury; heart failure;	
KW		immuno-compromised condition; HIV infection; NF-kappa-B regulation;	
KW		apoptosis regulation; NF-kappa-B activity; human.	
XX	OS	Homo sapiens.	
XX	PN	WO200294999-A2.	
XX	PD	28-NOV-2002.	
XX	PF	22-MAY-2002; 2002WO-US016164.	
XX	PR	22-MAY-2001; 2001US-0292599P.	
XX	PR	08-MAR-2002; 2002US-0362944P.	
XX	PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.	
XX	PI	Lee N, Chen J, Feder J, Wu S, Chang H, Lee L, Blonar M, Bol D;	
XX	DR	WPI; 2003-148463/14.	
XX	DR	N-PSDB; ADG67845.	
PT	PT	New TRP-PLIK2 nucleic acid and its splice variants, useful for	
PT	PT	manufacturing a medicament for preventing, treating or ameliorating a	
PT	PT	medical condition, e.g. renal, inflammatory or reproductive disorders.	
XX	PS	Claim 5; SEQ ID NO 98; 457pp; English.	
XX	XX		







Db	242	DNKDYLDLKDYIFLAEGKW-----TKAIKQAEFDAFNL-----KMGLKIPSG	285
QY	96	DMGPOQLPD-----GQSL-----PIPPVILAEAGSDPTKGTVCFYGHLDVQPADRG	141
Db	286	IFGYSE--DITFRCHTFQGQISNTWLQKLKPCSVIILGGSLRDLTVSPEGYLD---NDQS	340
QY	142	DGWLTDPP-----YVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI	194
Db	341	DGIADNSDRKLIILNVLTEYHG--GNGFVFKGNL-----SRFI	377
QY	195	IEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD-----NLWISQRKPAITYGTRGN	246
Db	378	I-----RSRYNKGKGVLFETPDAPGDNKAAQLWLE-----CTGNKRS	413
QY	247	SYFMVEVKCRDQDFHSGT-FGGILHEPM-ADLVALLGSLVDSSGHILVPGIYDEWVPLTE	304
Db	414	GFEM-DHSLVNPSYNSGNHFGTIISQNGADLVN-----DDKYDVVLSGYNNNLTIYTE	466
QY	305	EEINTYKAIHLDEE-----YRNSSRVEKFLFDTKEEILMHLWRYPSSLTHIEGAFDEP	359
Db	467	YGAGCW--HKDTLKGSRIFYTNMSHIN-----WK-----DEA	496
QY	360	GTK---TVIPG---RVI--GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKXNSSNKMWVS	410
Db	497	GDSNEVSYIPSAANGTRVIKYKGFQNVVVQNGNGQYSGKLTFTTH-----TANNKF--E	546
QY	411	MTLGLHPWIANIDDTQYLAAKRAIRTVFGT-EPDMIRDG-----STIPIAKMFQEIIVHKS	464
Db	547	YILG---NSTADQNIYYDPDKLFLRKKGKGTFOPIFPRDNVVLNFGTIPAGRS-----VEKS	598
QY	465	VVLIPLG	471
Db	599	LSLLQLG	605

RESULT 706  
ADN26406

ID ADN26406 standard; protein; 672 AA.

AC ADN26406;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #9059.

Recombinant DNA construct; transformed plant; improved plant property;  
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
pathogen tolerance; pest tolerance; plant disease resistance;  
cell cycle pathway modification; plant growth regulator;  
homologous recombination; seed oil yield; protein yield; carbohydrate;  
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
bacterial polypeptide.

**OS Bacteria.**

PN US2003233675-A1.

PD 18-DEC-2003.

20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

PA (CAOY//) CAO Y.  
PA (HINK//) HINKLE G J.  
PA (SLAT//) SLATER S C.  
PA (CHEN//) CHEN X.  
PA (GOLD//) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI; 2004-061375/06.

XX

PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

Query Match 3.4%; Score 90; DB 8; Length 672;

Best Local Similarity 22.2%; Pred. No. -92;

Matches 93; Conservative 37; Mismatches 134; Indels 154; Gaps 20;

31 PPALLEKVFQ-----YIDLHQDEFVQTLKEWVAIESDSVQVPFRFRQELF 75  
QY

```

Db      | | | | : | | | | | | | | | |
1 PRTLFEKVWEAHLVRPETAETPAVLVIDLH-----LIHEVTSPOAFTELQRL 49
Dz      | | | | : | | | | | | | | | |

```

QY 76 RMMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVI-----114

[illegible]

QY 115 LAELGSD-----PTKG-----TVCFYGHLDVQPA-----DRGDGWLTDYPVL--- 151

Db 101 LPELGDENQGIHVHVGPEQGLTOPGMTIVCGDSHTSTHGAFGALFGTGTSEVGHVLATQ 160

```
QY 152 -----TEVDKLYRGATDNKGPVLAINAV-----SAFRALEQD 186
      :||:| | | | | | | | | | | | | | | | | | | | | | | | | |
      :||:| | | | | | | | | | | | | | | | | | | | | | | | | |
```

Db 161 CLLQRPKTC AVRIDGRL-GPGVT-AKDII LALIAKYGVGGTG YVF EYMG EAIRALSME 218

QY 187 LPVNI-KFIIEGMEEAGSVALEELV-EKEKDRFFS--GVDY-----IVISD----- 228

Db 219 ERMTCNMSIEGGARAGMVPDDTTFEYIAGRPFAPKGFADFEAAVARNWRLPSDEGATFD 278

QY 229 ---NLWISQRKPAITYGTRGNSYFMVEVKC-RDQDFHSGTFFGGILHEPMADL----- 276

279 HELTSASELKPMITYGTPNGMGPIDAPVPRPEDMPDARSRAALDKALAYMGLERPGKPL 338

ov 277 -----VALIGSLVDS-----SGHILVPGIYDEWPLTEEEINTYKAITHLD 316

27, 277, 339  
 b b  
 LGHPVDVVFIGSCTNSRLSLDLROAAOFFFRGRKVPGRVMVVPGSOOVKRAAAEGLD 396

RESULT 707

ABP73572

ID ABP73572 standard; protein; 799 AA.

AC ABP73572;

DT 30-JAN-2003 (first entry)



CC (ACE) that can be used in a comparison with the human angiotensin  
CC converting enzyme 2 (ACE-2 of the invention.  
XX  
SQ Sequence 1313 AA;  
  
Query Match 3.4%; Score 90; DB 7; Length 1313;  
Best Local Similarity 17.8%; Pred. No. 2.6e+02;  
Matches 125; Conservative 78; Mismatches 210; Indels 288; Gaps 34;  
  
QY 12 LLAVALLLERGMFSSPPPALLEKVFQYIDLHQDE-----FVQTL 53  
Db 19 MSLSLLLLL-----LPPSPAPA-LDPGLQPGNFSADEAGAQLFADSYNSSAEVVMFQSTA 72  
  
QY 54 KEWVAIESDSVQVPVPRFRQELFRMMAAAD-----TLQRLGARVASVD 96  
Db 73 ASW-AHDTNITEENARLQEEAALINQEFAEVWGKKAKELYESIWNQFTDQKLRRIGSVQ 131  
  
QY 97 -MGPOQLPDGQSLPIPPVILAELGSDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEVD 155  
Db 132 TLGPANPLTQRLQYNS-LLSNMSRIYSTGKVCF-----PNKTATCWSLDP-ELTNI- 181  
  
QY 156 GKLYGRGATDNKGPVL----AWINAVS-AFRALEQDLPV--NIKFIEGMEERAG----- 202  
Db 182 -----LASSRNYAKVLFAMEGWHDVAGIPLRPLYQDFTALSNEAYRQDGFSDTGAYWRSW 236  
  
QY 203 --SVALEELVE----- 211  
Db 237 YESPSFEESLEHLYHQVEPLYNLHLAFVRRALHRRYGDYINLRGPIPAHLLGDMWAQSW 296  
  
QY 212 -----KEKDRFFSGVDYIVISDNLWISQ--RK 236  
Db 297 ENIYDMVVPFDKPNLDVTSTMVQKGNATHMFRVAEEFTSLGLSPMPPEFWAESMLEK 356  
  
QY 237 PA-----ITYGTR-----GNSYFMVEVKCRDQDFHS 262  
Db 357 PADGREVVCHASAWDFYNRKDFRIKQCTRTVMDQLSTVHEMGHVQYLYQYK---DLHV 412  
  
QY 263 GTFGGI---LHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD--- 316  
Db 413 SLRRGANPGFHEAIGDVLAL---SVSTPAHLHKIGLLDRVANDIEDINYLKMALEKIA 469  
  
QY 317 -----LEEYR-----NSSRVEKFLFDTKKEILMHLWRYPSSLHGI-----EGAFD 357  
Db 470 FLPGYLVDQWQWGVFSGRTPPSRNYD-----WWYLRTKYQGI CPPVARNETHFD 520  
  
QY 358 EPGTKTVIPG-----RVIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSNKMVMSM 411  
Db 521 -GAKFHIPSVTPIRYFVSFVLQFQFHQALCKEAGHQGLHQCDIYQSTKAGAKLQQVL 579  
  
QY 412 TLGL-HPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSI-----PIAKMFQEIHKSV 465  
Db 580 QAGCSRPW-----QEVLKDLVGS-----ALDASALMEYFQPVSQLQE----- 618  
  
QY 466 VLIPLGAVDDGEHSQNEKINRW-----NYIEGTKL 495  
Db 619 -----QNQRNGEVLGWPEYQWRPPLPDNYPEGIDL 648  
  
RESULT 709  
ABB84545  
ID ABB84545 standard; protein; 1799 AA.  
XX  
AC ABB84545;  
XX  
DT 13-JAN-2003 (first entry)  
XX  
DE Transient receptor potential channel associated protein SEQ ID 11.  
XX  
KW Transient receptor potential channel; cytosstatic; cardiant; stroke;  
KW nootropic; neuroprotective; vasotropic; antiarrhythmic; hypotensive;  
KW anticonvulsant; antiparkinsonian; cerebroprotective; gene therapy; human;  
KW cancer; cardiovascular disorder; CNS disorder; heart failure; epilepsy;  
KW myocardial infarction; ischaemic disease; arrhythmia; hypertensive;

KW peripheral vascular disease; traumatic brain injury; sleep disorder;  
KW Parkinson's disease; Alzheimer's disease; motor unit disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200272824-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 19-FEB-2002; 2002WO-EP001727.  
XX  
PR 20-FEB-2001; 2001US-0269411P.  
PR 23-JAN-2002; 2002US-0350021P.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Smith TJ;  
XX  
WI; 2002-723353/78.  
DR N-PSDB; AAF88942.  
DR  
XX  
PT New isolated polynucleotides encoding transient receptor potential  
channel polypeptides, useful for treating, preventing and ameliorating  
diseases such as cancer, congestive heart failure, arrhythmias and  
Parkinson's disease.  
XX  
PS Claim 25; Fig 11; 189pp; English.  
XX  
CC This invention describes a novel polynucleotide encoding a human  
transient receptor potential channel polypeptide which has cytostatic,  
cardiant, nootropic, neuroprotective, vasotropic, antiarrhythmic,  
CC hypotensive, anticonvulsant, antiparkinsonian and cerebroprotective  
activity and can be used for gene therapy. Medicaments capable of  
modulating the activity of a transient receptor potential channel are  
useful for the treatment of diseases such as cancer, cardiovascular  
disorders or CNS disorders. The transient receptor potential channel  
polypeptides and polynucleotides are useful for treating, preventing and  
ameliorating diseases including congestive heart failure, myocardial  
infarction, ischaemic diseases, arrhythmias, hypertensive and peripheral  
vascular diseases, traumatic brain injury, epilepsy, Parkinson's disease,  
CC Alzheimer's disease, post-stroke, disorders of sleep and wakefulness, or  
diseases of motor unit. They are also useful in identifying test  
compounds that may act as activators or inhibitors at the enzyme's active  
site, or in raising specific antibodies that can block and effectively  
reduce its activity. Fusion proteins are useful for generating antibodies  
used in various assay system and drug screening. This sequence represents  
a polypeptide associated with the human transient receptor potential  
channel protein described in the disclosure of the invention  
XX  
SQ Sequence 1799 AA;  
  
Query Match 3.4%; Score 90; DB 5; Length 1799;  
Best Local Similarity 21.8%; Pred. No. 4.2e+02;  
Matches 42; Conservative 40; Mismatches 89; Indels 22; Gaps 8;  
  
QY 303 TEEEINTYKAHLDLEEYRNSSRVEKFLFDTKKEILMHL-----WR--YPSL--SIHGIEG 354  
Db 77 TKSPDTDTFTINFQDGEHTTHAKYIRTSYDTKLDHLLHMLKEWKMLPKLVISVHGGIQ 136  
  
QY 355 AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVMSMTLG 414  
Db 137 NFTMPSKFKEIFSQGLVKAAETTGAWIITEGINTGVSKHVGDAL-KSHSSHSLRKIWTVG 195  
  
QY 415 LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSIPIAKMFQ-EIVHKSVVLIPLGAV 473  
Db 196 IPPW--GVLENQ-----RDLIGKDVVCLYQTLDNPLSKLTILNSMHSFILSDDGTV 245  
  
QY 474 DDGEHSQNEKINR 486  
Db 246 --GKYGNEMKLRR 256  
  
RESULT 710



ADG67791  
ID ADG67791 standard; protein; 1939 AA.  
XX  
AC  
AC ADG67791;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
XX Human TRP-PLIK2c protein sequence.  
DE  
XX  
XX TRP-PLIK2; transient receptor potential channel; antiinflammatory;  
KW gynaecological; immunomodulatory; cardiant; cytostatic; neuroprotective;  
KW antiviral; anti-HIV; gene therapy; immune disorder;  
KW haematopoietic disorder; inflammatory disorder; renal disorder;  
KW reproductive disorder; hepatic disorder;  
KW hyper transient receptor potential activity; prostate cancer;  
KW testicular cancer; chromosome 9q21 aberration;  
KW amyotrophic lateral sclerosis; frontotemporal dementia;  
KW early-onset pulverulent cataract; infantile nephronophthisis;  
KW hypomagnesaemia;  
KW secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis;  
KW neuron degeneration; neurogenic inflammation; allergy; immunodeficiency;  
KW excessive immune activation; visual defect; hearing disorder; pain;  
KW cancer; hypertension; cardiovascular disease; Calcium homeostasis;  
KW osteoporosis; hypercalciuric stone disease; chronic renal failure;  
KW proliferative disorder; ischaemia-reperfusion injury; heart failure;  
KW immuno-compromised condition; HIV infection; NF-kappa-B regulation;  
KW apoptosis regulation; NF-kappa-B activity; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200294999-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 22-MAY-2002; 2002WO-US016164.  
XX  
PR 22-MAY-2001; 2001US-0292599P.  
PR 08-MAR-2002; 2002US-0362944P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Lee N, Chen J, Feder J, Wu S, Chang H, Lee L, Blonar M, Bol D;  
XX  
XX WPI; 2003-148463/14.  
DR N-PSDB; ADG67790.  
DR  
XX  
PT New TRP-PLIK2 nucleic acid and its splice variants, useful for  
PT manufacturing a medicament for preventing, treating or ameliorating a  
PT medical condition, e.g. renal, inflammatory or reproductive disorders.  
XX  
XX Claim 2; SEQ ID NO 6; 457pp; English.  
PS  
XX  
CC This invention relates to a novel isolated human TRP-PLIK2 (transient  
CC receptor potential channel) nucleic acid sequence and the protein encoded  
CC by it. The invention may be useful for the development of compounds with  
CC an antiinflammatory, gynaecological, immunomodulatory, cardiant,  
CC cytostatic, neuroprotective, antiviral or anti-HIV activity. In addition  
CC the DNA sequence may be useful for gene therapy. The invention may  
CC therefore be useful for manufacturing a medicament for preventing,  
CC treating or ameliorating a medical condition, for example immune  
CC disorders, haematopoietic disorders, inflammatory disorders, renal  
CC disorders, reproductive disorders, hepatic disorders, a disorder related  
CC to hyper transient receptor potential activity, prostate cancer,  
CC testicular cancer, diseases related to chromosome 9q21.2-22 aberrations,  
CC amyotrophic lateral sclerosis with frontotemporal dementia, early-onset  
CC pulverulent cataract, infantile nephronophthisis, hypomagnesaemia with  
CC secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis,  
CC neuron degeneration, neurogenic inflammation, allergy,  
CC immunodeficiency/excessive immune activation, visual defects, hearing  
CC disorder, pain, cancer, hypertension, cardiovascular diseases, diseases  
CC associated with disturbances in Calcium homeostasis including  
CC osteoporosis, hypercalciuric stone disease, chronic renal failure,  
CC proliferative disorders, ischaemia-reperfusion injury, heart failure,





Db 83 TKSPTDTFGTINFQDGEHTTHAKYIRTSYDTKLDHLLMLKWKMKELPKLVISVHGGIQ 142  
QY 355 AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLG 414  
Db 143 NFTMPSKFKEIFSQGLVKAAETTGAWIITEGINTGSKHVGDAL-KSHSSHSLRKIWTVG 201  
QY 415 LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRGDSITPIAKMFQ-EIVHKSVVLIPLGAV 473  
Db 202 IPPW--GVLENQ-----RDIGKDVVCLYQTLDNPLSKLTTLSNMHSHFILSDDGTV 251  
QY 474 DDGEHSQNEKINR 486  
Db 252 --GKYGNEMKLRR 262

RESULT 713  
ABB84546  
ID ABB84546 standard; protein; 2000 AA.  
XX ABB84546;  
XX 13-JAN-2003 (first entry)  
DE Transient receptor potential channel associated protein SEQ ID 12.  
XX Transient receptor potential channel; cytosstatic; cardiac; stroke;  
KW nootropic; neuroprotective; vasotropic; antiarrhythmic; hypotensive;  
KW anticonvulsant; antiparkinsonian; cerebroprotective; gene therapy; human;  
KW cancer; cardiovascular disorder; CNS disorder; heart failure; epilepsy;  
KW myocardial infarction; ischaemic disease; arrhythmia; hypertensive;  
KW peripheral vascular disease; traumatic brain injury; sleep disorder;  
KW Parkinson's disease; Alzheimer's disease; motor unit disease.

OS Homo sapiens.  
XX WO200272824-A2.  
XX 19-SEP-2002.  
PF 19-FEB-2002; 2002WO-EP001727.  
XX 20-FEB-2001; 2001US-0269411P.  
PR 23-JAN-2002; 2002US-0350021P.  
XX (FARB ) BAYER AG.  
XX Smith TJ;  
PI WPI; 2002-723353/78.  
DR N-PSDB; AAF88943.  
XX New isolated polynucleotides encoding transient receptor potential  
PT channel polypeptides, useful for treating, preventing and ameliorating  
PT diseases such as cancer, congestive heart failure, arrhythmias and  
PT Parkinson's disease.

PS Claim 25; Fig 12; 189pp; English.  
XX This invention describes a novel polynucleotide encoding a human  
CC transient receptor potential channel polypeptide which has cytostatic,  
CC cardiac, nootropic, neuroprotective, vasotropic, antiarrhythmic,  
CC hypotensive, anticonvulsant, antiparkinsonian and cerebroprotective  
CC activity and can be used for gene therapy. Medicaments capable of  
CC modulating the activity of a transient receptor potential channel are  
CC useful for the treatment of diseases such as cancer, cardiovascular  
CC disorders or CNS disorders. The transient receptor potential channel  
CC polypeptides and polynucleotides are useful for treating, preventing and  
CC ameliorating diseases including congestive heart failure, myocardial  
CC infarction, ischaemic diseases, arrhythmias, hypertensive and peripheral  
CC vascular diseases, traumatic brain injury, epilepsy, Parkinson's disease,  
CC Alzheimer's disease, post-stroke, disorders of sleep and wakefulness, or  
CC diseases of motor unit. They are also useful in identifying test

CC compounds that may act as activators or inhibitors at the enzyme's active  
CC site, or in raising specific antibodies that can block and effectively  
CC reduce its activity. Fusion proteins are useful for generating antibodies  
CC used in various assay system and drug screening. This sequence represents  
CC a polypeptide associated with the human transient receptor potential  
CC channel protein described in the disclosure of the invention  
XX

SQ Sequence 2000 AA;  
Query Match 3.4%; Score 90; DB 5; Length 2000;  
Best Local Similarity 21.8%; Pred. No. 5e+02;  
Matches 42; Conservative 40; Mismatches 89; Indels 22; Gaps 8;

QY 303 TEEINTYKAIHLDLEEYRNSSRVEKFLDFTKEEILMHL-----WR--YPSL--SIHGIEG 354  
Db 114 TKSPTDTFGTINFQDGEHTTHAKYIRTSYDTKLDHLLMLKWKMKELPKLVISVHGGIQ 173  
QY 355 AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLG 414  
Db 174 NFTMPSKFKEIFSQGLVKAAETTGAWIITEGINTGSKHVGDAL-KSHSSHSLRKIWTVG 232  
QY 415 LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRGDSITPIAKMFQ-EIVHKSVVLIPLGAV 473  
Db 233 IPPW--GVLENQ-----RDIGKDVVCLYQTLDNPLSKLTTLSNMHSHFILSDDGTV 282  
QY 474 DDGEHSQNEKINR 486  
Db 283 --GKYGNEMKLRR 293

RESULT 714  
AAE32072  
ID AAE32072 standard; protein; 2004 AA.

XX AAE32072;  
XX 24-MAR-2003 (first entry)  
DE Human TRICH-6 protein.  
XX Human; transporter and ion channel; TRICH; atherosclerosis; cancer;  
KW gene therapy.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT Domain 484..503  
FT /note= "Transmembrane domain"  
FT Domain 718..746  
FT /note= "Transmembrane domain"  
FT Domain 808..832  
FT /note= "Transmembrane domain"  
FT Domain 853..871  
FT /note= "Transmembrane domain"  
FT Domain 893..910  
FT /note= "Transmembrane domain"  
FT Domain 917..941  
FT /note= "Transmembrane domain"  
FT Domain 957..980  
FT /note= "Transmembrane domain"  
FT Domain 1026..1054  
FT /note= "Transmembrane domain"

XX WO200283712-A2.  
XX 24-OCT-2002.  
XX 12-APR-2002; 2002WO-US011760.  
XX 12-APR-2001; 2001US-0283440P.  
PR 20-APR-2001; 2001US-0285592P.  
PR 27-APR-2001; 2001US-0287263P.  
PR 04-MAY-2001; 2001US-0288666P.



PR 18-MAY-2001; 2001US-0292042P.  
PR 25-MAY-2001; 2001US-0293724P.  
PR 22-JAN-2002; 2002US-0351107P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Baughn MR, Elliott VS, Hafalia AJA, Yang J, Walia NK, Ramkumar J;  
PI Forsythe IJ, Lu Y, Tang YT, Yue H, Raumann BE, Lal PG, Azimzai Y;  
PI Lu DAM, Gandhi AR, Thornton M, Nguyen DB, Arvizu CS, Emerling BM;  
PI Swarnakar A, Yao MG, Ding L, He A, Griffin JA, Sanjanwala MM;  
PI Gietzen KJ, Lee EA, Xu Y, Au-Young JK, Das D, Lee SY, Chang H;  
XX  
XX WPI; 2003-092996/08.  
DR N-PSDB; AAD49504.  
DR  
XX  
XX New human functional transporters and ion channels (TRICH) polypeptides,  
PT useful for preparing a composition for diagnosing or treating a disease  
PT associated with decreased expression or overexpression of TRICH e.g.  
PT cancer.  
XX  
PS Claim 1; Page 157-162; 204pp; English.  
XX  
XX The invention relates to human transporters and ion channels (TRICH)  
CC polypeptides and nucleic acid molecules encoding such polypeptides. TRICH  
CC proteins are useful for preparing compositions for diagnosing or treating  
CC diseases or conditions associated with decreased expression or  
CC overexpression of functional TRICH e.g. atherosclerosis or cancer. The  
CC invention is useful in gene therapy. The present sequence is human TRICH  
CC protein  
XX  
SQ Sequence 2004 AA;  
  
Query Match 3.4%; Score 90; DB 6; Length 2004;  
Best Local Similarity 21.8%; Pred. No. 5e+02;  
Matches 42; Conservative 40; Mismatches 89; Indels 22; Gaps 8;  
  
QY 303 TEEEINTYKAHLDLEEYRNSRRVEKFLFDTKKEILMHL-----WR--YPSL--SIHGIEG 354  
Db 70 TKSPDTFTGTINFQDGEHTTHAKYIRTSYDTKLDHLLMLKEWKMLPKLVISVHGGIQ 129  
  
QY 355 AFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMKVVSMTLG 414  
Db 130 NFTMPSKFKEIFSQGLVKAETTGAWIITEGINTGVSKHVGDAL-KSHSSHSLRKIWTVG 188  
  
QY 415 LHPWIANIDDTQYLAAKRAIRTVFGTEPDMRDGSTIPIAKMFQ-EIVHKS VWLIPLGAV 473  
Db 189 IPPW--GVIEHQ-----RDLIGKDVVCLYQTLDNPLSKLTTLNSMHSHFILSDDGTV 238  
  
QY 474 DDGEHSQNEKINR 486  
Db 239 --GKYGNEMKLR 249  
  
RESULT 715  
ADG67787  
ID ADG67787 standard; protein; 2017 AA.  
XX  
AC ADG67787;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human TRP-PLIK2 protein sequence.  
XX  
XX TRP-PLIK2; transient receptor potential channel; antiinflammatory;  
KW gynaecological; immunomodulatory; cardiant; cytostatic; neuroprotective;  
KW antiviral; anti-HIV; gene therapy; immune disorder;  
KW haematopoietic disorder; inflammatory disorder; renal disorder;  
KW reproductive disorder; hepatic disorder;  
KW hyper transient receptor potential activity; prostate cancer;  
KW testicular cancer; chromosome 9q21 aberration;  
KW amyotrophic lateral sclerosis; frontotemporal dementia;  
KW early-onset pulverulent cataract; infantile nephronophthisis;  
KW hypomagnesaemia;

KW secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis;  
KW neuron degeneration; neurogenic inflammation; allergy; immunodeficiency;  
KW excessive immune activation; visual defect; hearing disorder; pain;  
KW cancer; hypertension; cardiovascular disease; Calcium homeostasis;  
KW osteoporosis; hypercalciuric stone disease; chronic renal failure;  
KW proliferative disorder; ischaemia-reperfusion injury; heart failure;  
KW immuno-compromised condition; HIV infection; NF-kappa-B regulation;  
KW apoptosis regulation; NF-kappa-B activity; human.  
XX Homo sapiens.  
XX WO200294999-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 22-MAY-2002; 2002WO-US016164.  
XX  
XX 22-MAY-2001; 2001US-0292599P.  
PR 08-MAR-2002; 2002US-0362944P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Lee N, Chen J, Feder J, Wu S, Chang H, Lee L, Blonar M, Bol D;  
PI WPI; 2003-148463/14.  
XX N-PSDB; ADG67786.  
DR  
XX New TRP-PLIK2 nucleic acid and its splice variants, useful for  
PT manufacturing a medicament for preventing, treating or ameliorating a  
PT medical condition, e.g. renal, inflammatory or reproductive disorders.  
XX  
PS Claim 2; SEQ ID NO 2; 457pp; English.  
XX  
XX This invention relates to a novel isolated human TRP-PLIK2 (transient  
CC receptor potential channel) nucleic acid sequence and the protein encoded  
CC by it. The invention may be useful for the development of compounds with  
CC an antiinflammatory, gynaecological, immunomodulatory, cardiant,  
CC cytostatic, neuroprotective, antiviral or anti-HIV activity. In addition,  
CC the DNA sequence may be useful for gene therapy. The invention may  
CC therefore be useful for manufacturing a medicament for preventing,  
CC treating or ameliorating a medical condition, for example immune  
CC disorders, haematopoietic disorders, inflammatory disorders, renal  
CC disorders, reproductive disorders, hepatic disorders, a disorder related  
CC to hyper transient receptor potential activity, prostate cancer,  
CC testicular cancer, diseases related to chromosome 9q21.2-22 aberrations,  
CC amyotrophic lateral sclerosis with frontotemporal dementia, early-onset  
CC pulverulent cataract, infantile nephronophthisis, hypomagnesaemia with  
CC secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis,  
CC neuron degeneration, neurogenic inflammation, allergy,  
CC immunodeficiency/excessive immune activation, visual defects, hearing  
CC disorder, pain, cancer, hypertension, cardiovascular diseases, diseases  
CC associated with disturbances in Calcium homeostasis including  
CC osteoporosis, hypercalciuric stone disease, chronic renal failure,  
CC proliferative disorders, ischaemia-reperfusion injury, heart failure,  
CC immuno-compromised conditions, HIV infection, disorders associated with  
CC aberrant NF-kappa-B regulation, disorders in which decreasing NF-kappa-B  
CC apoptosis regulation, disorders in which decreasing NF-kappa-B  
CC activity would be therapeutically desirable and disorders in which  
CC decreasing or increasing IkB activity would be therapeutically desirable.  
XX  
SQ Sequence 2017 AA;

Query Match 3.4%; Score 90; DB 7; Length 2017;  
Best Local Similarity 21.8%; Pred. No. 5e+02;  
Matches 42; Conservative 40; Mismatches 89; Indels 22; Gaps 8;  
  
QY 303 TEEEINTYKAHLDLEEYRNSRRVEKFLFDTKKEILMHL-----WR--YPSL--SIHGIEG 354  
Db 83 TKSPDTFTGTINFQDGEHTTHAKYIRTSYDTKLDHLLMLKEWKMLPKLVISVHGGIQ 142  
  
QY 355 AFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMKVVSMTLG 414  
Db 143 NFTMPSKFKEIFSQGLVKAETTGAWIITEGINTGVSKHVGDAL-KSHSSHSLRKIWTVG 201









XX Sequence 372 AA;  
SQ Query Match 3.4%; Score 89.5; DB 5; Length 372;  
Best Local Similarity 23.0%; Pred. No. 41;  
Matches 88; Conservative 32; Mismatches 118; Indels 145; Gaps 22;  
QY 106 QSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATD 165  
Db 83 QGKPPGPIPLAE-----PPKG-----DPTPAPAAASWYGHSSVLTIEVDGY---RVLAD 127  
QY 166 NKGpVLAWINAVSAFRAL-----EQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGV 221  
Db 128 ---PV--WSNRCSPSRAVGQPMHDVP-----VPLEAL-----PAV 158  
QY 222 DYIVIS---DNLWI-----SQRKPAIT---YGTRGNSYFMVEVKCRDQDFHSGTFG 266  
Db 159 DAVVISHDHYDHLDDITIVALAHTQAPFVPLGIGAHLRKWGVPEARIVELDWHEA--- 215  
QY 267 GILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTSEEINTYKAHLDLEEYRNSRV 326  
Db 216 ---HRIDDLTLVCTPARHFSGRLF---SRDSXXXLWASWVVT-----GSSHK 256  
QY 327 EKFLDFTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP----- 379  
Db 257 AFFGGDT-----GYTKSFAEIGDE-----YGPFDLTLPIGAYHPA 292  
QY 380 ---HMNVSAVEKQVTRHLEDVFSKRNSNMWV-----SMTLGLHPWIANIDDTQYLAA 430  
Db 293 FADIHMN---PEEAVRAHLD---LTEVDNSLMVPIHWATFRLAPHPW-----S 334  
QY 431 KRAIRTVFGTEPDMIRDGSTIPI 453  
Db 335 EPAERLLTAADAERV---LTVPI 355

RESULT 721  
AAY33270  
ID AAY33270 standard; protein; 401 AA.  
XX AAY33270;  
AC AAY33270;  
XX 23-NOV-1999 (first entry)  
DT Plasmid pHS1 bios1 fusion protein DNA.  
XX SAM; S-adenosyl methionine synthase; biosynthesis; biotin; bios1; bios2;  
KW bios3; cofactor; decarboxylation; Vitamin H; metK.  
XX Synthetic.  
OS DE19806872-A1.  
XX 26-AUG-1999.  
XX 19-FEB-1998; 98DE-01006872.  
XX 19-FEB-1998; 98DE-01006872.  
XX (BADI ) BASF AG.  
XX Schroeder H;  
XX WPI; 1999-480095/41.  
XX N-PSDB; AAZ09792.  
XX Production of biotin by expressing S-adenosyl-methionine synthase and  
PT second biotin synthesis gene in host cells.  
XX Example 3; Page 43-44; 48pp; German.  
XX This invention describes a novel method for the preparation of biotin (I)  
CC which comprises expressing, in a prokaryotic or eukaryotic host capable

CC of producing (I): (a) an S-adenosyl-methionine synthase (SAM) sequence  
CC (1), and (b) at least one of the other biotin biosynthesis genes bios1, 2  
CC or 3. (I) is a cofactor for enzyme-catalyzed (de)carboxylation reactions  
CC and is an essential vitamin (Vitamin H) for most animals and some  
CC microorganisms. Expression of biotin plus bios1, bios2 or bios3  
CC significantly increases productivity of biotin biosynthesis, particularly  
CC by at least 3 times. This sequence represents the bios1 protein used in  
CC the construction of a metK/bios1 fusion protein found in plasmid pHS1  
XX which is used in the method of the invention  
SQ Sequence 401 AA;  
Query Match 3.4%; Score 89.5; DB 2; Length 401;  
Best Local Similarity 20.9%; Pred. No. 46;  
Matches 78; Conservative 46; Mismatches 144; Indels 105; Gaps 18;  
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPV-----PRFRQELFRMMAVAAD--- 83  
Db 67 AAREKVAQLLNAPDDKTI---VWTRGTTESINMVAQCVCYARPLQPGDEIIVSVAEHAN 122  
QY 84 -----TLQRLGARVASVDMGPQQLPDGQSLP--IPP-----VILAEL-----GSDPTKGTV 127  
Db 123 LVPWLMVAQQTGAKVVKLPLNAQRLPDVDLLPELITPRSRILALQMSNVTGGCPDLARA 182  
QY 128 CFYGHLD--VQPADRGDWLTDPYVLTEVD-----GKLYGR---GATDNKGPVL--- 171  
Db 183 ITFAHSAGVMVMVDGAQGVHFFADVQQLDIDFYAFSGHKLYGPTGIGVLYGKSELLEAM 242  
QY 172 -AW-----INAVSAFRALEQDLPVNIKFIIEGMEEAG-----SVALEELVEKEK 214  
Db 243 SPWLGCGKVMHEVSFDGFTTQSAPWKL-----EAGTPNVAGVIGLSAALEWL----- 289  
QY 215 DRFFSGVDYIVISDNLW-----ISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268  
Db 290 -----ADYDINQAESWSRSLATLAEDALAKRPGFR-----SFRCDSSLLAFDFAGV 336  
QY 269 LHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTSEEINTYKAHLDLEEYRNSRV 328  
Db 337 HHSDMVTLLAEYGIALRAGQHCAQPLL-----AELGVTGTLRASFAFYNTKSDVDA 387  
QY 329 FL--FDTKEEILM 339  
Db 388 LVNAVDRALELLV 400

RESULT 722  
AAY33264  
ID AAY33264 standard; protein; 401 AA.  
XX AAY33264;  
AC AAY33264;  
XX 23-NOV-1999 (first entry)  
DT E. coli bios1 protein.  
XX SAM; S-adenosyl methionine synthase; biosynthesis; biotin; bios1; bios2;  
KW bios3; cofactor; decarboxylation; Vitamin H.  
XX Escherichia coli.  
XX DE19806872-A1.  
XX 26-AUG-1999.  
XX 19-FEB-1998; 98DE-01006872.  
XX 19-FEB-1998; 98DE-01006872.  
XX (BADI ) BASF AG.  
XX Schroeder H;  
XX WPI; 1999-480095/41.

DR N-PSDB; AAZ09785.  
XX Production of biotin by expressing S-adenosyl-methionine synthase and  
PT second biotin synthesis gene in host cells.  
XX  
XX Disclosure; Page 15-16; 48pp; German.  
XX  
CC This invention describes a novel method for the preparation of biotin (I)  
CC which comprises expressing, in a prokaryotic or eukaryotic host capable  
CC of producing (I): (a) an S-adenosyl-methionine synthase (SAM) sequence  
CC (1), and (b) at least one of the other biotin biosynthesis genes bios1, 2  
CC or 3. (I) is a cofactor for enzyme-catalyzed (de)carboxylation reactions  
CC and is an essential vitamin (Vitamin H) for most animals and some  
CC microorganisms. Expression of biotin plus bios1, bios2 or bios3  
CC significantly increases productivity of biotin biosynthesis, particularly  
CC by at least 3 times. This sequence represents the Escherichia coli bios1  
CC protein which is used in the method of the invention  
XX  
SQ Sequence 401 AA;  
Query Match 3.4%; Score 89.5; DB 2; Length 401;  
Best Local Similarity 20.9%; Pred. No. 46;  
Matches 78; Conservative 46; Mismatches 144; Indels 105; Gaps 18;  
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPV-----PRFRQELFRMMAVAAD--- 83  
Db 67 AAREKVAQLLNAPDDKTI-----VWTRGTTESINMVAAQCYARPRLOPGDEIIIVSVAEHHAN 122  
QY 84 -----TLQRLGARVASVDMGPPQQLPDGQSLP--IPP-----VILAEL-----GSDPTKGTV 127  
Db 123 LVPWLMVAQQTGAKVVKLPLNAQRLPDVDLLPELITPRSRILALGQMSNVTGGCPDLARA 182  
QY 128 CFYGHLD--VQPADRGDGLWTDPPYVLTEVD-----GKLYGR---GATDNKGPVL--- 171  
Db 183 ITFAHSAGVMVMVDGAQGVHFPADVQQLDIDFYAFSGHKLYGPTGIGVLYGKSELLEAM 242  
QY 172 -AW-----INAVSAFRALEQDLVPNIKFIIEGMEEAG-----SVALEELVEKEK 214  
Db 243 SPWLGKGKMHVEVSFDGFTTQSAPWKL-----EAGTPNVAGVIGLSAALEWL----- 289  
QY 215 DRFFSGVDYIVISDNLW-----ISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGI 268  
Db 290 -----ADYDINQAESWSRSLATLAEDALAKRPGFR-----SFRCDSSLLAFDFAGV 336  
QY 269 LHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAHLDLEEYRNSRVEK 328  
Db 337 HHSDMVTLLAEYGIALRAGQHCAQPLL-----AELGVTGTLRASFAFYNTKSDVDA 387  
QY 329 FL--FDTKEEILM 339  
Db 388 LVNAVDRALELLV 400  
RESULT 723  
AAV33268  
ID AAV33268 standard; protein; 401 AA.  
XX  
AC AAV33268;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
DE Plasmid pHS1 bios1 protein.  
XX  
KW SAM; S-adenosyl methionine synthase; biosynthesis; biotin; bios1; bios2;  
KW bios3; cofactor; decarboxylation; Vitamin H.  
XX  
OS Synthetic.  
XX  
PN DE19806872-A1.  
XX  
PD 26-AUG-1999.  
XX  
PF 19-FEB-1998; 98DE-01006872.

XX 19-FEB-1998; 98DE-01006872.  
PR (BADI ) BASF AG.  
XX  
XX Schroeder H;  
PI  
XX  
DR WPI; 1999-480095/41.  
DR N-PSDB; AAZ09791.  
XX  
PT Production of biotin by expressing S-adenosyl-methionine synthase and  
PT second biotin synthesis gene in host cells.  
XX  
PS Example 3; Page 34-35; 48pp; German.  
XX  
CC This invention describes a novel method for the preparation of biotin (I)  
CC which comprises expressing, in a prokaryotic or eukaryotic host capable  
CC of producing (I): (a) an S-adenosyl-methionine synthase (SAM) sequence  
CC (1), and (b) at least one of the other biotin biosynthesis genes bios1, 2  
CC or 3. (I) is a cofactor for enzyme-catalyzed (de)carboxylation reactions  
CC and is an essential vitamin (Vitamin H) for most animals and some  
CC microorganisms. Expression of biotin plus bios1, bios2 or bios3  
CC significantly increases productivity of biotin biosynthesis, particularly  
CC by at least 3 times. This sequence represents the bios1 protein from  
CC plasmid pHS1 which is used in the method of the invention  
XX  
SQ Sequence 401 AA;  
Query Match 3.4%; Score 89.5; DB 2; Length 401;  
Best Local Similarity 20.9%; Pred. No. 46;  
Matches 78; Conservative 46; Mismatches 144; Indels 105; Gaps 18;  
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPV-----PRFRQELFRMMAVAAD--- 83  
Db 67 AAREKVAQLLNAPDDKTI-----VWTRGTTESINMVAAQCYARPRLOPGDEIIIVSVAEHHAN 122  
QY 84 -----TLQRLGARVASVDMGPPQQLPDGQSLP--IPP-----VILAEL-----GSDPTKGTV 127  
Db 123 LVPWLMVAQQTGAKVVKLPLNAQRLPDVDLLPELITPRSRILALGQMSNVTGGCPDLARA 182  
QY 128 CFYGHLD--VQPADRGDGLWTDPPYVLTEVD-----GKLYGR---GATDNKGPVL--- 171  
Db 183 ITFAHSAGVMVMVDGAQGVHFPADVQQLDIDFYAFSGHKLYGPTGIGVLYGKSELLEAM 242  
QY 172 -AW-----INAVSAFRALEQDLVPNIKFIIEGMEEAG-----SVALEELVEKEK 214  
Db 243 SPWLGKGKMHVEVSFDGFTTQSAPWKL-----EAGTPNVAGVIGLSAALEWL----- 289  
QY 215 DRFFSGVDYIVISDNLW-----ISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGI 268  
Db 290 -----ADYDINQAESWSRSLATLAEDALAKRPGFR-----SFRCDSSLLAFDFAGV 336  
QY 269 LHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAHLDLEEYRNSRVEK 328  
Db 337 HHSDMVTLLAEYGIALRAGQHCAQPLL-----AELGVTGTLRASFAFYNTKSDVDA 387  
QY 329 FL--FDTKEEILM 339  
Db 388 LVNAVDRALELLV 400  
RESULT 724  
AAW92938  
ID AAW92938 standard; protein; 401 AA.  
XX  
AC AAW92938;  
XX  
DT 14-MAY-1999 (first entry)  
XX  
DE DE19731274 Seq ID 10.  
XX  
KW Biotin; synthesis; dethiobiotin; yield increase; industry; fermentation.  
XX



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OS Escherichia coli.
XX
XX DE19731274-A1.
XX
XX PD 28-JAN-1999.
XX
XX PF 22-JUL-1997; 97DE-01031274.
XX
XX PR 22-JUL-1997; 97DE-01031274.
XX
XX PA (BADI ) BASF AG.
XX
XX PI Schroeder H, Hauer B;
XX
XX DR WPI; 1999-107030/10.
XX
XX DR N-PSDB; AAX02814.
XX
XX
XX Improved synthesis of biotin by expressing the bios1 or bios2 sequence in
PT biotin-producing cells - and related gene constructs, provides increased
PT conversion of dethiobiotin in eukaryotic or prokaryotic hosts.
PT
XX
XX PS Disclosure; Page 35-37; 48pp; German.
XX
XX
XX This invention describes a method for the synthesis of biotin in
CC Escherichia coli. This method involves the expression of a biotin gene or
CC its functional variants, analogues and derivatives, in a prokaryote or
CC eukaryote that is able to produce biotin. The cells are grown and the
CC biotin produced either used directly, after separation of the biomass, or
CC after purification. Constructs containing this nucleic acid or protein or
CC their variants etc., can be coupled to one or more regulators for
CC increasing gene and/or protein expression, and/or having its natural
CC regulators 'switched off'. Expression of this biotin protein leads to
CC increased conversion, by at least 3-fold, of dethiobiotin to biotin, thus
CC increasing yield and making possible an industrially useful fermentative
CC method for biotin production
XX
XX SQ Sequence 401 AA;
XX
XX Query Match 3.4%; Score 89.5; DB 2; Length 401;
XX Best Local Similarity 20.9%; Pred. No. 46;
XX Matches 78; Conservative 46; Mismatches 144; Indels 105; Gaps 18;
XX
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPV-----PRFRQELFRMMAVAAD--- 83
Db 67 AAREKVAQLLNAPDDKTI-----VWTRGTTESINMVAQCYARPRILQPGDEIIVSVAEHHAN 122
QY 84 -----TLQRLGARVASVDMGPPQLPDGQSLP--IPP-----VILAEL-----GSDPTKGTV 127
Db 123 LVPWLMVAQQTGAKVKPLPLNAQRLPDVDLLPELITPRSRILALGQMSNVTGGCPDLARA 182
QY 128 CFYGHLD--VQPADRGDGLTDPYVLTEVD-----GKLYGR---GATDNKGPVL--- 171
Db 183 ITFAHSAGMVMVMDGAQGAHVFPADVQQLDIDFYAFSGHKLYGPTGIGLYKSELLEAM 242
QY 172 -AW-----INAVSAFRALEQDLPVNIKFIEGMEEAG-----SVALEELVEKEK 214
Db 243 SPWLGGMVHEVVSFDGFTTQSAPWKL-----EAGTPNVAGVIGLSAALEWL----- 289
QY 215 DRFFSGVDYIVISDNLW-----ISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268
Db 290 -----ADYDINQAESWSRSLATLAEDALAKRPGFR-----SFRQDSSLLAFDFAGV 336
QY 269 LHEPMADLVALLGSLVDSGGHILVPGIYDEWVPLTEEEINTYKAHLDLEEYRNSRVEK 328
Db 337 HHSDMVTLLAEYGIALRAGQHCAPQLL-----AELGVTGLRASFAFYNTKSDVDA 387
QY 329 FL--FDTKBEILM 339
Db 388 LVNAVDRALELLV 400
RESULT 725
AAW92934
```

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ID AAW92934 standard; protein; 401 AA.
XX
XX AC AAW92934;
XX
XX DT 14-MAY-1999 (first entry)
XX
XX DE E. coli biotin ORF401 protein.
XX
XX KW Biotin; ORF401; synthesis; dethiobiotin; yield increase; industry;
XX KW fermentation.
XX
XX OS Escherichia coli.
XX
XX FH Key Location/Qualifiers
XX FT Protein 1. .401
XX FT /note= "Partial sequence, no stop codon given"
XX
XX PN DE19731274-A1.
XX
XX PD 28-JAN-1999.
XX
XX PF 22-JUL-1997; 97DE-01031274.
XX
XX PR 22-JUL-1997; 97DE-01031274.
XX
XX PA (BADI ) BASF AG.
XX
XX PI Schroeder H, Hauer B;
XX
XX DR WPI; 1999-107030/10.
XX DR N-PSDB; AAX02810.
XX
XX Improved synthesis of biotin by expressing the bios1 or bios2 sequence in
PT biotin-producing cells - and related gene constructs, provides increased
PT conversion of dethiobiotin in eukaryotic or prokaryotic hosts.
PT
XX
XX PS Disclosure; Page 15-16; 48pp; German.
XX
XX
XX This invention describes a method for the synthesis of biotin in
CC Escherichia coli. This method involves the expression of a biotin gene or
CC its functional variants, analogues and derivatives, in a prokaryote or
CC eukaryote that is able to produce biotin. The cells are grown and the
CC biotin produced either used directly, after separation of the biomass, or
CC after purification. Constructs containing this nucleic acid or protein or
CC their variants etc., can be coupled to one or more regulators for
CC increasing gene and/or protein expression, and/or having its natural
CC regulators 'switched off'. Expression of this biotin protein leads to
CC increased conversion, by at least 3-fold, of dethiobiotin to biotin, thus
CC increasing yield and making possible an industrially useful fermentative
CC method for biotin production
XX
XX SQ Sequence 401 AA;
XX
XX Query Match 3.4%; Score 89.5; DB 2; Length 401;
XX Best Local Similarity 20.9%; Pred. No. 46;
XX Matches 78; Conservative 46; Mismatches 144; Indels 105; Gaps 18;
XX
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPV-----PRFRQELFRMMAVAAD--- 83
Db 67 AAREKVAQLLNAPDDKTI-----VWTRGTTESINMVAQCYARPRILQPGDEIIVSVAEHHAN 122
QY 84 -----TLQRLGARVASVDMGPPQLPDGQSLP--IPP-----VILAEL-----GSDPTKGTV 127
Db 123 LVPWLMVAQQTGAKVKPLPLNAQRLPDVDLLPELITPRSRILALGQMSNVTGGCPDLARA 182
QY 128 CFYGHLD--VQPADRGDGLTDPYVLTEVD-----GKLYGR---GATDNKGPVL--- 171
Db 183 ITFAHSAGMVMVMDGAQGAHVFPADVQQLDIDFYAFSGHKLYGPTGIGLYKSELLEAM 242
QY 172 -AW-----INAVSAFRALEQDLPVNIKFIEGMEEAG-----SVALEELVEKEK 214
Db 243 SPWLGGMVHEVVSFDGFTTQSAPWKL-----EAGTPNVAGVIGLSAALEWL----- 289
```



CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 416 AA;

Query Match 3.4%; Score 89.5; DB 6; Length 416;  
Best Local Similarity 22.5%; Pred. No. 49;  
Matches 81; Conservative 33; Mismatches 121; Indels 125; Gaps 18;

QY 6 GRMAASLLAVLLLL--LERGMFSSPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDS 63  
Db 125 GASAAALLACLALVGRDDEVLMPPDSYP-----CNRFVATAEGR 164  
QY 64 VQVPFRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS--D 121  
Db 165 AVLVPSPGPTFRQL--TADDVKTRWGERTRGVLLASPSNPTGTSLE-----PAELGRIID 217  
QY 122 PTKGTVCF-----YGHLDVQPADRGD-----GWLTDYPVL 151  
Db 218 AVRARGFSIVDEIYQGLSYDGA PVSALSFGDDVVTVNSFSKYFNMTGWRLGWLVP--- 274  
QY 152 TEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFTI-EGMEEAGSVALEE-- 208  
Db 275 -----VGTFEKLAQNL-----FICPSALAQHAALACFE PD 307  
QY 209 ---LVEXEKDRFFSGVDYIVISDNLWISQRKPAI-TYGTR-----GNSYFMVEVKCRDQDF 260  
Db 308 TLAIYEARRAEFRRRRDFIV-----PAIESLGFKVPVMPDGA FYVYAQC----- 351  
QY 261 HSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN-TYKA IHLDL EE 319  
Db 352 -----GGVAHPAAGDSAAALVNAMLHDAGVVLVPGM-DFGVHAPRDYIRLSYATAYSRL EE 405

RESULT 728  
ADH88873  
ID ADH88873 standard; protein; 426 AA.  
XX  
AC ADH88873;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Enterococcus faecalis polypeptide #3353.  
XX  
KW Enterococcus faecalis infection; transcription regulatory element;  
KW antibacterial.  
XX  
OS Enterococcus faecalis.  
XX  
PN US6617156-B1.  
XX  
PD 09-SEP-2003.  
XX  
PF 13-AUG-1998; 98US-00134000.

XX 15-AUG-1997; 97US-0055778P.  
PR  
XX (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-895394/82.  
DR N-PSDB; ADH85468.  
XX  
PT New nucleic acid comprising a sequence encoding an Enterococcus faecalis  
PT polypeptide, useful for preparing a composition for diagnosing or  
PT treating *E. faecalis* infection.  
XX  
PS Disclosure; SEQ ID NO 6758; 193pp; English.  
XX  
CC The invention relates to Enterococcus faecalis polynucleotides and  
CC polypeptides. The invention also relates to a recombinant expression  
CC vector comprising a polynucleotide operably linked to a transcription  
CC regulatory element, a cell comprising a recombinant vector, a method for  
CC producing an *E. faecalis* polypeptide, an isolated nucleic acid comprising  
CC a sequence not given in the specification, a recombinant vector  
CC comprising the nucleic acid and a cell comprising the recombinant vector.  
CC The polynucleotides can be used to detect the presence of *E. faecalis* in  
CC a sample. The sequences are useful for preparing a composition for  
CC diagnosing or treating Enterococcus faecalis infection. This sequence  
CC represents an *E. faecalis* polypeptide of the invention.

XX Sequence 426 AA;

Query Match 3.4%; Score 89.5; DB 7; Length 426;  
Best Local Similarity 19.9%; Pred. No. 50;  
Matches 66; Conservative 55; Mismatches 120; Indels 91; Gaps 17;

QY 161 RGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKEKDRFFSG 220  
Db 31 RKGDNNYQLYDWL--IHNLP TAQYVLGKLVKLILSNLTTGDEKQDEIL---NNFLYG 84  
QY 221 -----VDYIVISDNLWISQRKPAITYGTRGNSYF-----MVEVKCRDQDFHSGTFGGI 268  
Db 85 QTNPEGVNTYHVLVQSI-----KESIVYGRSGLRFLSKDDGLINVKCN---HFGV-AQI 134  
QY 269 LHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA IHLDL EEYRNSSRVEK 328  
Db 135 LNKEHYGYKELIGFVIDKKGRAITD-----VDLSEGEI-----DSEEFYFKG---I 177  
QY 329 FLPDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIP-GRVIGKFSIRLVP HNMVSAVE 387  
Db 178 FVFKNNDNILLPPEKFNLRV-----DTSTPKGSSVFDSDIQRV--LLIASVY 223  
QY 388 KOVTRHLE-----DVFSKRNSNKMVMSMTLGLHPWIANIDDTQYLA AKRAIR 435  
Db 224 KRLLYDIEYDGAGRLIFWADNANSNEESSNKF-----LNDTESATKRQDK 269  
QY 436 TVFGTEPDM--IRDG---STIPIAKMFQEI VH 462  
Db 270 YKKEVEEIMKLVKDSNSTSVLAVSNAFKKMDH 301

RESULT 729  
ABU48650  
ID ABU48650 standard; protein; 460 AA.  
XX  
AC ABU48650;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #34177.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Treponema pallidum.





CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 478 AA;

Query Match 3.4%; Score 89.5; DB 8; Length 478;  
Best Local Similarity 20.7%; Pred. No. 60;  
Matches 100; Conservative 66; Mismatches 143; Indels 175; Gaps 24;

QY 64 VQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIP-----P 112  
Db 54 IEMVREQSKLDRRVAILAD-LPGLKIRVGEIKGGYVELERGEKVTLTKDIEGETTIP 112  
QY 113 VILAEIGSDPTKGTVCFCYGHLDVQPADRGDGLWLTDPYVLTEVD-----GKL 158  
Db 113 VEYKDFPKLVSKGDVIY-----LSDGYIVLVRVEDVKENEVEAVVISGGKL 157  
QY 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIIE-----GMEEAGSV----- 204  
Db 158 FSR-----KG-----INIPKAYLPVEAITPRDIEIMKFAIEHGVDAIGLSFVGNVYDVLK 207  
QY 205 -----ALEELVEKEKDRFFSGV---DYIVIS-----DNLWISQR- 235  
Db 208 AKSFLERNAGDFTFVIAKIERPDVAVERNFEILNAADGIMIARGDLGVEMPIEQLPILQKR 267  
QY 236 -----KPAITYGTRGNSYFVMEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDS 286  
Db 268 LIRKANMEGKPVITATQMLVSMTMEKVPTR-----AEVTDVANAILDG 310  
QY 287 SGHILVPGIYDEVVPLTE-----EEINTYKAIHLDLEVRNS---SRVEKFLFDT- 333  
Db 311 T-----DAVMLSEETA VGKFFIEAVEMMARIKVTVEYRESFGITRMREFLEGTK 360  
QY 334 ---KEEILMHLWRYPSSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSA--VE 387  
Db 361 RGTIKEAITRSI--IDAICTIGIK--FILTPTKTGRTARLISRFK----PKQWILAFSTR 412  
QY 388 KOVTRHL-----EDVFSKRNSSNMVWSMTLGLHPWTANIDDTQYLAAKRAIRT 436  
Db 413 EKVCNNLMFSYGVYPPFCMEEGFNEND-----IVRLIKGL--GLVGSDDIVLMTGKPIEK 465  
QY 437 VFGT 440  
Db 466 TVGT 469

RESULT 731  
ADN18593  
ID ADN18593 standard; protein; 478 AA.

XX AC ADN18593;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #1246.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX Bacteria.  
OS  
XX US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR WPI; 2004-061375/06.  
XX

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.  
PS  
XX Claim 1; SEQ ID NO 1246; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX  
SQ Sequence 478 AA;

Query Match 3.4%; Score 89.5; DB 8; Length 478;  
Best Local Similarity 20.7%; Pred. No. 60;  
Matches 100; Conservative 66; Mismatches 143; Indels 175; Gaps 24;

QY 64 VQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIP-----P 112  
Db 54 IEMVREQSKLDRRVAILAD-LPGLKIRVGEIKGGYVELERGEKVTLTKDIEGETTIP 112  
QY 113 VILAEIGSDPTKGTVCFCYGHLDVQPADRGDGLWLTDPYVLTEVD-----GKL 158  
Db 113 VEYKDFPKLVSKGDVIY-----LSDGYIVLVRVEDVKENEVEAVVISGGKL 157  
QY 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNI---KFIIE-----GMEEAGSV----- 204  
Db 158 FSR-----KG-----INIPKAYLPVEAITPRDIEIMKFAIEHGVDAIGLSFVGNVYDVLK 207  
QY 205 -----ALEELVEKEKDRFFSGV---DYIVIS-----DNLWISQR- 235  
Db 208 AKSFLERNAGDFTFVIAKIERPDVAVERNFEILNAADGIMIARGDLGVEMPIEQLPILQKR 267





```
CC serine and/or threonine residues. The protein has potential antimicrobial
CC and antibacterial activity and is useful in screening for antagonists,
CC agonists and for compounds with antibiotic activity. The proteins are
CC also useful in determining their role in pathogenesis of infection,
CC dysfunction and disease and could be used as part of a vaccine and/or
CC peptide therapy
XX
SQ Sequence 530 AA;
    Query Match      3.4%; Score 89.5; DB 4; Length 530;
    Best Local Similarity 21.7%; Pred. No. 71;
    Matches 70; Conservative 48; Mismatches 110; Indels 95; Gaps 17;
QY 245 GNSYFMVEVKRQDQDFHSGTGGILHEPMADLVALLG---SLVDSSGHILVPGIYDEVVP 301
Db 32 GKSTLFNRLGRRSITSNT-SGVTRDSIEETVILRGFPRLRLVDTSGFTV----- 80
QY 302 LTEEEINTYKAHLDLEE-YRNSSRVEKFLF-----DTKEEILMHL---WRYPSLSI 349
Db 81 FSEKKASRQHIDTLVLEQTKYSIQCADKILLVDGTCESAEDEVIQYLRPYWGKLIAAV 140
QY 350 HGIEGA-----FDEPGTKTVI-----PCRVIKFSIRLPHMNVSAVEKQVTRHLEDVF 398
Db 141 NKTEGGEVHYNYARYGFSTLICVSAEHR-----NIDALERAIQNLFSD 187
QY 399 SKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTV---FGTEPDMIRD----- 447
Db 188 ERRELPKDDVVRLAIVGKPNNTGKSTLMNYL-MRRTVSLVCDRAGTRDVTGHVEFKQYK 246
QY 448 ---GSTIPI---AKMFQEIHKSVV--LIPLGAVD-----DGEHSQNEKI----- 484
Db 247 FIIADTAGIRKQKQVYESIEYSVIRAIISILNAVDIVLYIVDARDPSEQDKKIVSQISK 306
QY 485 -----NRWNYIEG-TKLFA 497
Db 307 RNLGVIFLNKWDLLEGSTSLIA 329
RESULT 734
ABP65706
ID ABP65706 standard; protein; 695 AA.
XX
AC ABP65706;
XX
DT 19-NOV-2002 (first entry)
XX
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:450.
XX
KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;
KW antidiarrheic; antibacterial; inhibitor of Salmonella; detection;
KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
KW rotavirus; food composition; pharmaceutical composition.
XX
OS Bifidobacterium longum.
XX
PN EP1227152-A1.
XX
PD 31-JUL-2002.
XX
PF 30-JAN-2001; 2001EP-00102050.
XX
PR 30-JAN-2001; 2001EP-00102050.
XX
PA (NEST ) SOC PROD NESTLE SA.
XX
DR WPI; 2002-668397/72.
XX
PT Novel polynucleotide comprising Bifidobacterium genome sequence useful as
PT a probe or primer for detecting and/or identifying Bifidobacterium longum
PT in a biological sample.
XX
PS Claim 3; SEQ ID NO 450; 80pp; English.
XX
```

```
CC The present invention describes a polynucleotide (I) comprising a
CC sequence of a Bifidobacterium genome selected from the nucleotide
CC sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at
CC least 90% identity or which hybridises with the sequences given in
CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a
CC fusion protein, comprising a sequence selected from 1097 sequences given
CC in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a
CC heterologous polypeptide. (I) has antidiarrheic and antibacterial
CC activities, and can be used as an inhibitor of Salmonella. (I) (which is
CC a probe) is useful for the detection and/or identification of
CC Bifidobacterium longum in a biological sample. A carrier containing the
CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be
CC used for preventing and/or treating diarrhoea brought about by pathogenic
CC bacteria and/or rotavirus. The carrier is a food composition selected
CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented
CC products, ice-creams, fermented cereal based products, milk based
CC powders, infant formula, pet food or a pharmaceutical composition
CC selected from tablets, liquid bacterial suspensions, dried oral
CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
CC (I) is useful in DNA arrays or chips to carry out analysis of the
CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
CC Bifidobacterium related nucleotide sequences given in the Sequence
CC Listing from the present invention but not mentioned further within the
CC specification. N.B. The sequence data for this patent is not represented
CC in the printed specification but is based on sequence information
CC supplied by the European Patent Office
XX
SQ Sequence 695 AA;
    Query Match      3.4%; Score 89.5; DB 5; Length 695;
    Best Local Similarity 20.4%; Pred. No. 1.1e+02;
    Matches 83; Conservative 53; Mismatches 139; Indels 131; Gaps 22;
QY 168 GPVLAWINA-----VSAFRALEQDLPVNIKFIIEGMEEGSVALEELVEKEKDRFF 218
Db 180 GAKVIGINARNLKNLVKVDNKNYNELAADLPDDVIKVAES-GVFGAVEVEDYAR----- 231
QY 219 SGVDYIVISDNLWISQRKPAITYGTRGNSYFMVE-----VKCRD-----QDFHSG 263
Db 232 AGADAVLVGEGV-----ATADNHELAVERLVKAGAQQKASSETTPLSEHQGPYWG 280
QY 264 TFGGILHEPMADLVALLGSLVDSSGHILV-----PGIYDEVVPLTEEEINTYKAHLDLE 318
Db 281 QFGG-RYVPEALITAL-----DELERVYTOAKADPEPHKEFMTLQQRYVGRPSPL----TE 331
QY 319 EYRNSSRV-EKFLFDT---KKEILMHLWRYPSLSIHGIEGAFDEP-----GTKTVIPG 367
Db 332 APRFSALVKEKTGLDARIFLKREDLNH-----TGAHKINNALGQALLVKRMGKTRVIAE 385
QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSN-----KMVVSMTLG----- 414
Db 386 TGAGQHG VATATVCAMLGKCR I--YMGQIDARRQALNVARMRMLGAEVVEVTGLGKILK 443
QY 415 -----LHPWIANIDDTQYLAAKRAIRTVFGTE--PDMIRDGSTIPIAKMFQEIIV----- 461
Db 444 DAINEALRDWVTNVKDTHYL-----LGTVAGPHPPFPAVVRD-----FQKIIGEERK 489
QY 462 -----HKSVVLIPLGAVDDGHSQN-----EKINRWNYIEG 492
Db 490 QQLQDWYIGIDHPDAICACVGGGSNAIGVMNAFLDDERVNLYGYEAG 535
RESULT 735
ABU18600
ID ABU18600 standard; protein; 706 AA.
XX
AC ABU18600;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #4127.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
```









Db 76 VLSQY-----NGTVFAYGQTSSGKTHTMGVIGDNGLSGIIIPRIVADIFNHIY----- 123

QY 167 KGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEERAGSVALEELVEKEK----- 214

Db 124 -----SMDENLQFHIKV---SYETYNKIRDLLDPEKVNLSIHEDKNRV 165

QY 215 -----DRFFSGVDYIVISDNLWISQKPAIT-----YGTRGNSYFMVEVKRCDQDFHSG 263

Db 166 PYVKGATERFVGPDVQLAIEDGKSNRMVAVTNMNEHSSRSHSVFLITVKQEHQTTKKQ 225

QY 264 TFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNS 323

Db 226 LTGKLY-----LVDLAG-----SEKVSKTGAQGTVLEEAKNI 257

QY 324 SR-----VEKFLFDTKKEILMH---LWRYPSLSIHG-----IEGAFDEPGTK 362

Db 258 NKSLTALGIVISALAEGTKSHVPYRDSKLTIRLQESLGGNSRTTVIICASPSHFNEAETK 317

QY 363 TVIPGRVIGKFSIRLVPHMNVSAVEKQVT-----RHLEDVFSKRNSNKMVVSMTLGLHP 417

Db 318 STL-----LFGARAKTIKNVVQINEELTAEWKRRYEKEKEKTRLAALLQAAALELSR 371

QY 418 WIA--NIDDTQYL-----AAKRAIRTVEGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLG 471

Db 372 WRAGESVSEVEWVNLSDSAQMAVSEVSGGSTPLM-ERSTAPAPPLTSTT-----G 421

QY 472 AVDDGEHSQNEKINRWNYIEGTKLF 496

Db 422 PITDEEKKKYE-----ERVKLY 439

RESULT 738

ABU37382

ID ABU37382 standard; protein; 982 AA.

XX ABU37382;

DT 23-OCT-2003 (revised)

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #22909.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Neisseria gonorrhoeae.

PN WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA41252.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 65306; 1766pp; English.

PS The invention relates to an isolated nucleic acid comprising any one of

XX

CC

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to

CC standardise OS field)

XX

SQ Sequence 982 AA;

Query Match 3.4%; Score 89.5; DB 6; Length 982;

Best Local Similarity 19.3%; Pred. No. 1.8e+02;

Matches 105; Conservative 72; Mismatches 190; Indels 177; Gaps 26;

QY 32 PALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQ--PVPFRFRQEL-----FRMMAVAA 82

Db 197 PAVRERKGEFVDFADLQAQGFAR-VRVDGEVYQLDEVPKLEKNIKHNIDVIDRVKKA 255

QY 83 DTLQRLG-----ARVASVDMGPQQLPDGQ-SLPIPPVILABL----- 118

Db 256 DIKQRLAESPETALRHGNERALAMEMDSGEHWFSAFACPVCSYSLPELPRLSFNPN 315

QY 119 -GSDPT---KGTVCFCYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWI 174

Db 316 MGSCPTCDGLGNTNFF-----DPEKVVAHPELSLATGAID-----GWD 353

QY 175 NAVSAFRALEQDLPVNIKFIIEGMEERAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ 234

Db 354 KRNQFYFQMIQSLAHYKFDV-----NVAWETLPEKVKVKVVLHSGSKEVI-DFTYLSE 405

QY 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPG 294

Db 406 R-----GTTFN-----RSHAFEGI-----IPN 422

QY 295 I---YDEVVPLTEEEINTYKAHLDLEEYRN-----SSRVEK---FLFDTKEEILMH 340

Db 423 LERRYRE---TDSE-----TVREKLERYQNHACPCSGGARLRKEARYVY-VGGEPLHE 472

QY 341 LWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRL-----VPHMN-----VSAY 386

Db 473 VSAWPLTKTHRFFETLDDGNKKQIABKILKEITERLGLINVLNLSRSAETLSGG 532

QY 387 EKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVEGTEPDMIR 446

Db 533 EAQRIRLASQIGSGLTGVMYVLDPEPSIGLH---QRDNDRLLATLKRRLDL----- 579

QY 447 DGSTIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQN-----EKINRWNYIEGT 493

Db 580 -GNSVIVVEHDEDAIREADFVDMGP-GAGEHGGNVLIADTPENVAKCEKSVTGQYLGK 637



CC that contributes to the resistance of a diploid fungus to an antifungal  
CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
CC and for identifying a therapeutic agent for treatment of a mammalian  
CC disease. (M1) is useful for identifying a compound which modulates the  
CC activity of a gene product, preferably enzymatic activity, carbon  
CC compound catabolism, biosynthetic, transporter, transcriptional,  
CC translational, signal transduction, DNA replication and cell division  
CC activity. The method is useful for identifying a compound having the  
CC ability to inhibit growth or proliferation of C. albicans cells and for  
CC treating infection by C. albicans. The present sequence is that of an  
CC essential Candida albicans protein used in the method of the invention.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied to Derwent by  
CC the European Patent Office  
XX  
SQ Sequence 1070 AA;

Query Match 3.4%; Score 89.5; DB 5; Length 1070;  
Best Local Similarity 17.3%; Pred. No. 2.1e+02;  
Matches 110; Conservative 98; Mismatches 189; Indels 239; Gaps 32;

QY 15 VLLLLLGRGMFSSPPPAL----LEKVFQYIDLHQDEFVQTLKEWVAI----- 59  
Db 16 ITISFLEFNIDNTPPPRINNISTMNLDDLDDELDELETTTKPKVKILNKKKEDKPIV 75  
QY 60 -----ESD----SVQPVPRF---RQELFRMMAVAADTLQRLGARVASVDMGPQQL 102  
Db 76 DDDLDLDDDDDFNLKPKPTKFKMKREDALRIKETPSSL----SPSSSVPSKPQGV 131  
QY 103 PDGQSLPI---PPVILAEGLSDPTKGTVCFCYGLHDVQPADRGDWLTDPVYLTEVDGKL 158  
Db 132 --SSNLPFRPATPPV-----SEPS-----TYEEDLGDINL-DNFSNIEADREW 172  
QY 159 YRGATDNKGPVLAWINAVSAFRALEQDLPVNKPIIE-----GMEEAGSVALE 207  
Db 173 YN---IDEE-----SALARNEIDEDLPQQRKRIRNTRHPKKTPTKTSFNESGAFNE 222  
QY 208 --ELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGRGNSYFMVEVKCRDQDFHSGTF 265  
Db 223 FGEYIDYDQKSLNBLNRPITSHVIP-----PFLNSKQYLQLQIS-----GSSI 269  
QY 266 GGI-----LHEPMADLVAL-----GMEEAGSVALE 288  
Db 270 RGIGPTVNPVKDPTSELASMAKQGSFVVQVNRKRERALQAKEAGVENSIGSIIDTAN 329  
QY 289 HILVPGIYDEVVPLTEEEINTYKAIHLDLEEVRNS-----SRVEKFLFD 332  
Db 330 -----TTEEIKQEEKNADVNETHQDIOQQRKSLPAPAVRNDLLTTTRDNQVTVIGE 382  
QY 333 TKEEILHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 383 TSGGKTTQLTQF--LYEDGFGANIDKNGEK-----RIIACTQPRRVAAMSVA---KRVSE 432  
QY 393 HL-----EDV-----FSKRNSNKMVVS-MTLGL-----HPWIAN-----IDDT---- 425  
Db 433 EMNCKLGEVGSIRFEDKTDNKKTVIKYMTGILLREILADPMLANYSCIIMDEAHERS 492  
QY 426 -----QYLAAKRAIRTV-----FGTEPDMIRDGSGTIPIAKMFQ-- 458  
Db 493 LNTDILLGLFKNLLAKRKDLKLIVTSATWNNANRPTKFFGVAPQFHIPGRTFPVEVFFNRD 552  
QY 459 -----EIVHKSVVLIPLGAVDGGEHQSQEKINRW 488  
Db 553 VNMDYVEMAVKQVLTIHLG-----RWN 574

RESULT 741  
ABP28458  
ID ABP28458 standard; protein; 1090 AA.

XX

AC ABP28458;

XX

DT 02-JUL-2002. (first entry)

XX Streptococcus polypeptide SEQ ID NO 6092.  
DE  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX Streptococcus agalactiae.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C;  
PI Tettelin H;  
XX  
DR WPI; 2002-352536/38.  
DR N-PSDB; ABN69089.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 3772; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 1090 AA;

Query Match 3.4%; Score 89.5; DB 5; Length 1090;  
Best Local Similarity 19.2%; Pred. No. 2.2e+02;  
Matches 100; Conservative 76; Mismatches 175; Indels 169; Gaps 28;

QY 47 DEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQL--PD 104  
Db 604 DKFEVT---VTVHNKSDKP-----QELYQVTVQTDKVD--GKHFA---LAPKALYETS 649  
QY 105 GQSLPIP-----PV-----ILAEELGS-----DPTKGTVCFYGHLDV 135  
Db 650 WQKITIPANSSKQVTPIDASRFSKDLAQMKNGYFLEGFVRFKQDPTKEELMSIPYIGF 709  
QY 136 QPADRGDWLTDPVYLTEVDGKLYGRGATDN-----KGPVLAWINAVSAFRAAL--EQDLP 188  
Db 710 R-GDFGNLSALEKPIYDSKDGSSYYHEANSDAKDQDGLQFYALKNNFTALTTSNPW 768  
QY 189 VNIKFIEGMEEAGSVALEELVE-----KEKD-----RFFSGVDYIVISDNLWIS 233  
Db 769 TTIKAVKEGVENIEDIESSEITETIFAGTFAKQDDDDSHYYIHRHANGKPYAAISPN---- 824



QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVP 293  
Db 825 -----GDGN-----RDYVQFGTF-----LRNAKNLVAEVLDKEGNVVWT 859  
QY 294 GIYDEVVPLTEEEINTYKAHLDLEBYRNSRVEKFLFDTKKEILMHLWRYPSPLSIHGIE 353  
Db 860 S-----EVTEQVKNY---NNDLASTLGSTRFEKTRWDGKNK-----D 894  
QY 354 GAFDEPGTKTIPGRVIGKFSIRLVP-----HMNVSAVEKQVTRHL--EDVFSKRNS 403  
Db 895 GKVVANGTYT-----YRVRYTPISSGAKEQHTDFDVIVDNTTPEVATSATFSTEDS 945  
QY 404 SNKMVVSMTLGLHPWIA-----NIDDTQYLAAKRAIRTVFGTEPDMIRDG 448  
Db 946 -----RLTLASKPKTSQPVYRERIAITYMDEDLPTTEYISPNEGTFTLPEEAETM-EG 998  
QY 449 STIPIAKM--FQEIIVHK---SVVLIPLGAVDDGEHSQNEK 483  
Db 999 ATVPL-KMSDFTYVVEDMAGNITYTPVTVKLLEGHSNKPEQ 1037

RESULT 742  
ABB47667  
ID ABB47667 standard; protein; 1179 AA.  
AC  
XX  
AC ABB47667;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Listeria monocytogenes protein #371.  
XX  
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;  
KW vitamin B12; bacterial infection; disease.  
XX

OS Listeria monocytogenes.  
XX  
PN WO200177335-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 11-APR-2001; 2001WO-FR001118.  
XX  
PR 11-APR-2000; 2000FR-00004629.  
XX  
PA (INSP ) INST PASTEUR.  
XX  
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;  
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;  
PI Daniels J, Goebel W, Krefit J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;  
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;  
XX

DR WPI; 2002-010914/01.  
XX  
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related  
PT polypeptides.  
XX  
PS Claim 6; SEQ ID NO 372; 192pp; French.  
XX

CC The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin

CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccines compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1179 AA;

Query Match 3.4%; Score 89.5; DB 5; Length 1179;  
Best Local Similarity 18.8%; Pred. No. 2.4e+02;  
Matches 58; Conservative 55; Mismatches 106; Indels 89; Gaps 13;  
QY 215 DRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA 274  
Db 108 DFLLSGKPGIVIVPVAGLRKMLPPVSLWKHFN-ISIVEGEEIDPD-----VLRQKLV 158  
QY 275 DLVALLGSLVDSSGHILVPGIYDEVVPLTEE-----EINTYKAHLDLEEYRNS 324  
Db 159 TMGYTMSGMVNTPGFSVRGGIIDIYPITEEFPIRIELFDETEVDSLRF--FFDVETQRSTT 216  
QY 325 RVEKFLFDTKKEILMHLWRYPSPLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNV 384  
Db 217 RVEEFRLLPATEIILDQSYYPDI-----VK 241  
QY 385 AVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANI-DDTQYLAAKRAIRTVFGTEPD 443  
Db 242 RLEKKWMLTLNEL---KEQEDKQAL-----IENLEEDLEMLRS-----GVKPD 281  
QY 444 MIRD--GSTIP-IAKMFOIIVHKSIVLI-PLGAVDDGEHS-----QNEKINRWNVIE 491  
Db 282 MFFKYIGLAYPDPASLFDYLPKNTAILLDEFGRILETEESLEREEAEWQTETLSRMEIVR 341  
QY 492 GTKLFAAF 499  
Db 342 DVQVSHSF 349

RESULT 743  
ABU32719  
ID ABU32719 standard; protein; 1179 AA.  
XX  
AC ABU32719;  
XX

DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #18246.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Listeria monocytogenes.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX

PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.



Db 861 -----EVTEQVVKNY---NNDLASTLGSTRFEKTRWDGDK-----DG 895  
QY 355 AFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKRNSSNMVVS---- 410  
Db 896 KVVANGTYT-----YRVYTP---ISSGAKE--QHTDFDVIVDNTTPEVATSATES 941  
QY 411 -----MTLGLHPWIA-----NIDDTQYLAAKRAIRTVFGTEPDMIRDGST 450  
Db 942 TEDRLTLASKPKTSQPVYRERIATYMDDELPTTTEYISPNEDEGTFTLPEEAETM-EGAT 1000  
QY 451 IPIAKM--FQEIIVHK---SVVLPLGAVDDGEHSQNEK 483  
Db 1001 VPL-KMSDFTYVVEDMAGNITYTPTVTKLLEGHSNKPEQ 1037

RESULT 745  
ABU34837  
ID ABU34837 standard; protein; 1439 AA.  
XX  
AC ABU34837;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #20364.  
XX  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
OS Mycobacterium bovis.  
XX  
XX WO200277183-A2.  
PN  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA38707.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 62761; 1766pp; English.

XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1439 AA;

Query Match 3.4%; Score 89.5; DB 6; Length 1439;  
Best Local Similarity 22.5%; Pred. No. 3.3e+02;  
Matches 73; Conservative 33; Mismatches 100; Indels 119; Gaps 16;  
QY 59 IESDSVQVPVFRQEL--FRM-----MAVAADTLQRLGARVASVDMGPOQ 101  
Db 654 VPTDSTLLVERFRDELGWRVILHSPYGLRVHGPLALAVGRRRLDRYG-----IDEKPTA 708  
QY 102 LPDQQLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLTDPPYVLTEVDGK---- 157  
Db 709 SDNGIMVRLPDTVSA--GEDSPPGAELF-----VFDADG-----IDPIVTTEVAGSALFA 756  
QY 158 -----LYGRGATDNKGPVLAWINAVSAFRALE-----QDLPVNIKFIIEGMEEA 201  
Db 757 SRFESAARALLPRRHPGRSPL--WQORQRAARLLEVARKYPDFPIVLETVRECLQNV 814  
QY 202 GSV-ALBELVEKEKDR-----FSGVDYIVISDNLWISQKPAITY 241  
Db 815 YDVPILVELMARIAQRRVRVAEATAKPSPPFAASLLFGYVGAIFYEGDTPLAERRAALA 874  
QY 242 --GTRGNSYFMVEVKCR-----DQDFHSGTFFGGILH-----EPMADLVALLGS 282  
Db 875 LDGT-----LLAELLGRVELRELLDPDVIAATSRQLQHLAADRVARDAEGVADLLRLLG- 928  
QY 283 LVDSSGHILVPGIYDEVVPLTEEEI 307  
Db 929 -----PLTEDEI 935

RESULT 746  
AAY54373  
ID AAY54373 standard; protein; 1724 AA.  
XX  
AC AAY54373;  
XX  
DT 06-APR-2000 (first entry)  
XX  
DE cDNA sequence encoding the human minor vault protein p193.  
XX  
KW Human; minor vault protein p193; vault; multidrug resistant cancer.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 1. .94  
FT /note= "BRCT domain (this refers to the C-terminus of the  
FT BRCA-1 gene, and is a superfamily of conserved domains in  
FT DNA damage-response cell cycle checkpoint proteins"  
FT Misc-difference 143  
FT /note= "Phe encoded by CCT"  
FT Region 1562. .1724  
FT /note= "region necessary for interaction with the human  
FT major vault protein"  
XX WO9962547-A1.  
XX  
PD 09-DEC-1999.





QY 327 ---EKFL-----FDTKEEILMHLWRYPSLSIHGIEGAFD 357  
Db 688 EAQQEYLEAVTQGHGAYLMSQADPDVFTVSGNLPKAKVLIKITYITELSILGTGVFF 747  
QY 358 EPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK--RNSSNKMVVSMTLG 414  
Db 748 MPA--TVAPWQ-----QDKALNENLQDTVEKICIKEIGTKQSFSLTMS 788  
QY 415 LH-PWIAN--IDDTQYLAAGR-----AIRTVEGTEPD 443  
Db 789 IEMPYVIEFIFSDTHELKQKRTDCKAVISTMEGSSLD 825  
RESULT 748  
ADB46006  
ID ADB46006 standard; protein; 1724 AA.  
XX  
AC ADB46006;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human minor vault protein p193.  
XX  
KW Human; minor vault protein; p193; cancer; chemotherapy; tumour cell;  
KW chemotherapeutic agent; multidrug-resistant cancer; MDR;  
KW lung resistance-related protein; LRP; major vault protein; vault;  
KW ribonucleoprotein organelle; antisense gene therapy; gene therapy;  
KW cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US655347-B1.  
XX  
PD 29-APR-2003.  
XX  
PF 28-JUN-2000; 2000US-00607510.  
XX  
PR 03-JUN-1998; 98US-00089621.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
XX Rome LH, Kichhoefer VA;  
PI  
XX  
DR WPI; 2003-786291/74.  
DR N-PSDB; ADB46005.  
XX  
PT New purified polynucleotide encoding human minor vault protein p193 for  
PT making the protein and for diagnosing and treating multidrug resistance  
PT cancer.  
XX  
PS Claim 13; Fig 2; 25pp; English.  
XX  
CC The invention discloses a purified polynucleotide encoding human minor  
CC vault protein p193. Most cancer cannot be cured using chemotherapy  
CC because tumour cells tend to develop resistance to several  
CC chemotherapeutic agents over time. These cancers are referred to as  
CC multidrug-resistant cancers (MDR). Overexpression of a number of genes  
CC have been associated with MDR cell lines, including the lung resistance-  
CC related protein (LRP) which is also known as the human major vault  
CC protein. Vaults are large, barrel-shaped, multi-subunit, cytoplasmic,  
CC ribonucleoprotein organelles. Also claimed is a vector comprising the  
CC polynucleotide, an isolated prokaryotic or eukaryotic host cell stably  
CC transformed or transfected with a vector including the human minor vault  
CC protein, p193. The polynucleotide can be used in a method for making  
CC human minor vault protein p193. The polynucleotide, the protein it  
CC encodes, antibodies against the protein or antisense gene therapy can be  
CC used in methods for diagnosing and treating multidrug resistance cancer.  
CC The sequence presented is the human minor vault protein p193.  
XX  
SQ Sequence 1724 AA;

Query Match 3.4%; Score 89.5; DB 7; Length 1724;  
Best Local Similarity 20.3%; Pred. No. 4.4e+02;

Matches 105; Conservative 74; Mismatches 183; Indels 155; Gaps 29;  
QY 26 SSPSPPP-----ALLEKVEQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAV 80  
Db 365 SKPNPPSLAKYRALRCKI-EHVEQNTTEEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 420  
QY 81 AADT--LQRLGARVASVDMGPQQLPDG---QSLPIPPVILAELGSDPTKGTVCFCYGHLDV 135  
Db 421 NETTEFLSKLGNVRPLHCSPVQIVGILCRGLLPKV--EDRGVQRT-----DV 469  
QY 136 QPADRGDGWLTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRAL---EQDLPVNIK 192  
Db 470 --GNLGGIYFSDSLSTSI--KYSHPGETD--GTRLLLICDVALGKCMDLHEKDFPLTEA 523  
QY 193 ----FIIEGMEEAGSVALEELVEKEKDRFF-----SGVDYIV-----ISDN 229  
Db 524 PPGYDSVHGVSQTASVT-----TDFEDDEFVVKYKTNOVKMKYIIKFSMPGDQIKDFHPSDH 579  
QY 230 LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHE-----PMADLVALLGSLV 284  
Db 580 TELEEYRPEFSNFSKVEDYQLPDAKT-----SSSTKAGLQDASGNLVPLED-VHIKGRII 633  
QY 285 DSSGHILVPGIYDE-----VVPLTEEEINTYKAHLDLEEYRNSRV-----326  
Db 634 DTVAQVIVFQTYTNKSHVPIEAKYIFPLDD-----KAAVCGFEAFINGKHIIVGEIKEKE 687  
QY 327 ---EKFL-----FDTKEEILMHLWRYPSLSIHGIEGAFD 357  
Db 688 EAQQEYLEAVTQGHGAYLMSQADPDVFTVSGNLPKAKVLIKITYITELSILGTGVFF 747  
QY 358 EPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK--RNSSNKMVVSMTLG 414  
Db 748 MPA--TVAPWQ-----QDKALNENLQDTVEKICIKEIGTKQSFSLTMS 788  
QY 415 LH-PWIAN--IDDTQYLAAGR-----AIRTVEGTEPD 443  
Db 789 IEMPYVIEFIFSDTHELKQKRTDCKAVISTMEGSSLD 825  
RESULT 749  
ADB46006  
ID ADS17664 standard; protein; 1724 AA.  
XX  
AC ADS17664;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Human poly ADP-ribosyl polymerase (VPARP) protein.  
XX  
KW vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
XX  
OS Homo sapiens.  
XX  
PN WO2004081533-A2.  
XX  
PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Rome LH, Kichhoefer VA, Raval-Fernandes S, Stewart PL;  
XX  
DR WPI; 2004-690644/67.  
DR N-PSDB; ADS17665.  
XX  
PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.

XX	Claim 37; SEQ ID NO 3; 459pp; English.	ADSI17713	ID	ADSI17713 standard; protein; 1736 AA.
PS		XX	XX	
XX		AC	AC	ADSI17713;
CC	The invention relates to a novel method of using vaults as carrier	XX	XX	
CC	molecules to deliver one, or more than one, substance to an organism, or	DT	16-DEC-2004	(first entry)
CC	to a specific tissue or to specific cells, or to an environmental medium.	XX		
CC	The method comprises providing vaults, incorporating the substance into	DE		Cysteine rich peptide + human VPARP protein, CP-VPARP.
CC	the vaults, and administering the vaults comprising the substance to the	XX		
CC	organism, to the specific tissue, to the specific cells, or to the	KW		vault; carrier molecule; major vault protein; MVP;
CC	environmental medium. The invention further comprises: a vault-like	KW		vault poly-ADP ribose polymerase; VPARP; toxin.
CC	particle, comprising a major vault protein (MVP) or modified MVP, and/or	XX		
CC	further comprising a vault poly-ADP ribose polymerase (VPARP) or a	OS		Homo sapiens.
CC	portion of a VPARP, comprising at least about 150 consecutive residues of	OS		Synthetic.
CC	VPARP; a method of preventing damage by one, or more than one, substance	XX		
CC	to an organism, to a specific tissue, to specific cells, or to an	PN	WO2004081533-A2.	
CC	environmental medium by sequestering the substance within a vault-like	XX		
CC	particle; a method of delivering one or more than one substance,	PD	23-SEP-2004.	
CC	particularly a sensor to an organism, to a specific tissue, to specific	XX		
CC	cells, or to an environmental medium; a method of detecting a signal from	XX		
CC	a sensor within an organism, or a specific tissue or specific cells; a	PF	10-MAR-2004; 2004WO-US007434.	
CC	method of making vault-like particles; and a method of making vault-like	XX		
CC	particles comprising one, or more than one, substance. The method or the	XX		
CC	vault-like particles are useful for delivering substances to an organism,	PR	10-MAR-2003; 2003US-0453800P.	
CC	or to a specific tissue or to specific cells, or to an environmental	XX		
CC	medium. The vault-like particles are also useful for preventing damage by	PA	(REGC ) UNIV CALIFORNIA.	
CC	a substance (e.g., toxin) to an organism, to a specific tissue, to	XX		
CC	specific cells, or to an environmental medium. This sequence represents a	PI	Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;	
CC	Human poly ADP-ribosyl polymerase (VPARP) protein of the invention.	XX		
XX		DR	WPI; 2004-690644/67.	
CC		DR	N-PSDB; ADSI17714.	
CC		XX		
SQ	Sequence 1724 AA;	PT		Using vaults as carrier molecules to deliver substance(s) to an organism,
		PT		to a specific tissue, to specific cells, or to an environmental medium
		PT		comprises incorporating the substance(s) into the vaults and
		PT		administering them.
		XX		
		PS		Disclosure; SEQ ID NO 52; 459pp; English.
QY	26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80	XX		
Db	365 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 420	CC		The invention relates to a novel method of using vaults as carrier
QY	81 AADT--LQRLGARVASVDMGPPQQLPDG---QSLPIPPVILAEIGSDPTKGTVCYFGHLDV 135	CC		molecules to deliver one, or more than one, substance to an organism, or
Db	421 NETTEFLSKLGNVRPLHSGSPQVNIIVGILCRGLLPKVV-EDRGVQRT-----DV 469	CC		to a specific tissue or to specific cells, or to an environmental medium.
QY	136 QPADRGDGLTDPVLTTEVDGKLYGRGATDNKGPVLAWINAVSAFRAL---EQDLPVNIK 192	CC		The method comprises providing vaults, incorporating the substance into
Db	470 --GNLGGIYFSDSLSTSI--KYSHPGETD--GTRLLLLICDVALGKCMDLHEKDFPLTEA 523	CC		the vaults, and administering the vaults comprising the substance to the
QY	193 ----FIEGMEEAGSVALEELVEKEKORFF-----SGVDYIV-----ISDN 229	CC		organism, to the specific tissue, to the specific cells, or to the
Db	524 PPGYDSVHGVSQTASVT-----TDFEDDEFVVYKTNQVKMKYIIFKFSMPGDQIKDFHPSDH 579	CC		environmental medium. The invention further comprises: a vault-like
QY	230 LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHE-----PMADLVALLGSLV 284	CC		particle, comprising a major vault protein (MVP) or modified MVP, and/or
Db	580 TELEYRPEFSNFSKVEDYQLPDAKT-----SSSTKAGLQDASGNLVPLED-VHIKGRII 633	CC		further comprising a vault poly-ADP ribose polymerase (VPARP) or a
QY	285 DSSGHILVPGIYDE-----VVPLTEEEINTYKAIHLDLEEYRNSRV-----326	CC		portion of a VPARP, comprising at least about 150 consecutive residues of
Db	634 DTVAQVIVFQYTNKSHVPIEAKYIFPLDD-----KAAVCGFEAFINGKHIVGEIKEKE 687	CC		VPARP; a method of preventing damage by one, or more than one, substance
QY	327 ---EKFL-----FDTKEILMHLWRYPYSLSIHGIEGAFD 357	CC		to an organism, to a specific tissue, to specific cells, or to an
Db	688 EAQOEYLEAVTQGHGAYLMSQADPDVFTSVGNLPPKAKVLIKITYITELSLITGVGVFF 747	CC		environmental medium by sequestering the substance within a vault-like
QY	358 EPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK---RNSSNMVVSMTLG 414	CC		particle; a method of delivering one or more than one substance,
Db	748 MPA--TVAPWQ-----QDKALNENLQDTVEKICIKEIGTKQSFSLTMS 788	CC		particularly a sensor to an organism, to a specific tissue, to specific
QY	415 LH-PWIAN--IDDTQYLAAGR-----AIRTVFGTEPD 443	CC		cells, or to an environmental medium; a method of detecting a signal from
Db	789 IEMPVIVIEFISDTHLQKQRTDCKAVISTMEGSLD 825	CC		a sensor within an organism, or a specific tissue or specific cells; a
		CC		method of making vault-like particles; and a method of making vault-like
		CC		particles comprising one, or more than one, substance. The method or the
		CC		vault-like particles are useful for delivering substances to an organism,
		CC		or to a specific tissue or to specific cells, or to an environmental
		CC		medium. The vault-like particles are also useful for preventing damage by
		CC		a substance (e.g., toxin) to an organism, to a specific tissue, to
		CC		specific cells, or to an environmental medium. This sequence represents a
		CC		Human poly ADP-ribosyl polymerase (VPARP) protein of the invention.
		XX		
		SQ		Sequence 1724 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1724;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;
				Pred. No. 4.4e+02;
				Mismatches 183; Indels 155; Gaps 29;
				Matches 105; Conservative 74;
				Query
				26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAV 80
				Db
				377 SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRVGRV 432
				Sequence 1736 AA;
				Query Match
				Best Local Similarity 20.3%; Score 89.5; DB 8; Length 1736;



QY 81 AADT--LQRLGARVASVDMGPPQLPDG---QSLPIPPVILAELGSDPTKGTVCIFYGHLDV 135  
Db 433 NETTEFLSKLGNVRPLLLHGSPVQNIIVGILCRGLLLPKVV-EDRGVQRT-----DV 481  
QY 136 QPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRAL---EQDLPVNIK 192  
Db 482 --GNLGSGIYFSDSLSTSI--KYSHPGETD--GTRLLLLICDVALGKMDLHEKDFPLTEA 535  
QY 193 ----FIIEGMEEAGSVALEELVEKEKDRFF-----SGVDYIV-----ISDN 229  
Db 536 PPGYDSVHGVSQTASVT---TDFEDDEFVYKTNQVKMKYIIKFSMPGDQIKDFHPSDH 591  
QY 230 LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHE-----PMADLVALLGSLV 284  
Db 592 TELEEYRPEFSNFSKVEDYQLPDAKT-----SSSTKAGLQDASGNLVPLED-VHIKGRII 645  
QY 285 DSSGHILVPGIYDE-----VVPLTEEEINTYKAIHLDLEEYRNSRV----- 326  
Db 646 DTVAQVIVFQTYTNKSHVPIEAKYIFPLDD-----KAAVCGFEAFINGKHIIVGEIKEKE 699  
QY 327 ---EKFL-----FDTKEEILMHLWRYPSLSIHGIEGAFD 357  
Db 700 EAQOEYLEAVTQGHGAYLMSQDAPDVFTVSVGNLPPKAKVLIKITYITELSILGTVGVPFF 759  
QY 358 EPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK---RNSSNKMVVSMTLG 414  
Db 760 MPA--TVAPWQ-----QDKALNENLQDTVEKIKIKEIGTKQSFSLTMS 800  
QY 415 LH-PWIAN--IDDTQYLAAGR-----AIRTVFGTEPD 443  
Db 801 IEMPYVIEFIFSDTHELKQKRTDCKKAVISTMEGSSLD 837  
RESULT 751  
ADSI17717  
ID ADS17717 standard; protein; 1820 AA.  
XX  
AC ADS17717;  
XX  
DT 16-DEC-2004 (first entry)  
DE GAL4 peptide + human VPARP protein, GAL4-VPARP.  
XX  
KW vault; carrier molecule; major vault protein; MVP;  
KW vault poly-ADP ribose polymerase; VPARP; toxin.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO2004081533-A2.  
XX  
PD 23-SEP-2004.  
PF 10-MAR-2004; 2004WO-US007434.  
XX  
PR 10-MAR-2003; 2003US-0453800P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;  
XX  
DR WPI; 2004-690644/67.  
XX N-PSDB; ADS17718.  
PT Using vaults as carrier molecules to deliver substance(s) to an organism,  
PT to a specific tissue, to specific cells, or to an environmental medium  
PT comprises incorporating the substance(s) into the vaults and  
PT administering them.  
XX  
PS Disclosure; SEQ ID NO 56; 459pp; English.  
XX  
CC The invention relates to a novel method of using vaults as carrier  
CC molecules to deliver one, or more than one, substance to an organism, or

CC to a specific tissue or to specific cells, or to an environmental medium..  
CC The method comprises providing vaults, incorporating the substance into  
CC the vaults, and administering the vaults comprising the substance to the  
CC organism, to the specific tissue, to the specific cells, or to the  
CC environmental medium. The invention further comprises: a vault-like  
CC particle, comprising a major vault protein (MVP) or modified MVP, and/or  
CC further comprising a vault poly-ADP ribose polymerase (VPARP) or a  
CC portion of a VPARP, comprising at least about 150 consecutive residues of  
CC VPARP; a method of preventing damage by one, or more than one, substance  
CC to an organism, to a specific tissue, to specific cells, or to an  
CC environmental medium by sequestering the substance within a vault-like  
CC particle; a method of delivering one or more than one substance,  
CC particularly a sensor to an organism, to a specific tissue, to specific  
CC cells, or to an environmental medium; a method of detecting a signal from  
CC a sensor within an organism, or a specific tissue or specific cells; a  
CC method of making vault-like particles; and a method of making vault-like  
CC particles comprising one, or more than one, substance. The method or the  
CC vault-like particles are useful for delivering substances to an organism,  
CC or to a specific tissue or to specific cells, or to an environmental  
CC medium. The vault-like particles are also useful for preventing damage by  
CC a substance (e.g., toxin) to an organism, to a specific tissue, to  
CC specific cells, or to an environmental medium. This sequence represents a  
CC GAL4 peptide + human VPARP protein, GAL4-VPARP of the invention.  
XX  
SQ Sequence 1820 AA;  
Query Match 3.4%; Score 89.5; DB 8; Length 1820;  
Best Local Similarity 20.3%; Pred. No. 4.8e+02;  
Matches 105; Conservative 74; Mismatches 183; Indels 155; Gaps 29;  
QY 26 SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMMAV 80  
Db 461 SKPNPPSLAKYRALRCKI-EHVEQNTTEEFLRVKE-VLQNHHKSPVDVL--QIFRVGRV 516  
QY 81 AADT--LQRLGARVASVDMGPPQLPDG---QSLPIPPVILAELGSDPTKGTVCIFYGHLDV 135  
Db 517 NETTEFLSKLGNVRPLLLHGSPVQNIIVGILCRGLLLPKVV-EDRGVQRT-----DV 565  
QY 136 QPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRAL---EQDLPVNIK 192  
Db 566 --GNLGSGIYFSDSLSTSI--KYSHPGETD--GTRLLLLICDVALGKMDLHEKDFPLTEA 619  
QY 193 ----FIIEGMEEAGSVALEELVEKEKDRFF-----SGVDYIV-----ISDN 229  
Db 620 PPGYDSVHGVSQTASVT---TDFEDDEFVYKTNQVKMKYIIKFSMPGDQIKDFHPSDH 675  
QY 230 LWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHE-----PMADLVALLGSLV 284  
Db 676 TELEEYRPEFSNFSKVEDYQLPDAKT-----SSSTKAGLQDASGNLVPLED-VHIKGRII 729  
QY 285 DSSGHILVPGIYDE-----VVPLTEEEINTYKAIHLDLEEYRNSRV----- 326  
Db 730 DTVAQVIVFQTYTNKSHVPIEAKYIFPLDD-----KAAVCGFEAFINGKHIIVGEIKEKE 783  
QY 327 ---EKFL-----FDTKEEILMHLWRYPSLSIHGIEGAFD 357  
Db 784 EAQOEYLEAVTQGHGAYLMSQDAPDVFTVSVGNLPPKAKVLIKITYITELSILGTVGVPFF 843  
QY 358 EPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK---RNSSNKMVVSMTLG 414  
Db 844 MPA--TVAPWQ-----QDKALNENLQDTVEKIKIKEIGTKQSFSLTMS 884  
QY 415 LH-PWIAN--IDDTQYLAAGR-----AIRTVFGTEPD 443  
Db 885 IEMPYVIEFIFSDTHELKQKRTDCKKAVISTMEGSSLD 921  
RESULT 752  
ADSI17725  
ID ADS17725 standard; protein; 1854 AA.  
XX  
AC ADS17725;  
XX

DT	16-DEC-2004	(first entry)	
XX	MS2 peptide + human VPARP protein, MS2-VPARP.		
DE	vault; carrier molecule; major vault protein; MVP;		
XX	vault poly-ADP ribose polymerase; VPARP; toxin.		
KW	Homo sapiens.		
KW	Synthetic.		
XX	WO2004081533-A2.		
PN	23-SEP-2004.		
XX	10-MAR-2004; 2004WO-US007434.		
PF	10-MAR-2003; 2003US-0453800P.		
XX	(REGC ) UNIV CALIFORNIA.		
PA	Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;		
XX	WPI; 2004-690644/67.		
XX	N-PSDB; ADS17726.		
DR	Using vaults as carrier molecules to deliver substance(s) to an organism,		
XX	to a specific tissue, to specific cells, or to an environmental medium		
XX	comprises incorporating the substance(s) into the vaults and		
XX	administering them.		
PS	Disclosure; SEQ ID NO 64; 459pp; English.		
XX	The invention relates to a novel method of using vaults as carrier		
CC	molecules to deliver one, or more than one, substance to an organism, or		
CC	to a specific tissue or to specific cells, or to an environmental medium.		
CC	The method comprises providing vaults, incorporating the substance into		
CC	the vaults, and administering the vaults comprising the substance to the		
CC	organism, to the specific tissue, to the specific cells, or to the		
CC	environmental medium. The invention further comprises: a vault-like		
CC	particle, comprising a major vault protein (MVP) or modified MVP, and/or		
CC	further comprising a vault poly-ADP ribose polymerase (VPARP) or a		
CC	portion of a VPARP, comprising at least about 150 consecutive residues of		
CC	VPARP; a method of preventing damage by one, or more than one, substance		
CC	to an organism, to a specific tissue, to specific cells, or to an		
CC	environmental medium by sequestering the substance within a vault-like		
CC	particle; a method of delivering one or more than one substance,		
CC	particularly a sensor to an organism, to a specific tissue, to specific		
CC	cells, or to an environmental medium; a method of detecting a signal from		
CC	a sensor within an organism, or a specific tissue or specific cells; a		
CC	method of making vault-like particles; and a method of making vault-like		
CC	particles comprising one, or more than one, substance. The method or the		
CC	vault-like particles are useful for delivering substances to an organism,		
CC	or to a specific tissue or to specific cells, or to an environmental		
CC	medium. The vault-like particles are also useful for preventing damage by		
CC	a substance (e.g., toxin) to an organism, to a specific tissue, to		
CC	specific cells, or to an environmental medium. This sequence represents a		
CC	MS2 peptide + human VPARP protein, MS2-VPARP of the invention.		
XX			
SQ	Sequence 1854 AA;		
Query Match 3.4%; Score 89.5; DB 8; Length 1854;			
Best Local Similarity 20.3%; Pred. No. 4.9e+02;			
Matches 105; Conservative 74; Mismatches 183; Indels 155; Gaps 29;			
QY	26	SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAV 80	
DB	495	SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRGRV 550	
QY	81	AADT--LQRLGARVASVDMGFPQQLPDG---QSLPIPPVILAELGSDPTKGTVCFYGLHDV 135	
DB	551	NETTEFLSKLGNVRPLHGSVPQNVIGILCRGLLPLKVV-EDRGVQRT-----DV 599	
QY	136	QPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRAL---EQDLPVNIK 192	
DB	600	--GNLGSgiYfSDSLSTsi--KYshPGETD--GTRLLliCDVALGKMDLHEKDFPLTEA 653	
QY	193	----FiIEGMEeAGSvALEELVEKEKORFF-----SGVDYiV-----ISDN 229	
DB	654	PPGYDSvHGVSQTASVT---TDFEDDEFVVYKTNQVKMKYIIKFSPMGDQIKDFHPSDH 709	
QY	230	LWISQRKPAiTYGTRGNSYFMVEVKCRDQDFHSGTFGGILHE-----PMADLVALLGSLV 284	
DB	710	TELEeYRPEFSNFskVEDYQLPDAKT-----SSTKAGLQDASGNLVPLED-VHIKGRii 763	
QY	285	DSSGHILVPGiYDE-----VPLTEEEINtYKAiHLdLEeYRNssRV----- 326	
DB	764	DTVAQViVFQTYTNKSHVPIEAKYiFPLDD-----KAAVCGFEAFINGKHIVGEIKeKE 817	
QY	327	---EKFL-----FDTKEEiLMHLWRYPPSLSiHGIEGAfD 357	
DB	818	EAQQeYLEAVTQGHGAYLMSQDAPDVFTSVGNLPPKAKVLIKiTYITeLSiLGTVGvFF 877	
QY	358	EPGtKTViPGRViGKfSiRLVPHMNvSAVEKQVTRHLEDVfSK--RNSSNKMVVvSMtLG 414	
DB	878	MPA--TVAPWQ-----QDKALNENLQDTVEKiCIKeIGTKQSPSLTMS 918	
QY	415	LH-PWIAN--IDDTQYLAaKR-----AiRTVfGTEPD 443	
DB	919	IEmpYViEfIFSDThELKQKRTDCKAViSTMEGSSLD 955	
RESULT 753			
ADS17721			
ID	ADS17721	standard; protein; 1961 AA.	
XX	AC	ADS17721;	
XX	DT	16-DEC-2004 (first entry)	
XX	DE	Green fluorescent protein + human VPARP protein.	
XX	KW	vault; carrier molecule; major vault protein; MVP;	
XX	OS	vault poly-ADP ribose polymerase; VPARP; toxin.	
OS	OS	Homo sapiens.	
XX	PN	WO2004081533-A2.	
XX	PD	23-SEP-2004.	
XX	PF	10-MAR-2004; 2004WO-US007434.	
XX	PR	10-MAR-2003; 2003US-0453800P.	
XX	PA	(REGC ) UNIV CALIFORNIA.	
PI	Rome LH, Kickhoefer VA, Raval-Fernandes S, Stewart PL;		
XX	WPI; 2004-690644/67.		
DR	N-PSDB; ADS17726.		
XX	Using vaults as carrier molecules to deliver substance(s) to an organism,		
PT	to a specific tissue, to specific cells, or to an environmental medium		
PT	comprises incorporating the substance(s) into the vaults and		
PT	administering them.		
XX	Disclosure; SEQ ID NO 64; 459pp; English.		
XX	The invention relates to a novel method of using vaults as carrier		
CC	molecules to deliver one, or more than one, substance to an organism, or		
CC	to a specific tissue or to specific cells, or to an environmental medium.		
CC	The method comprises providing vaults, incorporating the substance into		
CC	the vaults, and administering the vaults comprising the substance to the		
CC	organism, to the specific tissue, to the specific cells, or to the		
CC	environmental medium. The invention further comprises: a vault-like		
CC	particle, comprising a major vault protein (MVP) or modified MVP, and/or		
CC	further comprising a vault poly-ADP ribose polymerase (VPARP) or a		
CC	portion of a VPARP, comprising at least about 150 consecutive residues of		
CC	VPARP; a method of preventing damage by one, or more than one, substance		
CC	to an organism, to a specific tissue, to specific cells, or to an		
CC	environmental medium by sequestering the substance within a vault-like		
CC	particle; a method of delivering one or more than one substance,		
CC	particularly a sensor to an organism, to a specific tissue, to specific		
CC	cells, or to an environmental medium; a method of detecting a signal from		
CC	a sensor within an organism, or a specific tissue or specific cells; a		
CC	method of making vault-like particles; and a method of making vault-like		
CC	particles comprising one, or more than one, substance. The method or the		
CC	vault-like particles are useful for delivering substances to an organism,		
CC	or to a specific tissue or to specific cells, or to an environmental		
CC	medium. The vault-like particles are also useful for preventing damage by		
CC	a substance (e.g., toxin) to an organism, to a specific tissue, to		
CC	specific cells, or to an environmental medium. This sequence represents a		
CC	MS2 peptide + human VPARP protein, MS2-VPARP of the invention.		
XX			
SQ	Sequence 1854 AA;		
Query Match 3.4%; Score 89.5; DB 8; Length 1854;			
Best Local Similarity 20.3%; Pred. No. 4.9e+02;			
Matches 105; Conservative 74; Mismatches 183; Indels 155; Gaps 29;			
QY	26	SSPSPPP-----ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAV 80	
DB	495	SKPNPPSLAKYRALRCKI-EHVEQNTTEFLVRKE-VLQNHHSKSPVDVL--QIFRGRV 550	
QY	81	AADT--LQRLGARVASVDMGFPQQLPDG---QSLPIPPVILAELGSDPTKGTVCFYGLHDV 135	
DB	551	NETTEFLSKLGNVRPLHGSVPQNVIGILCRGLLPLKVV-EDRGVQRT-----DV 599	
QY	136	QPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRAL---EQDLPVNIK 192	

Using vaults as carrier molecules to deliver substance(s) to an organism, to a specific tissue, to specific cells, or to an environmental medium comprises incorporating the substance(s) into the vaults and administering them.

Disclosure; SEQ ID NO 60; 459pp; English.

The invention relates to a novel method of using vaults as carrier molecules to deliver one, or more than one, substance to an organism, or to a specific tissue or to specific cells, or to an environmental medium. The method comprises providing vaults, incorporating the substance into the vaults, and administering the vaults comprising the substance to the organism, to the specific tissue, to the specific cells, or to the environmental medium. The invention further comprises: a vault-like





Db 1074 PPGYDSVHGVSQTASVT-----TDFEDDEFVYKTNQVMKYIIFKSPMGDQIKDFHPSDH 1129

QY 230 LWTISQKPAITYGTRGNSYFVVEVKCRDQDFHSGTGGILHE-----PMADLVALLGSLV 284

Db 1130 TELEEYRPEFSNFSKVEDYQLPDAKT-----SSSTKAGLQDASGNLVPLED-VHIKGRII 1183

QY 285 DSSGHILVPGIYDE-----VVLTEEEINTYKAIHLDLEEYRNSRV----- 326

Db 1184 DTVAQVIVFQYTNKSHVPIEAKYIFPLDD-----KAAVCGFEAFINGKHI VGEIKEKE 1237

QY 327 ---EKFL-----FDTKEEILMHLWRYPSLSIHGIEGAFD 357

Db 1238 EAQOEYLEAVTQGHGAYLMSODAPDVFTVSVGNLPPKAKVLIKITYITELSI LGTVGVFF 1297

QY 358 EPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEBDVFSK---RNSSNMVMVSMTLG 414

Db 1298 MPA--TVAPWQ-----QDKALNENLQDVTVEKICIKEIGTKQSFSLTMS 1338

QY 415 LH-PWIAN--IDDTQYLAAR-----AIRTVFGTEPD 443

Db 1339 IEMPYVIEFIFSDTHELKQKXTDCKAVISTMEGSSLD 1375

RESULT 755

ABP41753

ID ABP41753 standard; protein; 237 AA.

XX AC ABP41753;

XX DT 22-AUG-2002 (first entry)

XX DE Human ovarian antigen HPDRB76, SEQ ID NO:2885.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

KW ovarian cancer; breast cancer; tumour; reproductive system disorder;

KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;

KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;

KW gastrointestinal disorder; urinary system disorder; drug screening;

KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;

KW antiinflammatory; gynaecological; reproductive; chromosome 1p34.

XX OS Homo sapiens.

XX PN WO200200677-A1.

XX PD 03-JAN-2002.

XX PF 07-JUN-2001; 2001WO-US018569.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-147878/19.

DR N-PSDB; ABQ54830.

XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,

PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian

PT cancer), immune disorders, cardiovascular disorders and neurological

PT diseases.

XX PS Claim 11; SEQ ID NO 2885; 2922pp; English.

XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also

CC encompasses polypeptides 90% identical and polynucleotides 95% identical

CC to the sequences of the invention. The invention additionally relates to

CC recombinant vectors and host cells comprising human ovarian antigen

CC polynucleotides, antibodies against human ovarian antigens, and the use

CC of ovarian antigen polynucleotides and polypeptides in diagnosing,

CC treating, prognosing or preventing various ovarian and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,

CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and

CC vaginitis), immune disorders (e.g., congenital and acquired

CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC respiratory disorders, neurological disorders, gastrointestinal disorders

CC and urinary system disorders. Ovarian antigen polypeptides and

CC polynucleotides may also be used in screening for compounds which

CC modulate ovarian antigen expression or activity. The polynucleotides may

CC further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies

CC useful in disease diagnosis, drug targeting and phenotyping. The present

CC sequence represents a human ovarian antigen of the invention. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 237 AA;

Query Match 3.4%; Score 89; DB 5; Length 237;

Best Local Similarity 23.0%; Pred. No. 23;

Matches 69; Conservative 40; Mismatches 103; Indels 88; Gaps 16;

QY 94 SVDMPGQ-----QLPDGQSLPIPPVILAE LGS DPTKGT-----VCFYGHLDVQP 137

Db 3 SADMAPSVPAEPEYPKG----IRAVLLGPPGAG--KGTOAPRLAENFCVCHLATGDMRL 56

QY 138 ADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF-RALEQDLPVNIKFIIE 196

Db 57 AMVAG-----SELGKKL--KATMDAGKLVSDMMVELIEKNLETPLCNK-GFLLD 104

QY 197 GMEEAGSVA--LEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVK 254

Db 105 GFPRTVRQAEMLDLMEKRKEKLDVIEF-SIPDSLIRITRGLRIHPKSGRSY----- 157

QY 255 CRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIH 314

Db 158 --HEEFNPP-----KEPMKD-----DITGE-----PLIRSDDNEKALK 189

QY 315 LDLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374

Db 190 IRLQAYH-----TQTTPLIEYRK-----RGIHSAIDASQTPDVVPFASILA AFS 233

RESULT 756

ABG99179

ID ABG99179 standard; protein; 333 AA.

XX AC ABG99179;

XX DT 14-JAN-2003 (first entry)

XX DE Human endogenouc retrovirus k6 (herv-k6) prt.

XX KW Human; endogenous retrovirus; herv; prostate cancer; testicular cancer;

KW multiple sclerosis; insulin-dependent diabetes mellitus; HML-2 protease;

KW cancer; transgenic animal.

XX OS Human endogenous retrovirus.

XX PN WO200246477-A2.

XX PD 13-JUN-2002.

XX PF 07-DEC-2001; 2001WO-US047824.







DT 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #26937.  
DE  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
KW Pseudomonas syringae.  
XX  
XX WO200277183-A2.  
PN  
XX 03-OCT-2002.  
PD  
XX 21-MAR-2002; 2002WO-US009107.  
PF  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA45280.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 69334; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 409 AA;

Query Match 3.4%; Score 89; DB 6; Length 409;  
Best Local Similarity 25.0%; Pred. No. 53;  
Matches 28; Conservative 17; Mismatches 45; Indels 22; Gaps 4;

QY 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLE-----DVFSKRNSNKNMVSMTL 413

Db 121 GMHGVATATVAARFGLPCVIYMGATDIERQQANVFRMKLLGAEIVPVTSGTGLKDAWNE 180  
QY 414 GLHPWIANIDDTQYLAAKRAIRTVFGTE--PDMIRDGSTIPIAKMFOEIVHK 463  
Db 181 ALRDWVTNVDDTFYL-----IGTVAGPHPYPPAMVRD-----FQSVIGK 218

RESULT 761  
AAU55162  
ID AAU55162 standard; protein; 428 AA.  
XX  
AC AAU55162;  
XX  
DT 27-FEB-2002 (first entry)  
XX  
DE Propionibacterium acnes immunogenic protein #16058.  
XX  
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.  
XX  
OS Propionibacterium acnes.  
XX  
PN WO200181581-A2.  
XX  
PD 01-NOV-2001.  
XX  
XX 20-APR-2001; 2001WO-US012865.  
PF  
XX 21-APR-2000; 2000US-0199047P.  
PR 02-JUN-2000; 2000US-0208841P.  
PR 07-JUL-2000; 2000US-0216747P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX  
DR WPI; 2001-616774/71.  
DR N-PSDB; AAS59568.  
XX  
PT Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris.  
XX  
PS Example 1; SEQ ID NO 16357; 1069pp; English.  
XX  
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
CC polypeptides. The proteins and their associated DNA sequences are used in  
CC the treatment, prevention and diagnosis of medical conditions caused by  
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
CC P. acnes is also involved in infections of bone, joints and the central  
CC nervous system, however it is particularly involved in the inflammatory  
CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC specific for P. acnes proteins. These antibodies can be used to  
CC downregulate expression and activity of P. acnes polypeptides and  
CC therefore treat P. acnes infections. The antibodies may also be used as  
CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 428 AA;

Query Match 3.4%; Score 89; DB 4; Length 428;

Best Local Similarity 21.8%; Pred. No. 56;  
Matches 90; Conservative 61; Mismatches 130; Indels 132; Gaps 24;

QY 80 VAADTLQR-----LGARVASVDMGPPQLPDGQSLPPIPVILAEGLSDPTKGTVCIFYG 131  
Db 81 IAVDPLHRAAFFDVSAALGDEVVHV-----VRPVLGRI---TAASVLFDD 122

QY 132 HLD-----VQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPV-LAWINAVSAFRALE 184  
Db 123 DLDDRGVQGIRLVDRGSAALDVNVVRLVD-----DNQGPLELSEILGIHTEVGLQ 173

QY 185 QDLPVN-IKFIIEG-----MEEAGSVALEEL-----VEKEKDRFFS 219  
Db 174 RDGAVDTLRHVDEGATRPHRRVEGGELVVTTERDSAGKMLAEELRLLLSRSVSVEED---- 229

QY 220 GVDYIV--ISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLV 277  
Db 230 --DTLLAELLVNLVNVNHR-LVLGGNAGNQPIILLSLR-----DTQTVVGVLN----- 273

QY 278 ALLGSLVDSSGHILVPGIYD--EVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKE 335  
Db 274 --IGGKVLPGRCCLTLGTHEVLDLVKVNRAIDTTPGRHRLALEK-----LESLE 320

QY 336 EILMH-LW-----RYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQ 389  
Db 321 PHIEHPLWLMFHSRY---ATHDILGQ-SAPGSRGV-----SVRVVPTTFVATQGSQ 367

QY 390 VTRHLEDVFSKRNSSNMVVMVMTLGLHPWIANIDD--TQYLAAKRAIRTVEGT 440  
Db 368 V-----FVLGTGAREACGSVNLG-HEWSFRMDGLLDGSASARRVISTSTGT 413

RESULT 762  
ABM51681  
ID ABM51681 standard; protein; 428 AA.  
AC ABM51681;  
XX  
DT 20-OCT-2003 (first entry)  
XX  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16357.  
XX  
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
KW immunostimulant; immune response; vaccine.  
OS Propionibacterium acnes.  
XX  
PN WO2003033515-A1.  
XX  
PD 24-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032727.  
XX  
PR 15-OCT-2001; 2001US-00978825.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
PI Barth B, Vallieve-Douglass J;  
XX  
DR WPI; 2003-381789/36.  
DR N-PSDB; ACF64497.  
XX  
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the  
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
PT or for stimulating an immune response specific for a P. acnes protein.  
XX  
PS Example 1; SEQ ID NO 16357; 1481pp; English.  
XX  
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
CC encoding a Propionibacterium acnes protein. The invention also relates to  
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 428 AA;

Query Match 3.4%; Score 89; DB 6; Length 428;  
Best Local Similarity 21.8%; Pred. No. 56;  
Matches 90; Conservative 61; Mismatches 130; Indels 132; Gaps 24;

QY 80 VAADTLQR-----LGARVASVDMGPPQLPDGQSLPPIPVILAEGLSDPTKGTVCIFYG 131  
Db 81 IAVDPLHRAAFFDVSAALGDEVVHV-----VRPVLGRI---TAASVLFDD 122

QY 132 HLD-----VQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPV-LAWINAVSAFRALE 184  
Db 123 DLDDRGVQGIRLVDRGSAALDVNVVRLVD-----DNQGPLELSEILGIHTEVGLQ 173

QY 185 QDLPVN-IKFIIEG-----MEEAGSVALEEL-----VEKEKDRFFS 219  
Db 174 RDGAVDTLRHVDEGATRPHRRVEGGELVVTTERDSAGKMLAEELRLLLSRSVSVEED---- 229

QY 220 GVDYIV--ISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLV 277  
Db 230 --DTLLAELLVNLVNVNHR-LVLGGNAGNQPIILLSLR-----DTQTVVGVLN----- 273

QY 278 ALLGSLVDSSGHILVPGIYD--EVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKE 335  
Db 274 --IGGKVLPGRCCLTLGTHEVLDLVKVNRAIDTTPGRHRLALEK-----LESLE 320

QY 336 EILMH-LW-----RYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQ 389  
Db 321 PHIEHPLWLMFHSRY---ATHDILGQ-SAPGSRGV-----SVRVVPTTFVATQGSQ 367

QY 390 VTRHLEDVFSKRNSSNMVVMVMTLGLHPWIANIDD--TQYLAAKRAIRTVEGT 440  
Db 368 V-----FVLGTGAREACGSVNLG-HEWSFRMDGLLDGSASARRVISTSTGT 413

RESULT 763  
ADB07082  
ID ADB07082 standard; protein; 453 AA.  
XX  
AC ADB07082;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Alloicoccus otitis antigenic protein SEQ ID NO:1022.  
XX  
KW Alloicoccus otitidis; antigenic protein; immunogenic; immunisation;  
KW gene therapy; Gram-positive bacterium; infection.  
XX



OS Alloiococcus otitis.  
XX  
PN WO2003048304-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 25-NOV-2002; 2002WO-US036123.  
XX  
PR 29-NOV-2001; 2001US-0333777P.  
PR 18-NOV-2002; 2002US-0426742P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
XX  
PI Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;  
XX  
DR WPI; 2003-505284/47.  
DR N-PSDB; ADB07081.  
XX  
PT New Alloiococcus otitidis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.  
XX  
PS Claim 33; SEQ ID NO 1022; 1019pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I) of  
CC Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.  
CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its  
CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloiococcus otitidis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloiococcus  
CC otitidis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloiococcus  
CC otitidis. The present sequence represents an Alloiococcus otitidis  
CC antigen protein from the present invention.  
XX  
SQ Sequence 453 AA;  
Query Match 3.4%; Score 89; DB 6; Length 453;  
Best Local Similarity 20.5%; Pred. No. 62;  
Matches 70; Conservative 52; Mismatches 133; Indels 86; Gaps 14;  
QY 183 LEQDLPVNKFIEGMEEA-----GSVALEELVEKE----- 213  
Db 110 MENDL--NISLMINPEKEAAEDIMRVIQYPEALSIEEFANGRVNLSSELLIKENSPLIDVK 167  
QY 214 ----KDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKRCDQDFHSGTGGIL 269  
Db 168 ISDFRQRFGNILVTWVLRDQTLPISGGTVL--KEGDEIYVYSTKDKLNEFYAKVNGKVG 225  
QY 270 HEPMADLVA-----LLGSLVDSSGHILV-----PGIYDEWVP----- 301  
Db 226 QIKTALIIGGGRITHYLIIGLLLDKGVKVQIEQNTDAAKSLSSLYPKCVVEGDTQDSF 285  
QY 302 LTEEEINTYKAI--HLDLEEYRNSSRVEKFLFDTKEEILHMLWRYPSSLIHGIEGAFDEP 359  
Db 286 LEEERIGSYDAVISLTGVDESNIILTSMEAMTFDPK-KVITKVSRTDLLRIMSLGSI--- 341

QY 360 GTKTVI-PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPW 418  
Db 342 SLQTIPTPKRLIAYKIIRY-----VRALKYHYSSHFFENFRVANNAE-AMQFEVGSSEK 395  
QY 419 IANI-----DDTQYLAAKRAIRTVFGTEPDMIRDGSTI 451  
Db 396 IINIFLIDLKLDKDDLLJAFIVRGDDLFPPTGADRILPGDKV 436  
RESULT 764  
ADB07084  
ID ADB07084 standard; protein; 467 AA.  
XX  
AC ADB07084;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Alloiococcus otitis antigenic protein SEQ ID NO:1024.  
XX  
KW Alloiococcus otitidis; antigenic protein; immunogenic; immunisation;  
KW gene therapy; Gram-positive bacterium; infection.  
XX  
OS Alloiococcus otitis.  
XX  
PN WO2003048304-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 25-NOV-2002; 2002WO-US036123.  
XX  
PR 29-NOV-2001; 2001US-0333777P.  
PR 18-NOV-2002; 2002US-0426742P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
PI Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;  
XX  
DR WPI; 2003-505284/47.  
DR N-PSDB; ADB07083.  
XX  
PT New Alloiococcus otitidis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.  
XX  
PS Claim 33; SEQ ID NO 1024; 1019pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I) of  
CC Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.  
CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its  
CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloiococcus otitidis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloiococcus  
CC otitidis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloiococcus  
CC otitidis. The present sequence represents an Alloiococcus otitidis  
CC antigen protein from the present invention.  
XX



SQ Sequence 467 AA;  
Query Match 3.4%; Score 89; DB 6; Length 467;  
Best Local Similarity 20.5%; Pred. No. 65;  
Matches 70; Conservative 52; Mismatches 133; Indels 86; Gaps 14;  
QY 183 LEQDLPVNIKFIIEGMEA-----GSVALEELVEKE----- 213  
DB 124 MENDL--NISLMINPEKEAAEDIMRVIOYPEALSIEEFANGRVNLSSELLIKENSPLIDVK 181  
QY 214 ----KDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGIL 269  
DB 182 ISDFRQRFGNILVTVLRDGTLPISGQTVL--KEGDEIYVYSTDKLNEFYAKVNGKVG 239  
QY 270 HEPMADLVA-----LLGSLVDSSGHILV-----PGIYDEVVP----- 301  
DB 240 QIKTALIIGGRITHYLIGLLLDKGVKVIEQNTDAAKSLSSLYPKCVVVEGDGTQSF 299  
QY 302 LTEEEINTYKAI--HLDLEEYRNSRVEKFELEDTKEEILMHLWRYPSLSIHGIEGAFDEP 359  
DB 300 LEEERIGSYDAVISLTGVDESNILTSMFAMTFDPK-KVITKVSRTDLLRIMSLMGSF--- 355  
QY 360 GTKTVI-PCRVIKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVMVMTLGLHPW 418  
DB 356 SLQTIIVTPKRLIAYKIIRY-----VRALKYHYSSHFFENFRVANNOAE-AMQFEVGSSEK 409  
QY 419 IANI-----DDTQYLAAKRAIRTVFGTEPDMIRDGSTI 451  
DB 410 IINIPLIDLKLDKDDLLIAFIVRGDDLLFPTGADRILPGDKV 450  
RESULT 765  
ABM68874  
ID ABM68874 standard; protein; 589 AA.  
XX ABM68874;  
XX 20-NOV-2003 (first entry)  
DT Photorhabdus luminescens protein sequence #1971.  
DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
XX detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX Photorhabdus luminescens.  
OS WO200294867-A2.  
XX 28-NOV-2002.  
XX 07-FEB-2002; 2002WO-IB003040.  
PF 07-FEB-2001; 2001FR-00001659.  
XX (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
PI WPI; 2003-148459/14.  
DR Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX Claim 2; SEQ ID NO 1971; 1205pp; French.  
PS The invention relates to the isolation of genes and their encoded  
XX proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
SQ Sequence 589 AA;  
Query Match 3.4%; Score 89; DB 6; Length 589;  
Best Local Similarity 26.6%; Pred. No. 93;  
Matches 46; Conservative 28; Mismatches 53; Indels 46; Gaps 10;  
QY 349 IHGIEGAFD----EPGKTIVP---GRVIGKFSI--RLVPHMNVSAVEKQ----VTRHL 394  
DB 188 IEGVEKSFDRWLTGQPGERTVRKDRFGRVIEDISSVDSLAAHNLVLSIDERLQALVYREL 247  
QY 395 ED--VFSKRNSNKMVVMVMTLGLHPWIAN-----IDDTQYLAAKRAIRTVFGTEPD 443  
DB 248 TNAVAFNKAESGTAVLVDVNTGEVLAMANSPSYNPNRNINTPKEVMNRNRAITDIF--EP- 304  
QY 444 MIRDGSTIPIAKMFOEIVHKSVVLIPLGAVDDGEHSQNEKINRWNY-IEGTKL 495  
DB 305 ----GSTVK-----PMVMMAALNDGIKENTVINTVPYRISGKEI 340  
RESULT 766  
AAU10665  
ID AAU10665 standard; protein; 665 AA.  
XX AAU10665;  
XX 14-FEB-2002 (first entry)  
DT Human L1CAM F80 fusion polypeptide.  
XX Neurite outgrowth; fibronectin Type III repeat; cell adhesion molecule;  
KW F80; neurone; peripheral nerve damage; trauma; gliosis; infarction;  
KW degenerative disease; malignant disease; antibacterial;  
KW central nervous system lesion; virucide; antiparkinsonian; nootropic;  
KW neuroprotective; antiinflammatory; human; L1CAM; mutant; mutein.  
XX Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 615  
FT /label= Unknown  
FT  
XX US6313265-B1.  
PN 06-NOV-2001.  
XX 24-JUL-1995; 95US-00506296.  
XX 24-JUL-1995; 95US-00506296.  
XX (SCRI ) SCRIPPS RES INST.  
XX Phillips G, Cunningham BA, Crossin KL;  
PI WPI; 2002-017011/02.  
DR

XX Polypeptide for promoting neurite out-growth useful for treating diseases  
PT such as inflammation, Parkinson's disease, trauma, comprises fibronectin  
PT type III repeats derived from a family of cell adhesion molecules.  
XX  
PS Example 2; Fig 20; 132pp; English.  
XX  
CC The present invention relates to polypeptides that promote neurite  
CC growth. The polypeptides contain fibronectin Type III repeats derived  
CC from a family of cell adhesion molecules (CAMs). The polypeptides of the  
CC invention include the F80, 3-5, and 4-5 regions of the CAM family members  
CC chicken Ng-CAM, chicken Nr-CAM, mouse L1CAM and human L1CAM. The  
CC polypeptides of the invention are useful for promoting neurite outgrowth  
CC of neuronal cells in vitro e.g. in a cell culture system, or in vivo for  
CC treating disorders such as peripheral nerve damage associated with  
CC physical or surgical trauma, infarction, bacterial or viral infections,  
CC toxin exposure, degenerative disease, malignant disease that affects  
CC peripheral or central neurones, or in surgical or transplantation methods  
CC in which new neuronal cells from brain, spinal cord or dorsal root  
CC ganglia are introduced and require stimulation of neurite outgrowth from  
CC the implant and innervation into the recipient tissue, where the diseases  
CC include central nervous systems lesions, gliosis, Parkinson's disease,  
CC Alzheimer's disease, gliotic response or inflammation. The present  
CC sequence represents human L1CAM F80 fusion polypeptide  
XX  
SQ Sequence 665 AA;

Query Match 3.4%; Score 89; DB 5; Length 665;  
Best Local Similarity 26.0%; Pred. No. 1.1e+02;  
Matches 40; Conservative 23; Mismatches 41; Indels 50; Gaps 11;  
QY 264 TFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEWVPLTEEEINTYKAIHLDLEEY--R 321  
Db 209 TFGGGDHPPKSLVP-RGSI--HKDHVVVPANTTSVI---LSGLRPYSSYHLEVQAFNGR 262  
QY 322 NSSRVEKFLFDTKEEI-----LMHL-----WRYPSLSIHGIEGAF-----DE 358  
Db 263 GSGPASEFTFTPEGVPGHPALHLECCQNTSLLLRWQ-PPLSHNGVLTGYVLSYHPLDE 321  
QY 359 PGKTVIPGRVIGKFSIR-----LVPHM 381  
Db 322 GG-----KGQL--SFNLRDPELRTHNLTDLSPHL 348

RESULT 767  
ABU24641  
ID ABU24641 standard; protein; 702 AA.  
XX  
AC ABU24641;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #10168.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Clostridium botulinum.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA28511.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 52565; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 702 AA;

Query Match 3.4%; Score 89; DB 6; Length 702;  
Best Local Similarity 19.1%; Pred. No. 1.2e+02;  
Matches 94; Conservative 74; Mismatches 133; Indels 190; Gaps 24;  
QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRFQELFRMMVAADTLQRLGARV 92  
Db 266 AQLDKVKEKI---SEEFSEKVEDKVA---DIAEVIYKTQEIVRNMLNED----- 310  
QY 93 ASVDMGPPQQLPDGQSLPIPPVILAELGSDP-----TKG-----TVCFYGHL-DVQPA 138  
Db 311 -----RRPDGRAFDEVRPISCEVGILPRTHGTGLTRGLTQVMTVATLGALGDVQIL 362  
QY 139 DRGDGWLTDPPYVLTEVDGKLY-----IAEESKRYMHYNFPSYSGVEVRPLRGPGRREIGHGAL----- 403  
Db 363 DG-----IAEESKRYMHYNFPSYSGVEVRPLRGPGRREIGHGAL----- 403  
QY 174 INAVSAFRALE-----QDLPVNIKFIEGMEEAGSVA----- 205  
Db 404 -----AERALEPLIPSQSEFPYTIIRLVSEVLSSNGTSQASVCGSTLALLDAGVPIKRPA 458  
QY 206 -----LEELVEKEK-----DRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYF 249  
Db 459 AGIAMLITSEDLKEKEKVITDIQIEDFFGDMDFKVAGTEKGIT---SIQFDTK----- 509  
QY 250 MVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINT 309  
Db 510 -----IKGLNSCVKD--ALEGA---KKARLHLILGKIKECPEPRKELSK 549







QY 396 DVFSKRSSNMVSMVMTGLHP-----WIANIDDTQYLAAKRAIRTVFGTEPD 443  
Db 650 NAVSWYDENSASAKVIAKTLKPNELDALCORYQCOADELADFGYYATGKAGEVILYETSS 709  
QY 444 MIRDGSTIPI 453  
Db 710 DLRDSESIPL 719

RESULT 771  
ABU25821  
ID ABU25821 standard; protein; 914 AA.  
XX AC ABU25821;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #11348.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Corynebacterium diphtheriae.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US0009107.  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA29691.

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 53745; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 914 AA;  
Query Match 3.4%; Score 89; DB 6; Length 914;  
Best Local Similarity 19.0%; Pred. No. 1.8e+02;  
Matches 112; Conservative 87; Mismatches 236; Indels 154; Gaps 28;  
QY 4 KLGRMAASLLAVLLLLLGERGMFSSPS---PPPALLEK-----VFQYIDLHQDEFVQTLKE 55  
Db 342 KLASWLATRAGQSLALYVRGHGSPASGDAESAAIVDKQFHAVAFDFGDLDDADD-DQAFAQ 400  
QY 56 WVAIESDSVQVPRFRQE---LFRMMAVAADTLQRLGARVASVDMGPQLPDGQSLPIPP 112  
Db 401 WIA--SDS----PKYLHEAKAVFHMLAGRGYTLN--GIEHDTAIAGYLLRPGQRTYDLKD 452  
QY 113 V----ILAELGSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKG 168  
Db 453 VYQRLQRLGGSSSES-----GQLSLLDAPDAQELVDSAVAILELSKSL----- 497  
QY 169 PVLAWINAVSAFRAL-EQDLPV-----NIKFIIEGMEEAGSVALEELVEKEK-DR 216  
Db 498 --TAQLQAI DAYEL YREMELEPLVGVLARMEATGICVDVATLREQRDIFVEQVKEESAAR 555  
QY 217 FFSQVD-----YIVISDNLWISQRKPAIT-YGTRGNSYFMVEVK----- 254  
Db 556 ELAGDETLNLSSPKQLQVLFDTLGLPKTKTKTGYSTAAKEIESLAVKNPHPFDLHLLA 615  
QY 255 CRDQDFHSGTFGGI-----LHEPMADLVALLGSLVDSSSHILVPGIYDEVVPLTEE 305  
Db 616 HREFQKMTTLDGLIKAVGDDGRIHTTFNQTVASTGRLSSTEPNL-----QNIPTVPTP 668  
QY 306 EINTYKAIHLDLEYSR-----NSSRVEKFLFTKKEILMHLWRYPSL-----SIHGI 352  
Db 669 AGRKIRSAFVVGQYKSLLTADYSQIEM-----RVMAHLSDEPGLIEAYQTGEDLHNF 721  
QY 353 EGA--FDEP-----GKTVIPGRVIGKFSIRLPHMNVSAVEKQ----- 389  
Db 722 VGSKVDFVPVDQVTPELRRRVKAMSYGLVYGLSAFGLSQQLNIPAGEAKVIMESYFERFG 781  
QY 390 -VTRHLEDVFSKRNSSNMVSMVMTGLHPWTIANIDDTQYLAAKRAIRT-----VFGTEPD 443  
Db 782 GVKRYLDQVVEQARKDG--FTSTLFGRRRYLPELSSDNRVARENAERALNAPIQGTAAAD 839  
QY 444 MIRDGSTIPIAKMFQE-----IVHKSVVLIPLGAVDDGGEHSQNEKI 484  
Db 840 IIKIAMLRVDARLTAENCQSRVLLQVHDELVL---EVASGEQEKVQQL 884

RESULT 772  
AAU33401  
ID AAU33401 standard; protein; 989 AA.  
XX AC AAU33401;  
XX DT 14-FEB-2002 (first entry)  
XX DE Enterococcus faecalis cellular proliferation protein #37.  
XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
XX antibacterial; drug design.  
XX OS Enterococcus faecalis.  
XX PN WO200170955-A2.  
XX







XX AC ABG91809;

XX DT 29-NOV-2002 (first entry)

XX DE Human intracellular signalling molecule protein INSTIG-11.

XX KW Human; intracellular signalling molecule; INTSIG; atherosclerosis;

XX KW cell proliferative disease; cancer; autoimmune disease; AIDS;

XX KW inflammatory disease; acquired immunodeficiency syndrome; allergy;

XX KW neurological disorder; stroke; Parkinson's disease; epilepsy;

XX KW gastrointestinal disorder; ulcer; cirrhosis; reproductive disorder;

XX KW endometriosis; developmental disorder; vesicle trafficking disorder;

XX KW bacterial infection; viral infection; parasitic infection;

XX KW protozoal infection.

XX OS Homo sapiens.

XX PN WO200263008-A2.

XX PD 15-AUG-2002.

XX PF 07-FEB-2002; 2002WO-US003966.

XX PR 08-FEB-2001; 2001US-0267925P.

XX PR 09-MAR-2001; 2001US-0274435P.

XX PR 21-MAR-2001; 2001US-0277819P.

XX PR 03-APR-2001; 2001US-0281326P.

XX PR 15-MAY-2001; 2001US-0291195P.

XX PR 16-MAY-2001; 2001US-0291550P.

XX PR 25-MAY-2001; 2001US-0293591P.

XX PR 01-JUN-2001; 2001US-0295348P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Ding L, Warren BA, Elliot VS, Tang YT, Yue H, Burford N, Lee S;

XX PI Richardson TW, Lal P, Nguyen DB, Yang J, Hafalia AJA, Ison CH;

XX PI Gururajan R, Baughin MR, Wang YE, Yao MG, Thangavelu K, Swarnakar A;

XX PI Griffin JA, Forsythe IJ, Emerling BM, Walia NK;

XX DR WPI; 2002-627561/67.

XX DR N-PSDB; ABS67751.

XX PT New human intracellular signaling molecules (INTSIG), useful for

XX PT diagnosing, treating and preventing diseases or conditions associated

XX PT with the aberrant INTSIG expression, e.g. cancer, AIDS, atherosclerosis,

XX PT infections.

XX PS Claim 2; Page 163-166; 195pp; English.

XX CC The present invention relates to a new intracellular signalling molecule

XX CC (INTSIG) polypeptide. The polypeptides and polynucleotides of the

XX CC invention are useful in diagnosing, treating and preventing diseases or

XX CC conditions associated with the decreased expression or overexpression of

XX CC INTSIG, such as cell proliferative diseases (e.g. cancer,

XX CC atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS (acquired

XX CC immunodeficiency syndrome), allergies), neurological disorders (e.g.

XX CC stroke, Parkinson's disease, epilepsy), gastrointestinal (e.g. ulcer,

XX CC cirrhosis), reproductive (e.g. endometriosis), developmental, vesicle

XX CC trafficking disorders, and infections (e.g. bacterial, viral, parasitic,

XX CC protozoal). These are also useful in assessing the effects of exogenous

XX CC compounds on the expression of nucleic acid and amino acid sequences of

XX CC INTSIG. The INTSIG or its fragments are useful in screening compounds for

XX CC effectiveness as agonist or antagonist of the polypeptides, or in

XX CC altering the expression of the target polynucleotide and compounds that

XX CC specifically bind to or modulate the activity of the polypeptide. The

XX CC microarray is useful in monitoring or measuring protein-protein

XX CC interactions, drug-target interactions, and gene expression profiles. The

XX CC present amino acid sequence represents a human INSTIG protein of the

XX CC invention

XX SQ Sequence 1725 AA;

Query Match 3.4%; Score 89; DB 5; Length 1725;

Best Local Similarity 21.2%; Pred. No. 4.9e+02;

Matches 106; Conservative 55; Mismatches 164; Indels 174; Gaps 27;

QY 1 MDPKLGKMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60

Db 649 MDSKMKMAELQSVV-----SDPKNRKAIENQI-----QQW----- 680

QY 61 SDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120

Db 681 ---EQNLEKFHMDLFRMRCVLA-SLQ-----GGELPNPKSLLA-AAS 717

QY 121 DPTKGTVCIFYCHLDVQP-----ADRGDGLWTDPPYV-LTE-----VDGKLYGRGATDNK 167

Db 718 RPSKLALGRLGILSVSSFHALVCSRDDSSALRKRTLSTLQGRNKKGIFSSLKGLDTLARK 777

QY 168 G----PVLAWINAVSAFRALE-QDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVD 222

Db 778 GKEKRPSITQIFDSSGSHGFSGTQLPON-----SSNSSEVDELLH-----IYGSTVD 824

QY 223 YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGGILHEPMDLVAL--- 279

Db 825 G-VPRDNTWEIQ-----TY-----VHFQDNHGVTVGIKPEHRVEDILT LACK 865

QY 280 -----LGSLVDSSGHILVPG-----IYD--EVVPLTEEEINTYK----- 311

Db 866 MRQLEPSHYGLQLRKLVDNVEYCIPAPYEYMQQVYDEIEVFPNVDVQLTKTGSVCD 925

QY 312 ---AIHLDLEEYRNSSRVEKFLPDT-----KBEILMHLWRYPSLSIHGIEG 354

Db 926 FGFAVTAQVDERQHLSRI--FISDVLPDGLAYGEGELRKNGEIMTNGEAVSDLDLKQMEA 983

QY 355 AFDE-----PGTKTVI-----PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVF 398

Db 984 LFSEKSVGLTLIARPPDTKATICTSWSDSDLFSRDQKSLPPPN-----QSQ LLEEF LDNF 1039

QY 399 SKRNSNKM--VVSMTLGL 415

Db 1040 -KKN TANDFSNVPDIT TGL 1057

RESULT 776

AAR44929

ID AAR44929 standard; protein; 15281 AA.

XX AC AAR44929;

XX DT 16-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 08-JUL-1994 (first entry)

XX DE T. niveum Cyclosporin synthetase.

XX KW Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum;

XX KW T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase.

XX OS Tolypocladium inflatum.

XX PN EP578616-A2.

XX PD 12-JAN-1994.

XX PF 05-JUL-1993; 93EP-00810474.

XX PR 09-JUL-1992; 92AT-00001403.

XX PR 08-MAR-1993; 93AT-00000437.

XX PR 29-APR-1993; 93CH-00001310.

XX PR 04-MAY-1993; 93CH-00001375.

XX PA (SANO ) SANDOZ LTD.

XX PA (SANO ) SANDOZ PATENT GMBH.

XX PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX





XX	OS	Equine influenza virus H3N8.	KW	Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
XX	PN	WO200160849-A2.	XX	Listeria monocytogenes.
XX	PD	23-AUG-2001.	XX	WO200177335-A2.
XX	PF	16-FEB-2001; 2001WO-US005048.	XX	18-OCT-2001.
XX	PR	16-FEB-2000; 2000US-00506286.	PF	11-APR-2001; 2001WO-FR001118.
XX	XX	(UYPI-) UNIV PITTSBURGH.	XX	11-APR-2000; 2000FR-00004629.
XX	PI	Dowling PW, Youngner JS;	XX	(INSP ) INST PASTEUR.
XX	DR	WPI; 2001-522584/57.	XX	Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
DR	DR	N-PSDB; AAD15722.	PI	Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
XX	XX	Novel isolated equine influenza virus (wild-type and cold-adapted)	PI	Daniels J, Goebel W, Krefth J, Kuhn M, Ng E, Vazquez-Boland JA;
PT	PT	proteins and viruses containing nucleic acid molecules encoding the	PI	Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PT	PT	proteins, which are useful for protecting animals from influenza virus	PI	Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PT	PT	infections.	PI	Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
XX	XX		PI	Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PS	PS	Claim 5; Page 162-163; 172pp; English.	PI	Rose M, Voss H;
XX	XX	The patent discloses cold-adapted equine influenza viruses and	XX	WPI; 2002-010914/01.
CC	CC	reassortant influenza A viruses comprising atleast one genome segment of	XX	Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
CC	CC	such an equine influenza virus, wherein the equine influenza virus genome	PT	and prevention of Listeria and related bacterial infections, and related
CC	CC	segment confers atleast one identifying phenotype of the cold-adapted	PT	polypeptides.
CC	CC	equine influenza virus, such as cold adaptation, temperature sensitivity,	XX	Claim 6; SEQ ID NO 1516; 192pp; French.
CC	CC	dominant interference or attenuation. The viruses are useful for	PS	The present invention relates to the genome sequence of Listeria
CC	CC	protecting animals from diseases caused by influenza viruses. They are	XX	monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC	CC	also used as vaccines. The present sequence is equine influenza (ei)	CC	it are useful for selecting probes and primers for detecting genes in L.
CC	CC	virus H3N8 Peica2 (cold adapted) NP-N-245 protein which is encoded by	CC	monocytogenes and related organisms, and for studying genetic
CC	CC	neica2NP-N-735 DNA	CC	polymorphisms and other genomes. The present sequence is a protein
XX	XX		CC	encoded by the genome sequence of the present invention. Proteins
SQ	SQ	Sequence 245 AA;	CC	expressed from the genome sequence are useful for raising specific
		Query Match 3.4%; Score 88.5; DB 4; Length 245;	CC	antibodies, identification of L. monocytogenes and related organisms, and
		Best Local Similarity 20.8%; Pred. No. 26;	CC	for biosynthesis and biodegradation, especially biosynthesis of Vitamin
		Matches 60; Conservative 46; Mismatches 106; Indels 77; Gaps 15;	CC	B12. The genome sequence and proteins encoded by it are also useful for
QY	228	DNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSS 287	CC	selecting compounds that regulate gene expression and cell replication
Db	6	DNHSLSDIKIMASQGT-K-RSYEQMETDGERQN-----ATEIRASVGRMVVGI 51	CC	and modulate L. monocytogenes-related diseases. In addition, the genome
QY	288	GHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRRVEKFL---FDTKEEILMHLWRY 344	CC	sequence and proteins encoded by it are useful in pharmaceutical and
Db	52	GRFYVQ-----MCTELKLNDEG-----RLIQNSMTIERMVLSAFDERRN--KYLEEH 97	CC	vaccines compositions for the treatment or prevention of infections by L.
QY	345	PSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 404	CC	monocytogenes and related organisms. Note: The sequence data for this
Db	98	PS-----AGKDPKKTGGPIYRRKDGKWMRELILH-----DKEEIMR----IWRQANNG 141	CC	patent did not form part of the printed specification, but was obtained
QY	405	NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDM--IRDGSTIP----- 452	CC	in electronic format directly from WIPO at
Db	142	EDATAGLT-HMMIWHSNLNDTTYQRTALVRT--GMDPRMCSLMQGSTLPRRSGAAGAAV 198	CC	ftp.wipo.int/pub/published_pct_sequences
QY	453	--IAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLPAAF 499	XX	Sequence 396 AA;
Db	199	KGVGTMVMELIR---MIKRGINDR-----NFWRSENGRRTRIAY 234		Query Match 3.4%; Score 88.5; DB 5; Length 396;
				Best Local Similarity 19.7%; Pred. No. 56;
				Matches 85; Conservative 59; Mismatches 162; Indels 125; Gaps 18;
QY	107	SLPIPVILAEGLSDPTKGTVCFYGHL-DVQPADRGDGLTDPYV--LTEVDGKLYGRGA 163		
Db	40	ALPTIEYLLEQ-----NGKALFSLGKVKTEEDKEGSLRPVAVRLSELLGKEV-KFV 92		
QY	164	TDNKGVPVLAWINAVSAFRALEQDLPVNIKF-IIEGMEEAGSVALEELVEKEKDRFFSGVD 222		
Db	93	PTTRGPELE--KAIDELKDGEVLLFENTRFEDIDGKESKN-----DPELGKYWASLG 143		
QY	223	YIVISDNLMWISQRKPAITYGTRGN----SYFMVEVKCRDQDFHSGTGGILHEPMADLVA 278		
Db	144	DVFVNDAFGTAHRAHASNVGIASNLESAAGFLMEKEIK-----FIGGVVDNPARPLVA 196		
QY	279	LLG-----SLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRV 326		
Db	197	ILGGAQVSKIGVNIENLLTKADKVLVGG-----GMT 227		

QY 327 EKFLDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIP-GRVIGKFSIRLVPHMNVSA 385  
Db 228 FTFMAAQGEIGKSLLEADKVEL--AKGLLEKAGDKLVLPDVAVVSKEFSNDAPFHTVSA 285  
QY 386 -----VEKQVTRHLEDVFSKRNSSNMV-----SMTLGLHPWTIANIDD 424  
Db 286 DSIPADEMGLDIGQATIDLFTKELQCAKTVVWNGPMGVFELSNTFAKGTIGVCEAIANLTD 345  
QY 425 TQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 346 A-----TTIIG-----GGDSAAAAM-----DLGFADKFTTHISTGGG 376  
QY 485 NRWNYYIEGTKL 495  
Db 377 ASLEYLEGKEL 387

RESULT 780  
ABU32470  
ID ABU32470 standard; protein; 396 AA.  
XX AC ABU32470;  
DT 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #17997.  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Listeria monocytogenes.  
XX WO200277183-A2.  
PN 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA36340.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 60394; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 396 AA;

Query Match 3.4%; Score 88.5; DB 6; Length 396;  
Best Local Similarity 19.7%; Pred. No. 56;  
Matches 85; Conservative 59; Mismatches 162; Indels 125; Gaps 18;

QY 107 SLPIPPVILAEELGSDPTKGTVCFYGHL-DVQPADRGDWLTPYV--LTEVDGKLYGRGA 163  
Db 40 ALPTIEYILEQ-----NGKAILFSLGKVKTEEDKEGSLRPVAVRLSELLGKEV-KFV 92  
QY 164 TDNKGPPVLAWINAVSAFRALEQDLPVNIKF-IIEGMEEAGSVALEELVEKEKDRFFSGVD 222  
Db 93 PTTRGPELE--KAIDELKDGEVLLFENTRFEDIDGKESKN-----DPELGKYWASLG 143  
QY 223 YIVISDNLWISQRKPAITYGTRGN----SYFMVEVKCRDQDFHSGTGGILHEPMDLVA 278  
Db 144 DVFVNDAGFTAHRHASNVGSIASNLESAAGFLMEKEIK-----FIGGVVDNPARPLVA 196  
QY 279 LLG-----SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRV 326  
Db 197 ILGGAQVSDKIGVIENTLTAKDKVLVGG-----GMT 227  
QY 327 EKFLDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIP-GRVIGKFSIRLVPHMNVSA 385  
Db 228 FTFMAAQGEIGKSLLEADKVEL--AKGLLEKAGDKLVLPDVAVVSKEFSNDAPFHTVSA 285  
QY 386 -----VEKQVTRHLEDVFSKRNSSNMV-----SMTLGLHPWTIANIDD 424  
Db 286 DSIPADEMGLDIGQATIDLFTKELQCAKTVVWNGPMGVFELSNTFAKGTIGVCEAIANLTD 345  
QY 425 TQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 346 A-----TTIIG-----GGDSAAAAM-----DLGFADKFTTHISTGGG 376  
QY 485 NRWNYYIEGTKL 495  
Db 377 ASLEYLEGKEL 387

RESULT 781  
ADN18415  
ID ADN18415 standard; protein; 482 AA.  
XX AC ADN18415;  
XX 02-DEC-2004 (first entry)  
XX Bacterial polypeptide #1068.  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX

OS Bacteria.  
XX US2003233675-A1.  
PN 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
PF (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 1068; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transforming plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved lignin production and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 482 AA;  
  
Query Match 3.4%; Score 88.5; DB 8; Length 482;  
Best Local Similarity 20.2%; Pred. No. 76;  
Matches 77; Conservative 49; Mismatches 126; Indels 129; Gaps 18;  
  
Qy 157 KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSV-----ALEE 208  
Db 98 ELHRRGILDKYGIKLLGSN-----IRTIE--IAEDRELFAEAMAEINEPVTCKAVNSVDE 151  
Qy 209 LVEKEKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGI 268  
Db 152 AVE-----FAEEIGYPVIV-----RPAFTLG-----GTGGGI 178  
Qy 269 LHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEK 328  
Db 179 AHNK-----EELIDITSKGLKYSIINQV--LIDESVLGWKEFELEVMRDRKDTCI-- 226  
Qy 329 FLFDTKEEILMLWRYPYSLSIHGIEGAFDEPCTKTVIPGRVIGKF---SIRLVPHMNVS- 384  
Db 227 -----IVCGMENIDPMGIHTGESIVVSP--IQTLPDEFYQKLRNAAIKIIRHLGIEG 276

Qy 385 -----AVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWTIANIDDTQYLAAKRAI----- 434  
Db 277 GCNIQFAVNKEMTEYRVIEVNPVRSSALASKATG-YP-IARI-----AAKIAIGKTL 328  
Qy 435 -----RTVFGTEP-----DMIRDGSTIPIAKMFQE 459  
Db 329 DEILNDVTKETPASFEPTLDYVVVKIPRWPFDKFKTVDKKLGTSMKSTGEVMAIGRSFEE 388  
Qy 460 IVHKSVVLIPL---GAVDDGE 477  
Db 389 ALQKAIRSLDIGRFGIIGDGK 409  
  
RESULT 782  
ADN18857  
ID ADN18857 standard; protein; 500 AA.  
XX  
AC ADN18857;  
XX  
DT 02-DEC-2004 (first entry)  
DE Bacterial polypeptide #1510.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX US2003233675-A1.  
PN 18-DEC-2003.  
PD 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 1510; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transforming plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or





PR 14-FEB-2002; 2002US-0356937P.  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA Nakayama E, Ono T, Old LJ;  
XX WPI; 2003-075624/07.  
DR P-PSDB; ABT14648.  
XX New cancer-testis (CT) antigens, nucleic acids and encoded polypeptides,  
PT useful for diagnosing, monitoring or treating disorder or condition  
PT associated with the expression of human CT antigens, e.g. breast cancer  
PT or cervical cancer.  
XX Disclosure; Page 142-144; 165pp; English.  
PS The invention comprises the amino acid and coding sequences of human  
XX cancer-testis (CT) antigens that bind an HLA molecule. The CT antigens of  
CC the invention are useful for diagnosing, monitoring or treating cancer  
CC (e.g. breast cancer, colon cancer, cervical cancer or gastric cancer).  
CC The present sequence is a human cancer-testis (CT) antigen  
XX  
SQ Sequence 563 AA;  
Query Match 3.4%; Score 88.5; DB 6; Length 563;  
Best Local Similarity 20.3%; Pred. No. 96;  
Matches 72; Conservative 55; Mismatches 121; Indels 107; Gaps 19;  
QY 188 PVNIKFIEGMEEAGSVALE-----ELVEKEKDRFFSGVDYIVISDNLWISQRKPA 238  
Db 68 PATLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTQPVNAASFQKI-----IRQQFPQ 122  
QY 239 IT---YGTRGNS---YFMVEVKCRDQ--DFHSGTFGG-----ILHEPMAD 275  
Db 123 LTTRRLGTRGSKYHYGYIAVKESQYVDVMYSKKGAAWVSETGKKEVSKQTVAYSPRSK 182  
QY 276 LVALGSLVDSSGHILVPGIYDEVVP--LTEEEINTYKAHLDLEEYRNSR-----VEK 328  
Db 183 LGTLLPEF-----PNVKDLNLPASLPEEKVSTF-----IMMYRTHCQIRLDTVIR 227  
QY 329 FLFDTKEEILMHLWR-----YPSLSIHGIEGAFDE-----PGTKTVIPG- 367  
Db 228 ANFDEVQSFLHLFWQGMPPHMLPVLGSSSTVNVIVGCDSSILYKAISGLVLMPTVLQALPDS 287  
QY 368 --RVIGKFSIRL-----VPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVSMTLGL 415  
Db 288 LTQVIRKFAKQLDEWLKVALHDLPE-NLRNIKFELSRFRSQILRRQTSLNHLCOASRTVI 346  
QY 416 HPWIANIDDT-QYLAAKRAI-----RTVFGTEPDMIRDGSTITPIAKMFQEIIVH 462  
Db 347 H----SADITFQMLEDRNVLDNSITKQTLTYTMEDS--RDEHRKLITQLYQEFDH 395  
RESULT 785  
ABJ19253  
ID ABJ19253 standard; protein; 563 AA.  
XX ABJ19253;  
AC  
XX 28-MAR-2003 (first entry)  
DT Human cancer/testis antigen - SEQ ID No 33.  
XX Human; gene therapy; vaccine; cancer; cancer/testis antigen; CT antigen.  
XX Homo sapiens.  
OS  
XX WO200278526-A2.  
PN  
XX 10-OCT-2002.  
PD  
XX 29-MAR-2002; 2002WO-US009808.  
PF  
XX

PR 30-MAR-2001; 2001US-0280718P.  
PR 20-APR-2001; 2001US-0285154P.  
PR 05-OCT-2001; 2001US-0327432P.  
PR 22-JAN-2002; 2002US-00054683.  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (CORR ) CORNELL RES FOUND INC.  
XX Old LJ, Scanlan MJ, Chen Y;  
PI WPI; 2003-040608/03.  
XX N-PSDB; ABT15734.  
XX Diagnosing cancer comprises contacting a biological sample isolated from  
PT a subject with an agent that specifically binds to a nucleic acid  
PT molecule, its expression product or fragment or an antibody that binds to  
PT the product or fragment.  
XX Claim 40; Page 140-142; 155pp; English.  
PS The invention comprises a method for diagnosing cancer, the method  
XX involves detecting the DNA or protein sequences of human cancer/testis  
CC (CT) antigens that are disclosed in the invention. The method of the  
CC invention is useful for detecting/diagnosing, treating and monitoring a  
CC cancer or condition characterised by the expression of a human CT  
CC antigen. The present amino acid sequence represents a human CT antigen of  
CC the invention  
XX  
SQ Sequence 563 AA;  
Query Match 3.4%; Score 88.5; DB 6; Length 563;  
Best Local Similarity 20.3%; Pred. No. 96;  
Matches 72; Conservative 55; Mismatches 121; Indels 107; Gaps 19;  
QY 188 PVNIKFIEGMEEAGSVALE-----ELVEKEKDRFFSGVDYIVISDNLWISQRKPA 238  
Db 68 PATLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTQPVNAASFQKI-----IRQQFPQ 122  
QY 239 IT---YGTRGNS---YFMVEVKCRDQ--DFHSGTFGG-----ILHEPMAD 275  
Db 123 LTTRRLGTRGSKYHYGYIAVKESQYVDVMYSKKGAAWVSETGKKEVSKQTVAYSPRSK 182  
QY 276 LVALGSLVDSSGHILVPGIYDEVVP--LTEEEINTYKAHLDLEEYRNSR-----VEK 328  
Db 183 LGTLLPEF-----PNVKDLNLPASLPEEKVSTF-----IMMYRTHCQIRLDTVIR 227  
QY 329 FLFDTKEEILMHLWR-----YPSLSIHGIEGAFDE-----PGTKTVIPG- 367  
Db 228 ANFDEVQSFLHLFWQGMPPHMLPVLGSSSTVNVIVGCDSSILYKAISGLVLMPTVLQALPDS 287  
QY 368 --RVIGKFSIRL-----VPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVSMTLGL 415  
Db 288 LTQVIRKFAKQLDEWLKVALHDLPE-NLRNIKFELSRFRSQILRRQTSLNHLCOASRTVI 346  
QY 416 HPWIANIDDT-QYLAAKRAI-----RTVFGTEPDMIRDGSTITPIAKMFQEIIVH 462  
Db 347 H----SADITFQMLEDRNVLDNSITKQTLTYTMEDS--RDEHRKLITQLYQEFDH 395  
RESULT 786  
ADF18685  
ID ADF18685 standard; protein; 563 AA.  
XX ADF18685;  
AC  
XX 12-FEB-2004 (first entry)  
DT Human regulatory factor X 4 ( RFX4\_v2).  
XX Human; regulatory factor X 4; RFX4\_v2; hydrocephalus; cerebroprotective;  
KW gene therapy; transcription factor.  
XX  
OS Homo sapiens.







PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
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PR 18-OCT-1999; 99US-0159584P.

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PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160815P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match      3.4%; Score 88.5; DB 3; Length 617;
Best Local Similarity 18.6%; Pred. No. 1.1e+02;
Matches 60; Conservative 48; Mismatches 103; Indels 111; Gaps 13;

QY 134 DVQPADRGDGLTDPY-----VLTEVDGKLYGRGATDNKGPVLAWINAVSAFRA 182
Db 53 ELVPPEQGEGLLNSVPEISERGIPVDVSSVDG-----GGEENAFNIQEIDSVGGDAA 107

QY 183 LEQDLPVNIKFII-EGMEE---AGSVALBELVEKEK---DRF----- 217
Db 108 AVEEVLKSSSVGEGREEEAGASIVKEEDFVAEANLSGDRLEENKEVSMEEEPSSHEL 167

QY 218 ---FSGVDYIVISDNLWISQRKPAITYGTRGNSYF----- 249
Db 168 VCEVNGVDSLNDENREVGEQ---IVCGSMGGEIEIEDLESKKEKVDVIEEETTAQAASL 224

QY 250 -----MVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILV 292
Db 225 VNAIEIPDDKEVACVAGFTEISSQDKGLDESGNGLDEEPPVKEL-----QIGEGAKDLT 278

QY 293 PGYIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGI 352
Db 279 DGDAKEGVDVTEDE-----MDIQVLKKSKEEK--VDSTTELEIETMR---LEVHDV 325

QY 353 EGAFDEPGTKVIPGRVIGKFS 374
Db 326 A---TEMSDKTVISSAVVTQFT 344

RESULT 790
AAU37906
ID AAU37906 standard; protein; 623 AA.
XX
AC AAU37906;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #335.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
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PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS55765.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 13499; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 623 AA;

Query Match      3.4%; Score 88.5; DB 4; Length 623;
Best Local Similarity 19.6%; Pred. No. 1.1e+02;
Matches 111; Conservative 82; Mismatches 197; Indels 175; Gaps 28;

QY 35 LEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRFQELFRMMAVAADTLQRLGARVAS 94
Db 99 LIREYELIMLDYSEDKQARLERVMAEMDSLQ-----AWEIESQVKTVLSKLGIQDLS 150

QY 95 VDMGPOOLPDG--QSLPIPPVILAE---LGSDPKGTVCFYGHLDVQPADRGDWLT-- 146
Db 151 TPIG--ELSGGLRRRVQLAQVLLGNHDLILLDEPT-----NHLDAIAIE---WLTLF 197

QY 147 -----DPYVLTEVDGKLY---GRGATDNKG----- 168
Db 198 LKNSKKTVLFIETHRYFLDALSTRIFELDRAGLTEYQGNQDYVRLKAEQDERDAALLHK 257

QY 169 -----PVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEEL-VEKEKDRFFSGV 221
Db 258 KEQLYKQELAWMRROPQARATKQQARIN-RFHDLLKKKVSSSAETDLTMNFETSRI--GK 314

QY 222 DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFG--GILHEPMADLVAL 279
Db 315 KVIEFQAVSFAYENKPIL-----QDFNLLVQAKDR---IGIVGDNVGVKSTLLNLIA- 363

QY 280 LGSLLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLDFTKEEI-- 337
Db 364 -GSLEPTKGQWVI---GETVRIA-----YFSQQIEGLDESKRVINYLOEVAEEVKT 410

QY 338 -----LMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVE 387
Db 411 SGGSTTSIAELLEQLFPR-STHG-----TLIE-----KLSGGE 443

QY 388 KQVTRHLEDVFSKRN-----SSNKMVVSMTL-----GLHPWIANIDDTQYLAAKRA- 433
Db 433
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Db 444 KKRLYLLKLLLEKPNVLLLDDEPTNDLDIATLTVLENFLQFAGPVLTVSHDRYFLDKVAT 503  
QY 434 -----IRTVFGTEPDMIRDSG-TIPIAKMFQEIIVHKSVVLIPLGAVDDGSHSQNEK 483  
Db 504 KILAFEDGKIRPFPGHYTDYLDEKAFETDMANQVQKVEKEKVVKVR-----EDKKRMTYQE 559  
QY 484 INRWNYIEG-----TKLFAAFFLEM 503  
Db 560 KQEWASIEGDIETLEKRIAIAIEEM 584

RESULT 791  
ABU46161  
ID ABU46161 standard; protein; 623 AA.  
XX AC ABU46161;  
XX 19-JUN-2003 (first entry)  
DT Protein encoded by Prokaryotic essential gene #31698.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Streptococcus pneumoniae.  
XX WO200277183-A2.  
PN 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
PF 21-MAR-2001; 2001US-00815242.  
XX 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA50031.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 74085; 1766pp; English.  
PS The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 623 AA;

Query Match 3.4%; Score 88.5; DB 6; Length 623;  
Best Local Similarity 19.6%; Pred. No. 1.1e+02;  
Matches 111; Conservative 82; Mismatches 197; Indels 175; Gaps 28;  
QY 35 LEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVAS 94  
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QY 95 VDMGPQQLPDG--QSLPIPPVILAE----LGSDPTKGTVCFYGHLDVQPADRGDWLT-- 146  
Db 151 TPIG--ELSGGLRRRVQLAQVLLGNHDLILLDEPT-----NHLDAIIE----WLTLF 197  
QY 147 -----DPYVLTVEVDGKLY---GRGATDNKG----- 168  
Db 198 LKNSKKTVLFIHRYFLDALSTRIFELDRAGLTQYQGNQYDYVRLKAEQDERDAALLHK 257  
QY 169 -----PVLAWINAVSAFRALEQDLPVNIKFIIEGMBEAGSVALEEL-VEKEKDRFFSGV 221  
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QY 280 LGS�VDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKBEI-- 337  
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QY 338 -----LMHLWRYPVSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVE 387  
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Db 560 KQEWASIEGDIETLEKRIAIAIEEM 584

RESULT 792  
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ID AAG30568 standard; protein; 641 AA.  
XX AC AAG30568;  
XX 17-OCT-2000 (first entry)  
DT Arabidopsis thaliana protein fragment SEQ ID NO: 36568.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
XX

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PR	14-MAY-1999;	99US-0134219P.	PR	27-JUL-1999;	99US-0145913P.
PR	14-MAY-1999;	99US-0134370P.	PR	27-JUL-1999;	99US-0145918P.
PR	18-MAY-1999;	99US-0134768P.	PR	27-JUL-1999;	99US-0145919P.
PR	19-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-0135353P.	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
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PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
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PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
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PR	18-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.
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PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	21-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0151066P.
PR	22-JUN-1999;	99US-0139899P.	PR	27-AUG-1999;	99US-0151080P.
PR	23-JUN-1999;	99US-0140353P.	PR	30-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	99US-0140354P.	PR	31-AUG-1999;	99US-0151438P.
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PR	28-JUN-1999;	99US-0140823P.	PR	07-SEP-1999;	99US-0152363P.
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PR	30-JUN-1999;	99US-0141287P.	PR	13-SEP-1999;	99US-0153758P.
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PR	18-OCT-1999;	99US-0159584P.
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PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
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PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
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PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
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PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 3.4%; Score 88.5; DB 3; Length 641;		
Best Local Similarity 18.6%; Pred. No. 1.2e+02;		
Matches 60; Conservative 48; Mismatches 103; Indels 111; Gaps 13;		
QY	134 DVQPADRGDGLTDPY-----	182
Db	77 ELVPPEQEGALLNSVPEISERGIPVDVSSVDG-----	131
QY	183 LEQDLPVNIKFI-EGMEE---AGSVALEELVEKEK---DRF-----	217
Db	132 AVEEVPLKSSSVGEGREEAGASIVKEEDFVAEANLSGDRLEENKEVSMEEEPSSHEL	191
QY	218 ---FSGVDYIVISDNLWISQKPAITYGTRGNSYF-----	249
Db	192 VCEVNGVDSLNDENREVGREQ---IVCGSMGGEIEESDKKEKVDVIEEETTAQAASL	248
QY	250 -----MVEVKCRDQDFHSGTFCGILHEPMDLVALLGSLVDSSGHILV	292
Db	249 VNAIEIPDDKEVACVAGFTFESSQDKGLDESNGFLDEEPVKEL-----QIGEGAKDLT	302
QY	293 PGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLDTKEEILMHLWRYPSLSIHGI	352
Db	303 DGDAGEVDVTEDE-----MDIQVLKKSKEEK--VDSTTELEIETMR---LEVHDV	349
QY	353 EGAFDEPGTKTVIPGRVICKFS	374
Db	350 A---TEMSDKTVISSAVVTQFT	368

RESULT 793  
AAG30567  
ID AAG30567 standard; protein; 645 AA.

XX	AAG30567;	
AC	17-OCT-2000 (first entry)	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 36567.	
DT	Protein identification; signal transduction pathway; metabolic pathway;	
XX	hybridisation assay; genetic mapping; gene expression control; promoter;	
DE	termination sequence.	
XX	Arabidopsis thaliana.	
KW	EP1033405-A2.	
KW	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-00301439.	
PN	25-FEB-1999;	99US-0121825P.
XX	05-MAR-1999;	99US-0123180P.
PF	09-MAR-1999;	99US-0123548P.
XX	23-MAR-1999;	99US-0125788P.
XX	25-MAR-1999;	99US-0126264P.
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XX	28-MAY-1999;	99US-0136782P.
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XX	18-JUN-1999;	99US-0139461P.



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PR 23-AUG-1999; 99US-0149930P.

PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
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PR 04-OCT-1999; 99US-0157117P.  
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PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 3.4%; Score 88.5; DB 3; Length 645;  
Best Local Similarity 18.6%; Pred. No. 1.2e+02;  
Matches 60; Conservative 48; Mismatches 103; Indels 111; Gaps 13;

Qy 134 DVQPADRGDGLTDPY-----VLTEVDGKLYGRGATDNKGPVLAWINAVSAFRA 182  
Db 81 ELVPEQEGEALLNSVPEISERGI PVDVSVSDG-----GBENAAFNIQEIDS VGGDAA 135  
Qy 183 LEQDLPVNIKFI I-EGMEE---AGSVALEELVEKEK---DRF----- 217  
Db 136 AVEEVPLKSSSVVGE GREEEAGASIVKEEDFVAEANLSGDRLEENKEVSMEEEPSSSHEL S 195  
Qy 218 ---FSGVDYIVISDNLWISQRKPAITYGTRGNSYF----- 249  
Db 196 VCEVNGVDSLNDENREVGEQ---IVCGSMGEEIE S DLESKKEKVDVIEETTAQAASL 252  
Qy 250 -----MVEVKCRDQDFHSGTGGILHEPNADLVALLGSLVDSSGHILV 292  
Db 253 VNAIEIPDDKEVACVAGFTTEISSQDKGLDESGNGLDEEPPVKEL-----QIGEGAKDLT 306

QY 293 PGYDEVVPLTEEEINTYKAIHLDLEBYRNSSRVEKFLDTEKBEILMHLWRYPSLSIHGI 352  
| | | | | : | | | | : | | | | : | | | | :  
Db 307 DGAKEGVDTVEDE-----MDIQVLKKSKEEK--VDSTTELEIETMR---LEVHNV 353

QY 353 EGAFDEPGTKTVIPGRVIGKPS 374  
| | | | | : | | : | | :  
Db 354 A---TEMSDKTVISSAVVTQFT 372

RESULT 794  
AAU54939  
ID AAU54939 standard; protein; 718 AA.  
XX  
AC AAU54939;  
XX  
DT 27-FEB-2002 (first entry)  
XX  
DE Propionibacterium acnes immunogenic protein #15835.  
XX  
DE SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.  
XX  
OS Propionibacterium acnes.  
XX  
PN WO200181581-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 20-APR-2001; 2001WO-US012865.  
XX  
PR 21-APR-2000; 2000US-0199047P.  
PR 02-JUN-2000; 2000US-0208841P.  
PR 07-JUL-2000; 2000US-0216747P.  
XX  
XX (CORI-) CORIXA CORP.  
PA  
PA Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX  
DR WPI; 2001-616774/71.  
DR N-PSDB; AAS59567.  
XX  
PT Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris.  
XX  
PS Example 1; SEQ ID NO 16134; 1069pp; English.  
XX

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 718 AA;

Query Match 3.4%; Score 88.5; DB 4; Length 718;  
Best Local Similarity 19.1%; Pred. No. 1.4e+02;  
Matches 74; Conservative 55; Mismatches 121; Indels 137; Gaps 15;

QY 2 DPKLGRMAASLLAVLL---LLLRGMFSSPS--PPPALLEKVF-----QYIDLHQDE--- 48  
| | | | | : | | | | : | | | | : | | | | :  
Db 216 DPEVARPIAGELIDAGADYDIVHGGFGSPTKFPMPFTLLDALLVKGDPTSLDMAQNTCEH 275

QY 49 -----FVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMG---- 98  
| | | | | : | | | | : | | | | : | | | | :  
Db 276 LVRGGIFDQVGGGFHRYSTDSQWVVPHFEEKLYDNALLLA-TMARCWRRRTADHDSRRDL 334

QY 99 -----PQQLPDG-----QS 107  
| | | | | : | | | | : | | | | : | | | | :  
Db 335 YSHAARTTVAWLNREMLPGLYAAAGLDADSDDAAGHTEGIYYLWNQDLITDALGTDEA 394

QY 108 LPIPPVILAEELGSDPTKGTVCIFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRG----- 162  
| | | | | : | | | | : | | | | : | | | | :  
Db 395 EWLRLPLVHLEPCNDNGLGTLQLRGRVE-----W---ERINADMDTLLEARGRRSAP 442

QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALE-ELVEKEKDRFFSGV 221  
| | | | | : | | | | : | | | | : | | | | :  
Db 443 ARDEK-----AITAWNAM-----LIDGLVEAGMILREWSWVEQARE----- 478

QY 222 DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGG----- 267  
| | | | | : | | | | : | | | | : | | | | :  
Db 479 ----LADSLWTAHWDHGMALRTSFQDRPGVPVAVCEDYAWVALSFAGLAGATGESVWLDHA 534

QY 268 --ILHEPMADLVALLGSLVDSSGHILV 292  
| | | | | : | | | | : | | | | : | | | | :  
Db 535 VEVLGEAVARFSAVDGSFLDAEDSFLL 561

RESULT 795  
ABM51458  
ID ABM51458 standard; protein; 718 AA.  
XX  
AC ABM51458;  
XX  
DT 20-OCT-2003 (first entry)  
XX  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16134.  
XX  
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
KW immunostimulant; immune response; vaccine.  
XX  
OS Propionibacterium acnes.  
XX  
PN WO2003033515-A1.  
XX  
PD 24-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032727.  
XX  
PR 15-OCT-2001; 2001US-00978825.  
XX  
PA (CORI-) CORIXA CORP.  
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
PI Barth B, Vallieve-Douglas J;  
XX  
XX WPI; 2003-381789/36.  
DR N-PSDB; ACF64496.  
XX  
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the  
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
PT or for stimulating an immune response specific for a P. acnes protein.  
XX  
PS Example 1; SEQ ID NO 16134; 1481pp; English.  
XX  
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

CC encoding a Propionibacterium acnes protein. The invention also relates to  
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
CC immunogenic fragments of P. acnes polypeptides. The invention  
CC additionally encompasses expression, antibodies against polypeptides of the  
CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a  
CC invention; fusion proteins comprising a polypeptide of the invention; a  
CC method for stimulating an immune response specific for a P. acnes  
CC polypeptide and an isolated T cell population comprising T cells prepared  
CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
CC antigen-presenting cells that express the polypeptide); a method and kit  
CC for detecting or determining the presence or absence of P. acnes in a  
CC patient; and a method for inhibiting the development of P. acnes in a  
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations or antigen-presenting cells that express the  
CC polypeptides are useful for diagnosing, preventing or treating acne  
CC vulgaris, or for stimulating an immune response specific for a P. acnes  
CC protein. The polynucleotides can also be used as probes or primers for  
CC nucleic acid hybridisation. The vaccine composition is useful for the  
CC stimulation of an immune response against P. acnes, or for treating acne,  
CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence represents a polypeptide predicted to be encoded by an ORF (open  
CC reading frame) contained within the P. acnes polynucleotides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 718 AA;

Query Match 3.4%; Score 88.5; DB 6; Length 718;  
Best Local Similarity 19.1%; Pred. No. 1.4e+02;  
Matches 74; Conservative 55; Mismatches 121; Indels 137; Gaps 15;  
QY 2 DPKLGRMAASLLAVLL---LLLERGMFSSPS--PPPALLEKF-----QYIDLHQDE--- 48  
Db 216 DPEVARPIAGELIDAVGADYDIVHGGFSPTKFPMPPTLLDALLVKGDPTSLDMAQNTCEH 275  
QY 49 -----FVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLORLGARVASVDMG---- 98  
Db 276 LVRRGIFDQVGGFHRYSTDSQWVVRPEKMLYDNALLLA-TWRCWRRTADHDSRRDL 334  
QY 99 -----PQQLPDG-----PQQLPDG-----PQQLPDG-----PQQLPDG----- 107  
Db 335 YSHAARTTVAWLNREMLPNGLYAAGLDADSDDAAGHTHEGIYVLWNQDLITDALGTDEA 394  
QY 108 LPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRG----- 162  
Db 395 EWLRLPLVHLEPCNDNGLGTLQLRGRVE-----W---ERINADMDTLLLEARGRRSAP 442  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLFPVNIKFIIEGMEEAGSVALE-ELVEKEKDRFFSGV 221  
Db 443 ARDEK-----AITAWNAM-----LIDGLVEAGMILREWSWVEQARE----- 478  
QY 222 DYIVISDNLWISQKPKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGG----- 267  
Db 479 ----LADSLWTAHWDHGMALRTSFQDRPGVPACVEDYAWVALSFAGLAGATGESVWLDHA 534  
QY 268 --ILHEPMADLVALLGSLVDSSGHILV 292  
Db 535 VEVLGEAVARFSAVDGSFLDAEDSFLL 561

RESULT 796  
ADF18691  
ID ADF18691 standard; protein; 735 AA.  
XX  
AC ADF18691;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human regulatory factor X 4 ( RFX4\_v3 ).  
XX  
KW Human; regulatory factor X 4; RFX4\_v3; hydrocephalus; cerebroprotective;

gene therapy; transcription factor.  
XX Homo sapiens.  
OS  
XX WO2003088919-A2.  
XX  
PD 30-OCT-2003.  
XX  
PF 18-APR-2003; 2003WO-US012348.  
XX  
PR 19-APR-2002; 2002US-0374184P.  
PR 13-JUN-2002; 2002US-0388266P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Blackshear PJ, Zeldin DC, Graves JP, Stumpo DJ;  
XX  
DR WPI; 2003-854031/79.  
DR N-PSDB; ADF18690.  
XX  
PT New RFX4v3 polypeptide, useful in preparing a composition for diagnosing  
or treating congenital hydrocephalus.  
XX  
PS Claim 2; SEQ ID NO 8; 76pp; English.  
XX  
CC The present sequence is the protein sequence of human RFX4\_v3, a novel  
splice variant of the regulatory factor X 4 (RFX4) member of the winged  
helix transcription factor family. The human RFX4\_v3 polypeptide ADF18691  
inhibits the phenotypic expression of congenital hydrocephalus. When one  
allele is defective, there is universal congenital hydrocephalus with  
aqueductal stenosis, probably secondary to agenesis of the subcommissural  
organ. The defect appears to be compatible with life, and in some cases  
normal fertility. This hydrocephalus exhibits an autosomal dominant  
inheritance pattern. When 2 alleles are defective, there is severe  
disruption of brain formation and prenatal or perinatal death. The  
RFX4\_v3 transcript is novel in that it contains a mixture of exons from 2  
previously identified transcripts as well as a completely novel exon that  
encodes the N-terminus of the protein. The invention provides human,  
mouse and zebrafish RFX4\_v3 proteins and nucleic acids, as well as  
transgenic animals with altered RFX4\_v3 genes, and assays for the  
detection of RFX4\_v3 and RFX4\_v3 polymorphisms associated with disease  
states. Also provided are methods of determining a subject's risk of  
developing congenital hydrocephalus, methods of screening for drugs that  
inhibit or potentiate RFX4\_v3 action, and methods of using RFX4\_v3  
nucleic acid or polypeptide to treat congenital hydrocephalus.  
XX  
SQ Sequence 735 AA;

Query Match 3.4%; Score 88.5; DB 7; Length 735;  
Best Local Similarity 20.3%; Pred. No. 1.5e+02;  
Matches 72; Conservative 55; Mismatches 121; Indels 107; Gaps 19;  
QY 188 PVNIKFIIEGMEEAGSVALE-----ELVEKEKDRFSGVDYIVISDNLWISQKPA 238  
Db 59 PATLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTQPVNAASFGKI-----IRQQFPQ 113  
QY 239 IT---YGTRGNS---YFMVEVKCRDQ--DFHSGTFGG-----ILHEPMAD 275  
Db 114 LTTRRLGTRGQSKYHYGIAVKESQYDYVMYSKGAANVSETGKKEVSKQTVAYSRPSK 173  
QY 276 LVALLGSLVDSSGHILVPGIYDEVVP--LTEEEINTYKAHLDL EEYRNSR-----VEK 328  
Db 174 LGTLLPEF-----PNVKDLNLPASLPEEKVSTF-----IMMYRTHCQIRLDTVIR 218  
QY 329 FLFDTKKEILMHLWR-----YPSLSIHGIEGAFDE-----PGTKTVIPG- 367  
Db 219 ANFEVQSFLHFWQGMPPHMLPVLGSSTVNIVGVCDLSILYKAISGLVLMPTVLQALPDS 278  
QY 368 --RVICKFSIRL-----VPHMNVSAREKQVTRHLEDVFSKRNSSNKMVMSMTLGL 415  
Db 279 LTQVIRKFAQLDEWLKVALHDLPE-NLRNIKFELSRRESQILRRQTSNLHLCQASRTVI 337  
QY 416 HPWIANIDDT-QYLAAKRAI-----RTVFGTEPDMIRDGSTITPIAKMFQEIIVH 462





CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX  
SQ Sequence 873 AA;

Query Match 3.4%; Score 88.5; DB 8; Length 873;  
Best Local Similarity 21.6%; Pred. No. 1.9e+02;  
Matches 90; Conservative 58; Mismatches 169; Indels 99; Gaps 19;

Qy 31 PPALLEKVFQYIDLHQ-----DEFVQTLKEWVAIESDSVQPVPRFRQELFRM 77  
Db 69 PPARGDQLFIGEDLEQLLETADQVRGWGDRSIDVPQLIVAVGAD-----PRIGAELEFAA 123

Qy 78 MAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEAGSDPTKGTVCFYGHLDVQP 137  
Db 124 QGLAVDRLESLLRQPSVSPAPAP-----PPVPTAASAPAPTPTRSA-----P 164

Qy 138 ADRGDGWLTDPPYVLTEVDG---KLYGRGATD-----NKGPVLA---WINAVSAFRALEQ 185  
Db 165 APRVMAPEPEPMVELEREPSALEAYGRDLTEEAEGSLDPVIGRDSIRNLIKVLSRRSK 224

Qy 186 DLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNL-----WISQRKPAITY 241  
Db 225 NNPVLI-----GEPGVGKTAIAELLAQ---RIVAG----EVPDSLQGLRLIALDLGALIA 272

Qy 242 GTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVLALLGSLVDS--SGHILVPGIYDEV 299  
Db 273 GAKFRGQFEERLRSVLEEVSRSDSGVVLFF--IDELHTVVGSDRSSTDAGSLKPA----- 325

Qy 300 VPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSI----- 349  
Db 326 --LARGDLRCIGA--TTPEEYRRITVEKDPALNRRFQQVLI---REPDLELSLEILRLGLRE 378

Qy 350 -----HGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK 400  
Db 379 RYELHHGVITITDEAIOQTANRLADRYI---SDRCLPDKAIDLIDEEAAQKIEVTSK 431

RESULT 799  
ABM72914  
ID ABM72914 standard; protein; 901 AA.  
XX  
AC ABM72914;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
DE Staphylococcus aureus protein #2154.  
XX  
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;  
KW enzymatic assay; antibiotic target.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200294868-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 27-MAR-2002; 2002WO-IB002637.

PR 27-MAR-2001; 2001GB-00007661.  
XX (CHIR-) CHIRON SPA.  
XX Masignani V, Mora M, Scarselli M;  
PI WPI; 2003-120786/11.  
XX N-PSDB; ACF74474.  
DR  
XX New Staphylococcus aureus protein, useful as a vaccine for treating or  
PT preventing Staphylococcal infection, specifically an infection caused by  
PT S. aureus, e.g. sepsis.  
XX  
PS Claim 1; SEQ ID NO 4308; 49pp; English.  
XX  
CC The invention relates to novel genes and encoded proteins from  
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a  
CC nucleic acid encoding the protein, or an antibody to the protein, is  
CC useful as a pharmaceutical, particularly as a vaccine for treating or  
CC preventing infection due to Staphylococcus bacteria, specifically an  
CC infection caused by S. aureus. The composition is particularly useful for  
CC treating or preventing sepsis in a patient. The composition can also be  
CC used for diagnostics. The protein is also used in an assay for enzymatic  
CC studies and as a target for antibiotics. This sequence represents one of  
CC the novel S. aureus proteins of the invention  
XX  
SQ Sequence 901 AA;

Query Match 3.4%; Score 88.5; DB 6; Length 901;  
Best Local Similarity 20.2%; Pred. No. 2e+02;  
Matches 77; Conservative 63; Mismatches 153; Indels 89; Gaps 21;

Qy 143 GWLTD---PYVLTEVDGKLYGRGAT---DNKGPVLAWINAVSAFRALEQDLPVNIKFII 195  
Db 486 GYLDRDAGLQPY-LDDLGFNLVGYGCTTCIGNSGPLLPPEIEKAIA---DEDLLVT--SVL 538

Qy 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255  
Db 539 SG-----NRNFEGRIHPLVKAN-YLASPQLVVAALAGT-----VDIDL 576

Qy 256 RDQDFHSGTGGILHEPMDLVLALLGSLVDSGGHILVPGIYDEWVPLTEEEINTYKAHL 315  
Db 577 QNEPIGKNGDGEDVY--LKDIWPSIKEVSDTVDSVVTPELF-----IEEYNNVYN 624

Qy 316 DLEEYRNSRVEKFL--FDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPG-RVIGK 372  
Db 625 NNELWNEIDVTDQPLYDFDNPSTYIQN---PSF---FQGLSKEPGTIVPLNGLRVMGK 676

Qy 373 FSIRL-VPHMN-VSAVEKQVT--RHLED-----VFSKRNSNKMVVSMTLGLHPWI 419  
Db 677 FGDSVTTDHI SPAGAIGKDTPACKYLDHQVPIREFNSYCSRRGNHEVMVRGT-----F 730

Qy 420 ANIDDTQYLAAKRAIRTVFGTEPDMIR---DGSTIPIAKMFQEI VHKSVLIPLGAVDG 476  
Db 731 ANIRIKNQLAP-----GTEGGFTTYWPTNEVMPIFDAAMKYKEDGTGLVVLAGNDYG 782

Qy 477 EHSQNEKINRWNYIEGTKLFAA 498  
Db 783 MGSSRDWAAGTNLLGVKTVIA 804

RESULT 800  
AAG70871  
ID AAG70871 standard; protein; 1072 AA.  
XX  
AC AAG70871;  
XX  
DT 27-JUL-2001 (first entry)  
XX  
DE C albicans apoptosis associated protein #51.  
XX  
KW Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;  
KW autoimmune disease; ischaemia; neurodegeneration.





Db 683 DMAQVFPSTSTPDNFTSEAAVLPSFARGDASDISHPLSGSVVDTKAYVAALKEDSQWAE 742

Qy 209 -----LVEKEKDRFFSGVDYIVISDNLWISQRKPAI-----TYGTR 244

Db 743 ARLAYVALTRAKER-----LVVSWHQWRPRRKSGSLGPRGYADLLADMLGTVMWPDFGER 795

Qy 245 GNSYFVMEVKCRDQDFHSGTFCGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTE 304

Db 796 -----PDDDIQAGTPWPVFAKDVGH-----GLIDNTRSVDPPGQADRV----- 834

Qy 305 EEINTYKAIHLDL EYRNSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTV 364

Db 835 -----KAWRTDADTLLKDARRH-----IDLQDEV-----A 859

Qy 365 IPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSMTLGLHPW----- 418

Db 860 LPRLTTSQIVRL--HANPOAFRDDLRPMRPPADRG-----AGIGTAFHEWVSQRLA 910

Qy 419 -----IANIDD---TOYLA-----KRAIRTVFGTEPDMIRDGSTI-PIAK 455

Db 911 PAEPIPLFDAEEIAELDEESITQEAVAVEPSPGAENRALRSLCQAFESRWAGATVLAVEK 970

Qy 456 MFQEIYVHKSVMVLIPLGA-VDDGHSQNEKINRW 487

Db 971 SFVMTIGQTVVRGRLDVAVADPHFGDELVIDW 1003

RESULT 802

AAU02957

ID AAU02957 standard; protein; 1249 AA.

XX

AC AAU02957;

XX

DT 12-SEP-2001 (first entry)

XX

DE Angiotensin converting enzyme (ACEV) splice variant protein #57.

XX

KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;

KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;

KW platelet-derived endothelial cell growth factor; cardiovascular disease;

KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;

KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;

KW myocardial infarction; coronary arterial thrombosis; renal disease;

KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;

KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;

KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;

KW vascular disorder; asbestosis.

XX

OS Mus sp.

XX

XX WO200136632-A2.

XX

XX 25-MAY-2001.

XX

XX 17-NOV-2000; 2000WO-IL000766.

XX

XX 17-NOV-1999; 99IL-00132978.

PR

PR 10-DEC-1999; 99IL-00133455.

XX

XX (COMP-) COMPUGEN LTD.

PA

XX

XX Levine 2, David A, Azar I, Khosravi R, Bernstein J;

PI

XX

XX WPI; 2001-336004/35.

DR

DR N-PSDB; AAS06057.

XX

XX Novel alternative splicing variants e.g. variant of angiotensin

PT converting enzyme (ACEV), useful in identifying candidate compounds

PT capable of binding to the variant and to detect anti-variant antibodies.

XX

XX Claim 4; Fig 57; 519pp; English.

PS

XX The sequence represents an angiotensin converting enzyme splice variant

CC

CC (ACEV) polypeptide. The polypeptides of the invention include variants of

CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,

CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase

CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal

CC polypeptide receptor 2. The polypeptides and their associated nucleic

CC acids are useful for identification of variant sequences and detection of

CC candidate compounds capable of binding the molecules. The sequences of

CC the invention can be used in the treatment and diagnosis of various

CC disorders including cardiovascular diseases such as arteriosclerosis,

CC myocardial infarction and coronary arterial thrombosis, renal diseases

CC such as diabetic nephropathy, muscular diseases such as hypertrophy,

CC immune disorders such as immune complex nephritis, multiple sclerosis,

CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such

CC as asbestosis and vascular pathologies involving an endothelial

CC abnormality such as deep vein thrombosis

XX

SQ Sequence 1249 AA;

Query Match 3.4%; Score 88.5; DB 4; Length 1249;

Best Local Similarity 20.1%; Pred. No. 3.3e+02;

Matches 86; Conservative 62; Mismatches 181; Indels 99; Gaps 22;

Qy 56 WVAI-ESDSV-QPVPRFRQEL---FRMMAVAADTLQR-LGARVASVDMGPQQLPDGQSL 108

Db 830 WRSLYESDNLEQDLEKLYQELQPLLYNLHAYVRRSLRHVGSEYINLDG----- 878

Qy 109 PIPPVILAEELGSDPTKGTVCFYG-----HLDVQPADRGDGLTDPYVLTEVDGKLYGRG 162

Db 879 PIPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGW-TPRRIFKEADNFTSLG 937

Qy 163 ATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVD 222

Db 938 L-----LPVPPEFWNKSMLKPTDGREVVCHPSAWDFYNGKD 974

Qy 223 YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGS 282

Db 975 F-RIKQCTSVNMEDLVIAHEMGMHIQYFMQYKOLPVTTFREGANPG-FHEAIGDIMAL--- 1029

Qy 283 LVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD-----LEEYRNSRVEKEFLFD 332

Db 1030 SVSTPKHLYSLNLLSTEGSGYEYDINFLMKMALDKIAFIPPSYILIDQWRWR-----VFD 1083

Qy 333 ---TKEEILMHLW---RYPSL--SIHGIEGAFDEPGTKVIPG-----RVIGKFSIRLV 378

Db 1084 GSITKENYNQEWWSLRLYKQGLCPPVPRSQGDFD-PGSKFHV PANVPYRVYFVSFIQFQ 1142

Qy 379 PHNVV-SAVEKQVTRHLEDVFSKRNSNMVSMVMTLGL-HPWIANIDDTQYLAAKRAIRT 436

Db 1143 FHEALCRAAGHTGPLHKCDIYQSKEAGKLLADAMKLGSKPW-----PEAMKL 1190

Qy 437 VFGTEPDM 444

Db 1191 ITG-QPNM 1197

RESULT 803

AAU02985

ID AAU02985 standard; protein; 1252 AA.

XX

AC AAU02985;

XX

XX 12-SEP-2001 (first entry)

DT

XX

DE Angiotensin converting enzyme (ACEV) splice variant protein #85.

XX

KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;

KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;

KW platelet-derived endothelial cell growth factor; cardiovascular disease;

KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;

KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;

KW myocardial infarction; coronary arterial thrombosis; renal disease;

KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;

KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;

KW





for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)



QY	50	VQTLKEWVAIESD---SVQPVPRFRQELFRMMMAVAADTLQRLGARVASVDMGPPQQLPDGQ	108
Db	321	WQGLQCSLQGEDLLIGEVSQLOAFLQDLDDDFQAWLSITOK-----AVASEDM-PESLPEAE	375
QY	107	SLPIPPVILAEELGSDPTKGTVCIFYGHLDVQPADRGDGLWLTDPYVLTVEVGKLYGRGATDN	166
Db	376	QL-----LQQHAGIK--DEIDGH-QDSYQVRVKEGSEKVIQQTDP	412
QY	167	KGPVLA-----W-----INAVSAFALEQD-----LPVNIKFIIEGM	198
Db	413	EYLLLGORLEGLDTGWDALGRMWESRSHTLAOCLGFQFQKDAKQAEAILSNQEYTLAHL	472
QY	199	E-----EAGSVALEEL---VEKEKDRFFSGVD---YIVISDNLWISQRKPAITYGTR	244
Db	473	EPPDSLEAAEAGIRKFEDFLGSMENNRDKVLSPVDSGNKLVAEGLNYSDKIKEKVQ----	528
QY	245	GNSYFMVEVKCRDQDFHSGTGGILHEPM-----ADLVALLGSLVDSGSHILVPGI	295
Db	529	-----LIEDRHRKNNEKAQEAASVLLRDNLELQNLQNCQELTLWINDKLLTSQDV----S	579
QY	296	YDEVVPLTEEEINTYKAIHLDEEY-----RNSSRVEKFLEDTKEEILMHLWRYPSLSIHG	351
Db	580	YDEARNLHNKWLK-HQAFVAELASHEGWLENI DAEGKQLMDEKXPQTALV----SQKLEA	634
QY	352	IEGAFDEPGTKTVIPGRVIG---KFSIRLVPHMN-----VSAVEKQVTRHLEDVFSKRNS	404
Db	635	LHRLWDELQATTKEKTQHLSAARSSDLRLQTHADLNKWSAMEDQL--RSDDPGKDLTSV	692
QY	405	NKVVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDG--STIPIAKMFQEI VH	462
Db	693	NRMLAK-----LKRVED-QVNVVRKEELGELFAQVPSMGEEGDADLSIEKRFLDL--	741
QY	463	KSVVLIPLGAVDGDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQ	505
Db	742	-----LEPLGRRKKQLESSRAKLIQSRDLEDETLMWVEERLPLAQ	780

**RESULT 806**

ADI39480  
ADI39480 standard; protein; 1648 AA.  
ADI39480;  
22-APR-2004 (first entry)  
Arabidopsis thaliana DIM1 interacting molecule 7=40 (DIMIC7=40) protein.  
DIM1-interacting molecule; DIMIC; agriculture; plant yield;  
phytopharmaceuticals; screening assay; predictive medicine; diagnosis;  
clinical trial; phytotherapeutic; transcriptomics; proteomics;  
metabolomics; ligandomics; pharmacogenetics; pharmacogenomics.  
Arabidopsis thaliana.  
WO200253589-A2.  
11-JUL-2002.  
07-JAN-2002; 2002WO-EP000073.  
05-JAN-2001; 2001US-0259890P.  
(CROP-) CROPDESIGN NV.  
De Veylder L, Boudolf VKCK, Inze D, Frankard VM, Terras F;  
WPI; 2002-583602/62.  
N-PSDB; ADI39469.  
Isolated nucleic acid encoding DIM1-interacting molecule, which is useful  
for modulating the growth or cell cycle of plant, enhancing overall  
growth and yield of a plant, and modulating pre-mRNA splicing in a plant  
cell.

RESULT 807  
AAG50492  
ID AAG50492 standard; protein; 1752 AA.  
XX  
AC AAG50492;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63995.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
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KW	vascular endothelial growth factor; VEGF-stimulated proliferation;	PR	22-JUN-1998;	98US-0090254P.
KW	endothelial cell; T-lymphocyte proliferation; retinal neuron;	PR	23-JUN-1998;	98US-0090349P.
KW	rod photoreceptor cell; c-fos induction; adipocyte cell;	PR	23-JUN-1998;	98US-0090355P.
KW	chondrocyte differentiation;	PR	24-JUN-1998;	98US-0090429P.
KW	pancreatic beta-cell precursor differentiation;	PR	24-JUN-1998;	98US-0090431P.
KW	cardiac insufficiency disorder; wound; cancerous tumour;	PR	24-JUN-1998;	98US-0090435P.
KW	retinal disorders; loss of sight; retinitis pigmentosum; kidney disorder;	PR	24-JUN-1998;	98US-0090444P.
KW	obesity; diabetes; hyperinsulinaemia; hypoinsulinaemia; bone disorder;	PR	24-JUN-1998;	98US-0090445P.
KW	cartilage disorder; sports injury; arthritis; cancer; human.	PR	24-JUN-1998;	98US-0090472P.
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XX		PR	24-JUN-1998;	98US-0090542P.
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PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
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QY	250	-----MVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVSDSGHILV	292
Db	225	VNAIEIPDDKEVACVAGFTEISSQDKGLDESGNGFLDEEPVKEL-----QIGEGAKDLT	278
QY	293	PGIYDEVVPLTEEEINTYKAIHLDLSEYRNSRRVSKFLFDTKKEILMHLWRYPSSLIHGI	352
Db	279	DGDAKEGVDVTEDE-----MDIQVLKKSKEEK--VDSTTELEIETMR---LEVH	325
QY	353	EGAFDEPGTKTIPGRVIGKFS	374
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RESULT 808

ABR41636

ID ABR41636 standard; protein; 2141 AA.

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AC ABR41636;

XX

DT 02-JUN-2003 (first entry)

XX

DE Human DITHP cytoskeletal protein.

XX

KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
cancer; cell proliferative disorder; autoimmune disorder;  
inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
neurological disorder; gastrointestinal disorder; transport disorder;  
connective tissue disorder; drug screening; proteome analysis;  
gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
disease model; toxicological testing; transcript imaging;  
cytoskeletal protein.

OS Homo sapiens.

XX

PN WO200297031-A2.

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PD 05-DEC-2002.

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PF 27-MAR-2002; 2002WO-US010056.

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PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

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DR WPI; 2003-129518/12.

DR N-PSDB; ACC46573.

XX

PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
PT test compound which specifically binds to a polypeptide encoded by human  
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.

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PS Claim 27; SEQ ID NO 1171; 591pp; English.

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CC The invention relates to novel human diagnostic and therapeutic  
polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
proteins (DITHP; ABR41136-ABR41812). The invention also relates to  
polynucleotide sequences at least 90% identical to the dithp cDNA

CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
CC detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a DITHP protein which is a cytoskeletal  
CC protein. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence.2141 AA;

Query Match 3.4%; Score 88.5; DB 6; Length 2141;  
Best Local Similarity 19.6%; Pred. No. 7.6e+02;  
Matches 114; Conservative 92; Mismatches 232; Indels 145; Gaps 27;

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Db 1102 QL-----LQQHAGIK--DEIDGH-QDSYQVRKESGEKVIQQTDP 1138  
QY 167 KGPVLA-----W-----INAVSAFALEQD-----LPVNIKFIIEGM 198  
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Db 1255 -----LIEDHRKNNEKAQEAASVLLRDNLELQNLQNCQELTLWINDKLLTSQDV----S 1305  
QY 296 YDEVVPLTEEEINTYKAIHLDLEEY----RNSSRVEKFLFDTKEEILMHLWRYPSLSIHG 351  
Db 1306 YDEARNLHNKWLK-HQAFVAELASHEGWLENIDAEGKQLMDEKQPQTALV---SQKLEA 1360  
QY 352 IEGAFDEPGTKTIPGRVIG---KFSIRLVPHMN---VSAVEKQVTRHLEDVFSKRNSS 404  
Db 1361 LHRLWDELQATTKEKTQHLSAARSSDLRLQTHADLNKWKISAMEDQL--RSDDPGKDLTSV 1418  
QY 405 NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDG--STIPIAKMFQEIIVH 462  
Db 1419 NRMLAK-----LKRVED-QVNVKREELGELFAQVPSMGEEGGDADLSIEKRFLDL-- 1467  
QY 463 KSVLPIPLGAVDDGEHSQNEKINRWNYTEGTKLFAAFLEMAQ 505  
Db 1468 ----LEPLGRRKQLESRAKLQISRDELEDTLWVEERLPLAQ 1506

RESULT 809  
ADG42624  
ID ADG42624 standard; protein; 2991 AA.  
XX  
AC ADG42624;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human FAT tumour supressor 2 precursor #2.  
XX  
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;  
KW NOVX-associated disorder; cancer; human;  
KW FAT tumour supressor 2 precursor.  
XX  
OS Homo sapiens.  
XX  
PN US2003204052-A1.  
XX  
PD 30-OCT-2003.  
XX  
PF 04-OCT-2001; 2001US-00970944.  
XX  
PR 04-OCT-2000; 2000US-0237862P.  
XX  
PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
XX  
PI Herrmann JL, Rastelli L, Shimkets RA;  
XX  
DR WPI; 2003-900673/82.  
XX  
PT New NOVX gene or NOVX-specific antibody, useful for preparing a  
PT composition for treating or preventing a NOVX-associated disorder, e.g.,  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 22; 118pp; English.  
XX  
CC The invention describes a new isolated polypeptide comprising: a  
CC polypeptide or its mature form comprising a sequence not given in the  
CC specification; or a variant of (A), where one or more amino acid residues  
CC in the variant differs in no more than 15% from the amino acid sequence  
CC of the mature form. The pharmaceutical composition may be administered  
CC via oral, transdermal, rectal or parenteral route. The polypeptide,  
CC nucleic acid or antibody is useful for preparing a composition for  
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is  
CC the amino acid sequence of a transmembrane receptor homologue used in a  
CC comparison with the novel human proteins of the invention.  
XX  
SQ Sequence 2991 AA;

Query Match 3.4%; Score 88.5; DB 7; Length 2991;  
Best Local Similarity 20.4%; Pred. No. 1.3e+03;  
Matches 125; Conservative 78; Mismatches 210; Indels 201; Gaps 32;

QY 42 IDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARV-ASVDMGPQ 100  
Db 83 INHRPQFLETRYE-VRVPQDTPVGV-----ELLRVQAIQQDKGKSLIYTIHGSQDPGSA 136  
QY 101 QL--PDGQSLPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKL 158  
Db 137 SLFQDPPSSGLVTVGKLDLGSGPSQHTLTVMVRDQEIPKRNFWVVT----IHVEDGNL 192  
QY 159 -----YGRGATDNKGPVLAWINAVSAFALEQDLVPNIKF---IIEGMEEA----- 201  
Db 193 HPPRFTQLHYEASVPDTIAPGTPELLQV---RAMDADRGVNAEVHYSLLKGNSEGFENIN 248  
QY 202 ---GSVALEE-----LVEKEKDR-----FSGVDYI 224  
Db 249 ALLGIITLAQKLDQANHAPHHTLVTKAEDQGSQWHDLATVIHVPSDRSAPIFSKSEYF 308  
QY 225 VI-----SDNLWISQRKPA-ITYGTR-GNSYFMVEVKCRDQDFHSGTGGIL----- 269



Db 309 VEIPESIPVGSPIILLVSAMSPSEVTYELREGN-----KGVFSMNSYSGLISTQKK 359  
QY 270 --HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE-- 304  
Db 360 LDHEKISSYQLKIRGSNMAGAFDVMVVVDIIDENDNAPMFLKSTFVGQISEAAPLYSMI 419  
QY 305 -EEINTYKAIHL-DLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTK 362  
Db 420 MDKNNNPFVIHASDSKANSLLVYKIL---EPEALKFFKIDPSM-----GTL 464  
QY 363 TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNKMVVSMT 412  
Db 465 TIVSEMDYESMPSFQFCVYVHDQGSPLFAPRPAQVIIHVRDVNDSPPRFSEQIYEVAIV 524  
QY 413 LGLHPWI-----ANIDDTQY-----LAAKRAIR 435  
Db 525 GPIHPGMELLMVRASDESEVNYSIKTGNADAEVTIHPVTGSI SVLNPAFLGLSRKLTIR 584  
QY 436 TVFGTEPD--MIRDSGTIPIAKMFQ-----EIVHKS VVLIPLGAVDDGEHSQNE 482  
Db 585 ASDGLYQDTALVKISLTQVLDKSLQFDQDVYWAAVKENLQDRKALVILGA--QGNH-LND 641  
QY 483 KINRWNYIEGTKLF 496  
Db 642 TLS-YFLNGTDMF 654

RESULT 810  
ABB97541  
ID ABB97541 standard; protein; 4263 AA.  
XX  
AC ABB97541;  
XX  
DT 27-JUN-2002 (first entry)  
XX  
DE Novel human protein SEQ ID NO: 809.  
XX  
KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;  
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
KW neuroprotective; antiparkinsonian; protein therapy; EST;  
KW expressed sequence tag.  
XX  
OS Homo sapiens.  
XX  
PN WO200222660-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US026015.  
XX  
PR 11-SEP-2000; 2000US-00659671.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX  
DR WPI; 2002-292408/33.  
DR N-PSDB; ABN32727.  
XX  
PT An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis.  
XX  
PS Claim 20; SEQ ID NO 809; 509pp; English.  
XX  
CC The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke  
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

CC rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention  
XX  
SQ Sequence 4263 AA;  
Query Match 3.4%; Score 88.5; DB 5; Length 4263;  
Best Local Similarity 20.4%; Pred. No. 2.2e+03;  
Matches 125; Conservative 78; Mismatches 210; Indels 201; Gaps 32;  
QY 42 IDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV-ASVDMGPGQ 100  
Db 1441 INHHRPQFLETRYE-VRVPQDTPVGV-----ELLRVQAIDQDKGKSLIYTHGSDPGSA 1494  
QY 101 QL--PDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKL 158  
Db 1495 SLFQLDPSSGVLTVGKLDLGGSPSQHTLTVMVRDQEIPIKRNFWVT---IHVEDGNL 1550  
QY 159 -----YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKF---IIEGMEEA----- 201  
Db 1551 HPRFTQLHYEASVPDTPAGTELLQV----RAMDADRGVNAEVHYSLLKNGSEGFNIN 1606  
QY 202 ---GSVALEE-----LVEKEKDR-----FFSGVDYI 224  
Db 1607 ALLGIITLAQKLDQANHAPHTLTVKAEDQGSQWHDLATVIIHVYPSDRSAPIFSKSEYF 1666  
QY 225 VI-----SDNLWISQRKA-ITYGTR-GNSYFMVEVKCRDQDFHSGTGGIL----- 269  
Db 1667 VEIPESIPVGSPIILLVSAMSPSEVTYELREGN-----KGVFSMNSYSGLISTQKK 1717  
QY 270 --HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE-- 304  
Db 1718 LDHEKISSYQLKIRGSNMAGAFDVMVVVDIIDENDNAPMFLKSTFVGQISEAAPLYSMI 1777  
QY 305 -EEINTYKAIHL-DLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTK 362  
Db 1778 MDKNNNPFVIHASDSKANSLLVYKIL---EPEALKFFKIDPSM-----GTL 1822  
QY 363 TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNKMVVSMT 412  
Db 1823 TIVSEMDYESMPSFQFCVYVHDQGSPLFAPRPAQVIIHVRDVNDSPPRFSEQIYEVAIV 1882  
QY 413 LGLHPWI-----ANIDDTQY-----LAAKRAIR 435  
Db 1883 GPIHPGMELLMVRASDESEVNYSIKTGNADAEVTIHPVTGSI SVLNPAFLGLSRKLTIR 1942  
QY 436 TVFGTEPD--MIRDSGTIPIAKMFQ-----EIVHKS VVLIPLGAVDDGEHSQNE 482  
Db 1943 ASDGLYQDTALVKISLTQVLDKSLQFDQDVYWAAVKENLQDRKALVILGA--QGNH-LND 1999  
QY 483 KINRWNYIEGTKLF 496  
Db 2000 TLS-YFLNGTDMF 2012

RESULT 811  
ADM47281  
ID ADM47281 standard; protein; 4264 AA.  
XX  
AC ADM47281;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Protocadherin FAT-like NOVX 28b protein.  
XX  
KW NOVX; cytostatic; gene therapy; vaccine; cancer; chromosome mapping.  
XX  
OS Unidentified.  
XX  
PN WO2003083039-A2.  
XX  
PD 09-OCT-2003.  
XX  
PF 03-JUL-2002; 2002WO-US021485.

05-JUL-2001; 2001US-0303046P.  
09-JUL-2001; 2001US-0303828P.  
11-JUL-2001; 2001US-0304502P.  
12-JUL-2001; 2001US-0305011P.  
13-JUL-2001; 2001US-0305262P.  
16-JUL-2001; 2001US-0305673P.  
17-JUL-2001; 2001US-0306085P.  
24-JUL-2001; 2001US-0307536P.  
27-JUL-2001; 2001US-0308228P.  
30-JUL-2001; 2001US-0308877P.  
14-AUG-2001; 2001US-0312203P.  
17-SEP-2001; 2001US-0322640P.  
19-SEP-2001; 2001US-0323484P.  
21-SEP-2001; 2001US-0323821P.  
21-SEP-2001; 2001US-0323948P.  
25-SEP-2001; 2001US-0324711P.  
09-OCT-2001; 2001US-0327893P.  
21-NOV-2001; 2001US-0331768P.  
21-FEB-2002; 2002US-0359191P.  
22-FEB-2002; 2002US-0358939P.  
28-FEB-2002; 2002US-0360923P.  
01-MAR-2002; 2002US-0360830P.  
01-MAR-2002; 2002US-0361178P.  
05-MAR-2002; 2002US-0361748P.  
12-MAR-2002; 2002US-0363429P.  
12-MAR-2002; 2002US-0363683P.  
12-APR-2002; 2002US-0372141P.  
16-APR-2002; 2002US-0372967P.  
16-APR-2002; 2002US-0373051P.  
16-APR-2002; 2002US-0373063P.  
17-APR-2002; 2002US-0373280P.  
17-APR-2002; 2002US-0373287P.  
19-APR-2002; 2002US-0373881P.  
02-JUL-2002; 2002US-00187975.  
(CURA-) CURAGEN CORP.  
Li L, Shenoy SG, Patturajan M, Ellerman K, Gorman L, Zhong M; Catterton E, Spytek KA, Miller CE, Edinger SR, Hjalt T, Gerlach VL; Shimkets RA, Taupier RJ, Anderson DW, Guo X, Baumgartner JC; Padigar M, Peyman JA, Smithson G, Casman SJ, Voss EZ, Boldog FL; Pena CEA, Chapoval A, Rastelli L, Kekuda R, Vernet CAM;  
WPI; 2003-812538/76.  
N-PSDB; ADM47280.  
New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.  
Claim 2; SEQ ID NO 114; 433pp; English.  
The invention relates to a novel isolated polypeptide, designated NOVX. The novel polypeptide comprises a sequence comprising 109-1671 amino acids, or its mature form; a sequence that is at least 95% identical to the 109-1671 amino acid polypeptide; or a sequence comprising one or more conservative substitutions in the 109-1671 amino acid polypeptide. The invention further comprises: a composition; a kit comprising the composition; a method for determining the presence or amount of the polypeptide or nucleic acid molecule in a sample; determining the presence of, or predisposition to, a disease associated with the altered levels of nucleic acid or of expression of an agent that binds to the mammalian subject; identification of a potential therapeutic agent for treating a pathology related to aberrant expression or physiological interactions of the polypeptide; a method of screening for a modulator of activity or latency of, or predisposition to, a pathology associated with the polypeptide; a method for modulating the activity of the polypeptide; treating or preventing a pathology associated with the polypeptide; treating a pathological state in a mammal; an isolated nucleic acid molecule; a vector comprising the nucleic acid molecule; a cell comprising the vector; an antibody that immunospecifically binds to the polypeptide; and a method for producing the polypeptide. The NOVX





QY	101	QL--PDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKL	158
Db	1495	SLFQLDPSSGVLTVGKLDLGGSPSQHTLTVMVRDQEIPIKRNFWVVT---IHVEDGNL	1550
QY	159	-----YGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKF---IIEGMEEA-----	201
Db	1551	HPPRFTQLHYEASVPDTIAPGTELLQV-----RAMDADRGVNAEVHYSLKGNSEGFNIN	1606
QY	202	---GSVALEE-----LVEKEKOR-----FFSGVDYI	224
Db	1607	ALLGIITLAQKLDQANHAPHTLTVKAEDQGSQPQWHDLATVIIHVYPSDRSAPIFSKSEYF	1666
QY	225	VI-----SDNLWISQKPA-ITYGTR-GNSYFMVEVKCRDQDFHSGTGGIL-----	269
Db	1667	VEIPESIPVGSPILLVSAMSPSEVTYELREGN-----KGVFMSNYSYGLISTQKK	1717
QY	270	---HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE--	304
Db	1718	LDHEKISSYQLKIRGSMNAGAFDTVMVVVDIIDENDNAPMELKSTFVGQISEAAPLYSMI	1777
QY	305	EEINTYKAIHL-DLEEYRNSRVEKFLEFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTK	362
Db	1778	MDKNNPFIHASDSKKEANSLLVYKIL---EPEALKPFKIDPSM-----GTL	1822
QY	363	TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK---RNSSNKMVVSMT	412
Db	1823	TIVSEMDYESMPSEQFCVYVHDQGSPLFAPRPAQVIIHVRDVNDSPPRFSEQIYEVAIV	1882
QY	413	LGLHPWI-----ANIDDTQY-----LAACKRAIR	435
Db	1883	GPIHPGMELLMVRASDESEVNYSIKTGNADAETTHPVTGSISVLNPAFLGLSRKLTIR	1942
QY	436	TVFGTEPD--MIRDGSTIPIAKMFQ-----EIVHKSVLVLIPLGAVDDEHSQNE	482
Db	1943	ASDGLYQDTALVKISLTQVLDKSLQDFDQDVYAAVKENLQDRKALVILGA--QGNH-LND	1999
QY	483	KINRWNYIEGTKLF	496
Db	2000	TLS-YFLNGTDMF	2012

RESULT 814  
AAO26792  
ID AAO26792 standard; protein; 4349 AA.  
XX  
XX AAO26792;  
XX AC  
XX AC  
DT 03-APR-2003 (first entry)  
XX  
DE Human cadherin (CAD) protein. SEQ ID NO 15.

Cytostatic; p53 pathway modulating agent; cadherin; CAD; cancer; breast cancer; colon cancer; kidney cancer; lung cancer; ovary cancer; human.

OS Homo sapiens.

PN WO200299042-A2.

PD 12-DEC-2002.

PF 03-JUN-2002; 2002WO-US017315.

PR 05-JUN-2001; 2001US-0296076P.

PR 15-FEB-2002; 2002US-0357253P.

PA (EXEL-) EXELIXIS INC.

PI Friedman L, plowman

DR WPI; 2003-167332/16.

PT Identifying p53 pathway modulators that are useful as targets for  
PT therapeutics or for diagnosing cancers associated with defective p53  
PT function, by providing assay systems comprising a purified cadherin (CAD)  
PT polypeptide.  
XX  
XX Claim 13; Page 160-178; 192pp; English.  
PS  
XX The invention relates to a novel method for identifying a candidate p53  
CC pathway modulating agent. The method comprises providing an assay system  
CC comprising a purified cadherin (CAD) polypeptide or nucleic acid, or  
CC their functionally active fragment or derivative. The method is useful  
CC for identifying a candidate p53 pathway modulating agent, modulating a  
CC p53 pathway of a cell and for diagnosing a disease in a patient. In  
CC particular, the disease is cancer, e.g. breast cancer, colon cancer,  
CC kidney cancer, lung cancer or cancer of the ovary, which has an  
CC expression level of greater than 25%. The identified modulators are  
CC useful as targets for novel therapeutics. This sequence represents a  
CC cadherin (CAD) protein of the invention  
XX  
SQ Sequence 4349 AA;

	Query Match	3.4%;	Score 88.5;	DB 6;	Length 4349;
	Best Local Similarity	20.4%;	Pred. No. 2.3e+03;		
	Matches 125;	Conservative	78;	Mismatches 210;	Indels 201; Gaps 32;
QY	42	IDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARV-ASVDMGPQ	100		
Db	1441	INHRRPQFLETRYE-VRVPQDTVPGV-----ELLRVQAIDQDKGKSLYTIHGSQDPGSA	1494		
QY	101	QL--PDGQSLPIPPVILAEGLSDPTKGTVCIFYGHLDVQPADRGDGLWLTDPYVLTEVDGKL	158		
Db	1495	SLFQLDPSSGVLVTVGKLDLGGSPSQHTLTVMVRDQEIPIKRNFWVT-----IHVEDGNL	1550		
QY	159	-----YGRGATDNKGPVLAWINAVSAFRALEQDLVNIKF-----IEGMEEA-----	201		
Db	1551	HPPRFTQLHYEASVPDTIAPGTELLQV-----RAMDADRGVNAEVHYSLLKGNSEGGFFNIN	1606		
QY	202	---GSVALEE-----LVEKEKDR-----FFSGVDYI	224		
Db	1607	ALLGIITLAQKLDQANHAPHTLTVKAEDQGSQWHDLATVIIHVYPSDRSAPIFSKSEYF	1666		
QY	225	VI-----SDNLWISQRKPA-ITYGTR-GNSYFMVEVKCRDQDFHSGTFFGIL-----	269		
Db	1667	VEIPESIPVGPILLVSAMSPSEVTVELREGN-----KDGFSMNSYSGLISTQKK	1717		
QY	270	--HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE--	304		
Db	1718	LDHEKISSYQLKIRGSNMAGAFDVMVVVDIIDENDNAPMFLKSTFVCQISEAAPLYSMI	1777		
QY	305	-EEINTYKAHL-DLEEYRNSRVEKFLPDTKEEILMHLWRYPSPLSIHGIEGAFDEPGTK	362		
Db	1778	MDKNNPNFVIHASDSKANSLLVYKIL--EPEALKFFKIDPSM-----GTL	1822		
QY	363	TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNMWVVSMT	412		
Db	1823	TIVSEMDYESMPSPFQFCVYVHDQGSPLFAPRPAQVIIHVRDVNDSPRPFSEQIYEVAIV	1882		
QY	413	LGLHPWI-----ANIDDTQY-----LAACKRAIR	435		
Db	1883	GPIHPGMELLMVRASEDESEVNYSIKTGNADAEVTHPVTGSISVLNPAFLGLSRKLTIR	1942		
QY	436	TVFGTEPD--MIRDGSTIPIAKMFQ-----EIVHKSUVLLPLGCAVDGGEHSQNE	482		
Db	1943	ASDGLYQDTALVKISLTQVLDKSLQFDQDVYAAVKENLQDRKALVILGA--QGNH-LND	1999		
QY	483	KINRWNYIEGTKLF	496		
Db	2000	TLS-YFLNGTDMF	2012		

RESULT 815  
ABU62305  
ID ABU62305 standard; protein: 4349 AA.







QY 270 --HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE-- 304  
Db 1718 LDHEKISSYQLKIRGSNMAGFTDVMVVVDIIDENDNAPMFLKSTFVGQISEAPLYSMI 1777  
QY 305 -EEINTYKAIHL-DLEEYRNSRVEKFLFTDKEEILMHLWRYPSLSIHGIEGAFDEPGTK 362  
Db 1778 MDKNNPFIHASDSKANSLLVYKIL---EPEALKFFKIDPSM-----GTL 1822  
QY 363 TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNKMVVSMT 412  
Db 1823 TIVSEMDYESMPSFQFCVYVHDQGSPLFAPRPAQVVIHVRDVNDSPPRFSEQIYEVAIV 1882  
QY 413 LGLHPWI-----ANIDDTQY-----LAAKRAIR 435  
Db 1883 GPIHPGMELLMVRASDEDESEVNSIKTGNADAEAVTIHPVTGSISVLNPAFLGLSRKLTIR 1942  
QY 436 TVFGTEPD--MIRDSGTIPIAKMFQ-----EIVHKSVVLIPLGAVDDGEHSQNE 482  
Db 1943 ASDGLYQDTALVKISLTQVLDKSLQFDQDVYWAAVKENLQDRKALVILGA--QGNH-LND 1999  
QY 483 KINRWNYIEGTKLF 496  
Db 2000 TLS-YFLNGTDMF 2012  
RESULT 818  
ADG42620  
ID ADG42620 standard; protein; 4349 AA.  
XX  
AC ADG42620;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human FAT tumour suppressor 2 precursor #1.  
XX  
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;  
KW NOVX-associated disorder; cancer; human;  
KW FAT tumour suppressor 2 precursor.  
XX  
OS Homo sapiens.  
XX  
PN US2003204052-A1.  
XX  
PD 30-OCT-2003.  
XX  
PF 04-OCT-2001; 2001US-00970944.  
XX  
PR 04-OCT-2000; 2000US-0237862P.  
XX  
PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
XX  
PI Herrmann JL, Rastelli L, Shimkets RA;  
XX  
DR WPI; 2003-900673/82.  
XX  
PT New NOVX gene or NOVX-specific antibody, useful for preparing a  
PT composition for treating or preventing a NOVX-associated disorder, e.g.,  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 18; 118pp; English.  
XX  
CC The invention describes a new isolated polypeptide comprising: a  
CC polypeptide or its mature form comprising a sequence not given in the  
CC specification; or a variant of (A), where one or more amino acid residues  
CC in the variant differs in no more than 15% from the amino acid sequence  
CC of the mature form. The pharmaceutical composition may be administered  
CC via oral, transdermal, rectal or parenteral route. The polypeptide,  
CC nucleic acid or antibody is useful for preparing a composition for  
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is  
CC the amino acid sequence of a transmembrane receptor homologue used in a  
CC comparison with the novel human proteins of the invention.

XX  
SQ Sequence 4349 AA;  
Query Match 3.4%; Score 88.5; DB 7; Length 4349;  
Best Local Similarity 20.4%; Pred. No. 2.3e+03;  
Matches 125; Conservative 78; Mismatches 210; Indels 201; Gaps 32;  
QY 42 IDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV-ASVDMGPQ 100  
Db 1441 INHHRPQFLETRYE-VRVPQDTVPGV-----ELLRVQAIDQDKGKSLIYTHGSQDPGSA 1494  
QY 101 QL--PDGQSLPIPPVILAEELGSDPTKGTVCYFCHLDVQPADRGDGLTDPVYLTEVDGKL 158  
Db 1495 SLFQLDPSSGVLTVGKLDLGSGPSQHTLTVMVRDQEIPIKRNFWVT-----IHVEDGNL 1550  
QY 159 -----YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKF---IEGMEEA----- 201  
Db 1551 HPPRFTQLHYEASVPDTIAPGTELLQV-----RAMDADRGVNAEVHYSLLKGNSEGGFFNIN 1606  
QY 202 ---GSVALEE-----LVEKEKDR-----FFSGVDYI 224  
Db 1607 ALLGIITLAQKLDQANHAPHTLTVKAEDQGSPPQWHDLATVIIHVYPSDRSAPIFSKSEYF 1666  
QY 225 VI-----SDNLWISQRKPA-ITYGTR-GNSYFMVEVKCRDQDHSFGFGIL----- 269  
Db 1667 VEIPESIPVGSPIILLVSAMSPSEVTYELREGN-----KDGVFMSNSYSGLISTQKK 1717  
QY 270 --HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE-- 304  
Db 1718 LDHEKISSYQLKIRGSNMAGFTDVMVVVDIIDENDNAPMFLKSTFVGQISEAPLYSMI 1777  
QY 305 -EEINTYKAIHL-DLEEYRNSRVEKFLFTDKEEILMHLWRYPSLSIHGIEGAFDEPGTK 362  
Db 1778 MDKNNPFIHASDSKANSLLVYKIL---EPEALKFFKIDPSM-----GTL 1822  
QY 363 TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNKMVVSMT 412  
Db 1823 TIVSEMDYESMPSFQFCVYVHDQGSPLFAPRPAQVVIHVRDVNDSPPRFSEQIYEVAIV 1882  
QY 413 LGLHPWI-----ANIDDTQY-----LAAKRAIR 435  
Db 1883 GPIHPGMELLMVRASDEDESEVNSIKTGNADAEAVTIHPVTGSISVLNPAFLGLSRKLTIR 1942  
QY 436 TVFGTEPD--MIRDSGTIPIAKMFQ-----EIVHKSVVLIPLGAVDDGEHSQNE 482  
Db 1943 ASDGLYQDTALVKISLTQVLDKSLQFDQDVYWAAVKENLQDRKALVILGA--QGNH-LND 1999  
QY 483 KINRWNYIEGTKLF 496  
Db 2000 TLS-YFLNGTDMF 2012  
RESULT 819  
ADJ69933  
ID ADJ69933 standard; protein; 4349 AA.  
XX  
AC ADJ69933;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human heat mitochondrial protein as a therapeutic target SeqID1739.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003087768-A2.

XX 23-OCT-2003.  
PD 04-APR-2003; 2003WO-US010870.  
XX 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX WPI; 2003-845369/78.  
DR  
XX Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX Claim 1; SEQ ID NO 1739; 180pp; English.  
XX This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytotstatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX Sequence 4349 AA;  
SQ  
Query Match 3.4%; Score 88.5; DB 7; Length 4349;  
Best local similarity 20.4%; Pred. No. 2.3e+03;  
Matches 125; Conservative 78; Mismatches 210; Indels 201; Gaps 32;  
QY 42 IDLHQDEFVQTLKEWVAIESDSVQVPVPRFQELFRMMAVAADTLQRLGARV-ASVDMGPQ 100  
Db 1441 INHHRPQFLETRYE-VRVPQDTVPGV-----ELLRVQAIDQDKGSLIYTHGSDPGSA 1494  
QY 101 QL--PDGQSLPIPPVILAEELGSDPTKGTVCYFGHLDVQPADRGDGLWLTDPVLTVEVDGKL 158  
Db 1495 SLFQLDPSSGLVTVGKLDLGGSPSQHTLTVMVRDQEIPKRNFWVT----IHVEDGNL 1550  
QY 159 -----YGRGATDNKGPVLAWINAVSAFRALEQDLFVNIKF---IIEGMEEA----- 201  
Db 1551 HPPRFTQLHYEASVPDTIAPGTELLQV-----RAMDADRGVNAEVHYSLKGNSEGFNIN 1606  
QY 202 ---GSVALEE-----LVEKEKDR-----FMSGVDYI 224  
Db 1607 ALLGIITLAQKLDQANHAPHTLTIVKAEDQSPQWHDLATVIIHVYPSDRSAPIFSKSEYF 1666  
QY 225 VI-----SDNLWISQRKPA-ITYGTR-GNSYFMVEVKCRDQDFHSGTFFGIL----- 269  
Db 1667 VEIPESIPVGSPIILLVSAMSPSEVTYELREGN-----KDGVFSMNSYSLISTQKK 1717  
QY 270 --HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE-- 304  
Db 1718 LDHEKISSYQLKIRGSNMAGAFDVMVVVDIIDENDNAPMFLKSTFVGQISEAAPLYSMI 1777  
QY 305 -EEINTYKAIHL-DLEEYRNSSRVEKFLDFTKEIIMHLWRYPYSIHGIEGAFDEPGTK 362  
Db 1778 MDKNNNPFVHASDSDKEANSLLVYKIL---EPEALKFKKIDPSM-----GTL 1822

QY 363 TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNMVVVSMT 412  
Db 1823 TIVSEMDYESMPSPQFCVYVHDQGSPLFAPRPAQVLIHVRDVNDSPPRFSEQIYEVAIV 1882  
QY 413 LGLHPWI-----ANIDDTQY-----LAACKRAIR 435  
Db 1883 GPIHPGMELLMVRASDESEVNYSIKTGNADAEAVTIHPVTGTSISVLNPAFLGLSRKLTIR 1942  
QY 436 TVFGTEPD--MIRDSGTIPIAKMFQ-----EIVHKSVVLIPLGAVDDGEHSONE 482  
Db 1943 ASDGLYQDTALVKISLTQVLDKSLQFDQDVYWAAVKENLQDRKALVILGA--QGNH-LND 1999  
QY 483 KINRWNVIEGTKLF 496  
Db 2000 TLS-YFLLNGTDMF 2012  
RESULT 820  
ADM47279  
ID ADM47279 standard; protein; 4349 AA.  
XX  
AC ADM47279;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Protocadherin like NOVX 28a protein.  
XX  
KW NOVX; cytotstatic; gene therapy; vaccine; cancer; chromosome mapping.  
XX  
OS Unidentified.  
XX WO2003083039-A2.  
PN  
XX  
PD 09-OCT-2003.  
XX  
PF 03-JUL-2002; 2002WO-US021485.  
XX  
PR 05-JUL-2001; 2001US-0303046P.  
PR 09-JUL-2001; 2001US-0303828P.  
PR 11-JUL-2001; 2001US-0304502P.  
PR 12-JUL-2001; 2001US-0305011P.  
PR 13-JUL-2001; 2001US-0305262P.  
PR 16-JUL-2001; 2001US-0305673P.  
PR 17-JUL-2001; 2001US-0306085P.  
PR 24-JUL-2001; 2001US-0307536P.  
PR 27-JUL-2001; 2001US-0308228P.  
PR 30-JUL-2001; 2001US-0308877P.  
PR 14-AUG-2001; 2001US-0312203P.  
PR 17-SEP-2001; 2001US-0322640P.  
PR 19-SEP-2001; 2001US-0323484P.  
PR 21-SEP-2001; 2001US-0323821P.  
PR 25-SEP-2001; 2001US-0324711P.  
PR 09-OCT-2001; 2001US-0327893P.  
PR 21-NOV-2001; 2001US-0331768P.  
PR 21-FEB-2002; 2002US-0359191P.  
PR 22-FEB-2002; 2002US-0358939P.  
PR 28-FEB-2002; 2002US-0360923P.  
PR 01-MAR-2002; 2002US-0360830P.  
PR 01-MAR-2002; 2002US-0361178P.  
PR 05-MAR-2002; 2002US-0361748P.  
PR 12-MAR-2002; 2002US-0363429P.  
PR 12-MAR-2002; 2002US-0363683P.  
PR 12-APR-2002; 2002US-0372141P.  
PR 16-APR-2002; 2002US-0372967P.  
PR 16-APR-2002; 2002US-0373051P.  
PR 16-APR-2002; 2002US-0373063P.  
PR 17-APR-2002; 2002US-0373280P.  
PR 17-APR-2002; 2002US-0373287P.  
PR 19-APR-2002; 2002US-0373881P.  
PR 02-JUL-2002; 2002US-00187975.  
XX

PA (CURA-) CURAGEN CORP.

XX Li L, Shenoy SG, Patturajan M, Ellerman K, Gorman L, Zhong M;

PI Catterton E, Spytek KA, Miller CE, Edinger SR, Hjalt T, Gerlach VL;

PI Shimkets RA, Taupier RJ, Anderson DW, Guo X, Baumgartner JC;

PI Padigaru M, Peyman JA, Smithson G, Casman SJ, Voss EZ, Boldog FL;

PI Pena CEA, Chapoval A, Rastelli L, Kekuda R, Vernet CAM;

XX WPI; 2003-812538/76.

DR N-PSDB; ADM47278.

XX

PT New NOVX polypeptide, useful for preparing a composition for treating or

PT preventing e.g. cancer or for chromosome mapping.

XX

PS Claim 2; SEQ ID NO 112; 433pp; English.

XX

CC The invention relates to a novel isolated polypeptide, designated NOVX.

CC The novel polypeptide comprises a sequence comprising 109-1671 amino

CC acids, or its mature form; a sequence that is at least 95% identical to

CC the 109-1671 amino acid polypeptide; or a sequence comprising one or more

CC conservative substitutions in the 109-1671 amino acid polypeptide. The

CC invention further comprises: a composition; a kit comprising the

CC composition; a method for determining the presence or amount of the

CC polypeptide or nucleic acid molecule in a sample; determining the

CC presence of, or predisposition to, a disease associated with the altered

CC levels of nucleic acid or of expression of the polypeptide in a first

CC mammalian subject; identification of an agent that binds to the

CC polypeptide; identification of a potential therapeutic agent for treating

CC a pathology related to aberrant expression or physiological interactions

CC of the polypeptide; a method of screening for a modulator of activity or

CC latency of, or predisposition to, a pathology associated with the

CC polypeptide; a method for modulating the activity of the polypeptide;

CC treating or preventing a pathology associated with the polypeptide;

CC treating a pathological state in a mammal; an isolated nucleic acid

CC molecule; a vector comprising the nucleic acid molecule; a cell

CC comprising the vector; an antibody that immunospecifically binds to the

CC polypeptide; and a method for producing the polypeptide. The NOVX

CC polypeptide and its encoding nucleic acid have cytostatic activity. The

CC NOVX polynucleotide can be used in gene therapy to treat disorders. The

CC NOVX polypeptide can be used to create a vaccine. The polypeptide is

CC useful for preparing a composition for treating or preventing a

CC pathological state in a mammal, e.g., cancer, or for chromosome mapping.

CC This sequence represents a NOVX polypeptide of the invention.

XX

SQ Sequence 4349 AA;

Query Match 3.4%; Score 88.5; DB 7; Length 4349;

Best Local Similarity 20.4%; Pred. No. 2.3e+03;

Matches 125; Conservative 78; Mismatches 210; Indels 201; Gaps 32;

QY 42 IDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMVAADTLQRLGARV-ASVDMGPQ 100

Db 1441 INHHRPQFLETRYE-VRVPQDTPGV-----ELLRVAIDQDKGKSLIYTHGSDPGSA 1494

QY 101 QL--PDGQSLPIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKL 158

Db 1495 SLFQLDPSSGVLVTVGKLDLGSGPSQHTLTVMVRDQEIPIKRNFWVVT----IHVEDGNL 1550

QY 159 -----YGRGATDNKGPVLAWINAVSAFRALEODLPVNIKF---IIEGMEEA----- 201

Db 1551 HPPRFTQLHYEASVPDTIAPGTELLQV---RAMDADRGVNAEVHYSLLKGNSEGFNNIN 1606

QY 202 ---GSVALEE-----LVEKEKDR-----FPGVDYI 224

Db 1607 ALLGIITLAQKLDQANHAPHTLTVKAEDQGSQWHDLATVIIHVYPSDRSAPIFSKEYF 1666

QY 225 VI-----SDNLWISQKPA-ITYGTR-GNSYFMVEVKCRDQDFHSGTGGIL----- 269

Db 1667 VEIPESIPVGSPIILLVSAMSPSEVTYELREGN-----KGVFMSMNSGLISTQKK 1717

QY 270 --HEPMADL-----VALLGSLVDSSGHI-----LVPGIYDEVVPLTE-- 304

Db 1718 LDHEKISSYQLKIRGSNNMAGFTDVMVVVDIIDENDNAPMFLKSTFVGQISEAAPLYSMI 1777

QY 305 -EEINTYKAHL-DLEEYRNSRRVEKFLFDTKBEILMHLWRYPSLSIHGIEGAFDEPGTK 362

Db 1778 MDKNNNPFVIHASDSDKEANSLLVYKIL---EPEALKFFKIDPSM-----GTL 1822

QY 363 TVIPG---RVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSK--RNSSNKMVVVSM 412

Db 1823 TIVSEMDYESMPSPFQFCVVYVHDQGSPLFAPRPAQVIIHVRDVNDSPPRFSEQIYEVAIV 1882

QY 413 IGLHPWI-----ANIDDTQY-----LAAKRAIR 435

Db 1883 GPIHPGMELLMVRASDEDESEVNYSIKTGNDAEAVTIHPVTGSISVLNPAPFLGLSRKLTIR 1942

QY 436 TVFGTEPD--MIRDSGSTIPIAKMFQ-----EIVHKSUVLIPLGAVDGGEHSQNE 482

Db 1943 ASDGLYQDTALVKISLTQVLDKSLQFDQDVYVAAVKENLQDRKALVILGA--QGNH-LND 1999

QY 483 KINRWNYIEGTKLF 496

Db 2000 TLS-YFLNGTDMF 2012

RESULT 821

ADM74201

ID ADM74201 standard; protein; 4349 AA.

XX ADM74201;

XX 03-JUN-2004 (first entry)

DE Human NOV6A protein sequence SeqID40.

XX

KW NOVX; antiarteriosclerotic; cytostatic; antidiabetic; antiparkinsonian;

KW neuroprotective; nootropic; antiasthmatic; antiallergic;

KW immunosuppressive; antiarthritic; antirheumatic; osteopathic;

KW dermatological; antiinflammatory; anti-HIV; hypotensive; haemostatic;

KW anorectic; gastrointestinal-Gen; anabolic; antimicrobial; antipsoriatic;

KW neuroleptic; antidepressant; anabolic; eating disorders-Gen;

KW antiinfertility; nephrotropic; gene therapy; antisense gene therapy;

KW human disease; atherosclerosis; cancer; diabetes; Alzheimer's disease;

KW Parkinson's disease; asthma; allergy; immune disease;

KW graft-versus-host disease; osteoarthritis; rheumatoid arthritis;

KW scleroderma; systemic lupus erythematosus; AIDS; hypertension;

KW haemophilia; idiopathic thrombocytopenic purpura; obesity;

KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW infectious disease; psoriasis; multiple sclerosis; schizophrenia;

KW depression; anorexia; fertility; glomerulonephritis; chromosome mapping;

KW tissue typing; NOV6A; human.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT Misc-difference 3494. .3524

FT /label= OTHER

FT /note= "OTHER= All Xaa's in this region are unidentified

FT amino acid, probably Gln"

XX

PN WO2004015079-A2.

XX

PD 19-FEB-2004.

XX

PF 07-AUG-2003; 2003WO-US024931.

XX

PR 07-AUG-2002; 2002US-0401597P.

PR 09-AUG-2002; 2002US-0402205P.

PR 09-AUG-2002; 2002US-0402209P.

PR 13-AUG-2002; 2002US-0403517P.

PR 13-AUG-2002; 2002US-0403548P.

PR 15-AUG-2002; 2002US-0403696P.

PR 26-AUG-2002; 2002US-0406318P.

PR 27-AUG-2002; 2002US-0406202P.

PR 06-SEP-2002; 2002US-00236392.

PR 13-SEP-2002; 2002US-00242943.





CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX  
SQ Sequence 75 AA;  
  
Query Match 3.4%; Score 88; DB 3; Length 75;  
Best Local Similarity 30.8%; Pred. No. 4.7;  
Matches 20; Conservative 14; Mismatches 29; Indels 2; Gaps 2;  
  
QY 114 ILAELGSDPTKGTVCYGHLDVQPADRGDGLTDPY-VLTEVDGKLYGRGATDNKGPVLA 172  
Db 10 VLTWXGNTPTLSSILLNSHTDVVPVFK-EHWSHDPFAFKDSEGYIYARGAQDMKCVSIQ 68  
  
QY 173 WINAV 177  
Db 69 YLEAV 73  
  
RESULT 823  
ADP07863  
ID ADP07863 standard; protein; 335 AA.  
XX  
AC ADP07863;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein, seq id 346.  
XX  
KW Cytostatic; antidiabetic; anorectic; gynaecological; antipsoriatic;  
KW dermatological; antiarteriosclerotic; antiasthmatic; neuroprotective;  
KW nootropic; antiparkinsonian; nephrotropic; human; secreted protein;  
KW diagnostic; pharmaceutical; cancer; lung; oesophageal; liver; diabetes;  
KW obesity; metabolic disorder; cardiovascular disorder;  
KW reproductive disorder; psoriasis; eczema; bronchitis; cystic fibrosis;  
KW atherosclerosis; benign prostatic hyperplasia; asthma;  
KW Alzheimer's disease; Parkinson's disease; renal disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO2004042000-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 16-MAY-2003; 2003WO-US015439.  
XX  
PR 17-MAY-2002; 2002US-0381592P.  
PR 12-JUN-2002; 2002US-0388543P.  
PR 08-AUG-2002; 2002US-0401757P.  
PR 12-AUG-2002; 2002US-0402585P.  
PR 13-AUG-2002; 2002US-0402799P.  
PR 22-AUG-2002; 2002US-0404959P.  
PR 04-OCT-2002; 2002US-0415902P.  
XX  
PA (HUWA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM, Olsen H, Baker KP, Fiscella M, Wei P;  
PI Birse CE, Komatsoulis G, Choi GH, Moore PA, Gupta R, Shi Y;  
XX  
DR WPI; 2004-400658/37..  
DR N-PSDB; ADP07681.  
XX  
PT New human secreted polypeptides and nucleic acid molecules for  
PT diagnosing, preventing or treating disorders associated with the secreted  
PT proteins, such as cancer, diabetes, obesity, cardiovascular disorders or  
PT renal disorders.  
XX  
PS Claim 1; SEQ ID NO 346; 1157pp; English.  
XX  
CC The invention relates to a human secreted polypeptide for diagnosing,  
CC preventing or treating disorders associated with the secreted proteins.  
CC The polypeptides and nucleic acid molecules of the invention are useful

CC for preparing a diagnostic or pharmaceutical composition for diagnosing  
CC or treating a medical condition. These may be used for diagnosing,  
CC preventing or treating disorders related to the human secreted proteins,  
CC such as cancer (e.g. lung, oesophageal or liver cancer), diabetes,  
CC obesity, metabolic disorders, cardiovascular disorders, reproductive  
CC disorders, psoriasis, eczema, bronchitis, cystic fibrosis,  
CC atherosclerosis, benign prostatic hyperplasia, asthma, Alzheimer's  
CC disease, Parkinson's disease or renal disorders. Sequences given in  
CC records for ADP07710-ADP07891 represent human secreted proteins of the  
CC invention.  
XX  
SQ Sequence 335 AA;  
  
Query Match 3.4%; Score 88; DB 8; Length 335;  
Best Local Similarity 22.2%; Pred. No. 48;  
Matches 42; Conservative 25; Mismatches 80; Indels 42; Gaps 6;  
  
QY 176 AVSAFRALEQDLFPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQR 235  
Db 169 AVRKARRYSASLPAPVKLILPALEMVYVWNGFSIVSKRKD-----LSENLLVTVE 218  
  
QY 236 KPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGTILHEPMADLVALLGSLVDSS-----GHI 290  
Db 219 KAEALQSQNFNSFSDDECLVKLLKGCCUKNLQRPLOAEL--CYNHVVESEKLLKYDHY 276  
  
QY 291 LVP-----GIYDEVVPLTETEEINTYKAHLDLEEYRNSRVEKFLFDTKEEI 337  
Db 277 LVPFTLFELASLYKSQGEIDKAIFLETARNYK-----DYSLESRLH-----FRIQA 324  
  
QY 338 LMHLWRYPs 346  
Db 325 ALHLWRKPS 333  
  
RESULT 824  
AAB48844  
ID AAB48844 standard; protein; 357 AA.  
XX  
AC AAB48844;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Human RAP (receptor associated protein).  
XX  
KW RAP; receptor associated protein; human; factor VIII clearance;  
KW LRP-mediated plasma clearance; receptor-dependent clearance;  
KW receptor-independent clearance; ligand internalisation;  
KW low density lipoprotein related protein; haemophilia; half-life.  
XX  
OS Homo sapiens.  
XX  
PN WO2000071714-A2.  
XX  
PD 30-NOV-2000.  
XX  
PF 24-MAY-2000; 2000WO-US014111.  
XX  
PR 24-MAY-1999; 99US-0135847P.  
XX  
PA (AMNA-) AMERICAN NAT RED CROSS.  
XX  
PI Saenko EL, Strickland DK;  
XX  
DR WPI; 2001-025163/03.  
DR N-PSDB; AAC48844.  
XX  
PT Factor VIII mutants having increased half-life useful for treating  
PT hemophilia, comprise one or more amino acid substitutions in the A2  
PT and/or C2 domain of factor VIII.  
XX  
PS Claim 59; Fig 4; 121pp; English.  
XX  
CC The invention relates to human factor VIII mutants comprising an amino

CC acid substitution at one or more positions in the A2 domain and/or an  
CC amino acid substitution at one or more positions in the C2 domain. The  
CC invention also encompasses a factor VIII mutant which lacks a B domain  
CC (AAB48842). The factor VIII mutants have an increased half-life in the  
CC bloodstream. The A2 domain mutants exhibit reduced LRP-dependent  
CC (receptor-dependent) clearance of factor VIII, while C2 domain mutants  
CC have reduced receptor-independent clearance. The invention also relates  
CC to a method of using RAP (receptor associated protein), a protein which  
CC inhibits LRP (low density lipoprotein related protein)-mediated ligand  
CC internalisation, to increase the half-life of factor VIII. The mutant  
CC factor VIII proteins, and nucleotides encoding them, are useful for  
CC treating haemophilia. RAP, LRP-binding RAP mutants or fragments, and  
CC nucleic acids encoding them may also be used in the treatment of  
CC haemophilia, in combination with a mutant factor VIII protein or DNA of  
CC the invention. The invention provides means of increasing the half-life  
CC of factor VIII by reducing its clearance from plasma. The present  
CC sequence represents human RAP

XX  
SQ Sequence 357 AA;

Query Match 3.4%; Score 88; DB 4; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLL---LFLGPWPAAS-----HGGKYSR-----E 38  
QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE 119  
Db 39 KNQPKSPKRESGEEFRM-----EKLNLWEK-----AQRHLPPVRLAE 80  
QY 120 SDPTKGTVCYFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLKLGLDGEDGEKEARLIRNLNVILAKYGLDGK 129  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLWHKAKTSG 162  
QY 217 FFSGVYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL-----DKLW----REFLHKEKVHEYNVLLETLSRTEIHNVISPSDSL 214  
QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307  
Db 215 SVLHRSRHTELKEKLR SINQGLDRLRRVSHQGYSTEAEEFEP RVIDLWDLAQSANLT 274  
QY 308 NTYKAHLDLEEYRN-SSRVEKFLFDTKKEILMH 340  
Db 275 EAFR-----EELKHFEAKIEKHNHYQKLEIAH 302

RESULT 825  
AAO18621  
ID AAO18621 standard; protein; 357 AA.  
XX  
AC AAO18621;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Human receptor-associated protein.  
XX  
KW Human; factor VIII; fVIII; half-life; mutant; haemophilia;  
KW heparan sulfate proteoglycan-mediated clearance; RAP;  
KW receptor-associated protein; haemostatic; gene therapy;  
KW alpha2 macroglobulin receptor-associated protein.

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..34  
/note= "signal peptide"

FT Protein 35..357  
FT /note= "mature RAP"  
FT Region 237..353  
FT /label= LDL\_binding\_region  
XX  
PN WO200260951-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 11-JAN-2002; 2002WO-US000583.  
XX  
PR 12-JAN-2001; 2001US-0260904P.  
XX  
PA (AMNA-) AMERICAN NAT RED CROSS.  
XX  
PI Saenko EL, Sarafanov AG;  
XX  
XX WPI; 2002-608501/65.  
DR N-PSDB; AAL48893.  
XX

PT New mutant factor VIII with reduced sulfate proteoglycan (HSPG)-dependent  
PT or receptor-independent clearance and procoagulant activity for treating  
PT hemophilia.  
XX

PS Disclosure; Fig 14; 161pp; English.

XX  
CC The present invention relates to a mutant factor VIII protein with  
CC reduced sulfate proteoglycan (HSPG)-dependent or receptor-independent  
CC clearance and procoagulant activity, which has a nonconservative amino  
CC acid substitution at one or more positions in the A2 domain consisting of  
CC Lys(380, 512, 556, 570 or 659) or Arg(490, 527, 562 or 571) or in the C2  
CC domain relative to the wild-type. The mutant factor VIII or the  
CC polynucleotide encoding it and a receptor-associated protein (alpha2  
CC macroglobulin receptor-associated protein or RAP) are useful for treating  
CC haemophilia. The mutated protein has a longer half-life. The present  
CC sequence is the human receptor-associated protein

XX  
SQ Sequence 357 AA;

Query Match 3.4%; Score 88; DB 5; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLL---LFLGPWPAAS-----HGGKYSR-----E 38  
QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE 119  
Db 39 KNQPKSPKRESGEEFRM-----EKLNLWEK-----AQRHLPPVRLAE 80  
QY 120 SDPTKGTVCYFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLKLGLDGEDGEKEARLIRNLNVILAKYGLDGK 129  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLWHKAKTSG 162  
QY 217 FFSGVYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL-----DKLW----REFLHKEKVHEYNVLLETLSRTEIHNVISPSDSL 214  
QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307  
Db 215 SVLHRSRHTELKEKLR SINQGLDRLRRVSHQGYSTEAEEFEP RVIDLWDLAQSANLT 274  
QY 308 NTYKAHLDLEEYRN-SSRVEKFLFDTKKEILMH 340  
Db 275 EAFR-----EELKHFEAKIEKHNHYQKLEIAH 302

RESULT 826



ADD44975  
ID ADD44975 standard; protein; 357 AA.  
XX  
AC ADD44975;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P30533, SEQ ID NO 10406.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
DR GENBANK; P30533.  
DR  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 357 AA;  
  
Query Match 3.4%; Score 88; DB 7; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;  
  
Qy 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60

Db 1 MAPRRVRSFLRGLPALLLLL--LFLGPWPAAS-----HGGKYSR-----E 38  
Qy 61 SDSVQVPV-RFRQELFRMMVAADTLQRLGARVASVDMGPQLPDGQSLPIPPVILAELG 119  
Db 39 KNQPKPSPKRESGEFRM-----EKLNLWEK-----AQRHLFPVRLAELH 80  
Qy 120 SDPTKGTVCFYGHLDVQPAD-----RGDWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLKLGDGDEGEKEARLIRNLNVILAKYGLDGKKD 129  
Qy 160 GRGATDNKGPVLAWINAVSAFRALEQDLFVNKFIIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLMWHKAKTSG 162  
Qy 217 FFGVDYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL-----DKLW----REFLHKKEKVHEYNVLLTSLRTEEHENVISPSDLSDIKG 214  
Qy 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307  
Db 215 SVLHSRHTELKEKILRSINQGLDRLRRVSHQGYSTEAEFEPRVIDLWDLAQSANLTDKEL 274  
Qy 308 NTYKAIHLDLLEYRN-SSRVEKFLFDTKKEILMH 340  
Db 275 EAFR-----BELKHFEAKIEKHNHYQKQLEIAH 302  
  
RESULT 827  
ADD44979  
ID ADD44979 standard; protein; 357 AA.  
XX  
AC ADD44979;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P30533, SEQ ID NO 10410.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P30533.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 357 AA;

CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
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XX Sequence 357 AA;

Query Match 3.4%; Score 88; DB 7; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;  
QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLLL---LFLGPWPAAS-----HGGKYSR-----E 38  
QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQRHLPPVRLAELH 80  
QY 120 SDPTKGTVCIFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLDGLDEGEKEARLIRNLNVILAKYGLDGKKD 129  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLWHKAKTSG 162  
QY 217 FFSGVYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL-----DKLW---REFLHHKEKVHEYNVLLTSLRTEEHENVISPSDLSIDKG 214  
QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307  
Db 215 SVLHSRHTELKEKLSINQGLDRLRVSHQGYSTEAEEFEPVRVIDLWDLAQSANLTDKEL 274  
QY 308 NTYKAIHLDLEEYRN-SSRVEKFLFOTKKEILMH 340  
Db 275 EAFR-----BELKHFEAKIEKHNHYQKLEIAH 302

RESULT 828  
ADD44971  
ID ADD44971 standard; protein; 357 AA.  
XX  
AC ADD44971;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P30533, SEQ ID NO 10402.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX

PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P30533.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 357 AA;

Query Match 3.4%; Score 88; DB 7; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLLL---LFLGPWPAAS-----HGGKYSR-----E 38  
QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQRHLPPVRLAELH 80  
QY 120 SDPTKGTVCIFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLDGLDEGEKEARLIRNLNVILAKYGLDGKKD 129  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLWHKAKTSG 162

QY	217	PFSGVDYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G	267
Db	163	KFSGEEL-----DKLW-----REFLHKEKVHEYNVLLLETLRSRTTEIHNENVISPSDLSDIKG	214
QY	267	GILHEPMADLVALGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI	307
Db	215	SVLHSRHTELKEKLRSLNQGLDRLRRVSHQGYSTAEFEPRVIDLWDLAQSANLTDKEL	274
QY	308	NTYKAHLDLEEYRN-SSRVEKFLFDTKEEILMH	340
Db	275	EAFR-----EELKHFEAKIEKHNYQKQLEIAH	302
RESULT 829			
ADD44967			
ID	ADD44967 standard; protein; 357 AA.		
XX			
AC	ADD44967;		
XX			
DT	29-JAN-2004 (first entry)		
XX			
DE	Human Protein P30533, SEQ ID NO 10398.		
XX			
KW	Human; pain; neuronal tissue; gene therapy;		
KW	spinal segmental nerve injury; chronic constriction injury; CCI;		
KW	spared nerve injury; SNI; Chung.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003016475-A2.		
XX			
PD	27-FEB-2003.		
XX			
PF	14-AUG-2002; 2002WO-US025765.		
XX			
PR	14-AUG-2001; 2001US-0312147P.		
PR	01-NOV-2001; 2001US-0346382P.		
PR	26-NOV-2001; 2001US-0333347P.		
XX			
PA	(GEHO ) GEN HOSPITAL CORP.		
PA	(FARB ) BAYER AG.		
XX			
PI	Woolf C, D'urso D, Befort K, Costigan M;		
XX			
DR	WPI; 2003-268312/26.		
XX	GENBANK; P30533.		
PT	New composition comprising two or more isolated polypeptides, useful for		
PT	preparing a medicament for treating pain in an animal.		
XX			
PS	Claim 1; Page; 1017pp; English.		
XX			
CC	The invention discloses a composition comprising two or more isolated rat		
CC	or human polynucleotides or a polynucleotide which represents a fragment,		
CC	derivative or allelic variation of the nucleic acid sequence. Also		
CC	claimed are a vector comprising the novel polynucleotide, a host cell		
CC	comprising the vector, a method for identifying a nucleotide sequence		
CC	which is differentially regulated in an animal subjected to pain and a		
CC	kit to perform the method, an array, a method for identifying an agent		
CC	that increases or decreases the expression of the polynucleotide sequence		
CC	that is differentially expressed in neuronal tissue of a first animal		
CC	subjected to pain, a method for identifying a compound which regulates		
CC	the expression of a polynucleotide sequence which is differentially		
CC	expressed in an animal subjected to pain, a method for identifying a		
CC	compound that regulates the activity of one or more of the		
CC	polynucleotides, a method for producing a pharmaceutical composition, a		
CC	method for identifying a compound or small molecule that regulates the		
CC	activity in an animal of one or more of the polypeptides given in the		
CC	specification, a method for identifying a compound useful in treating		
CC	pain and a pharmaceutical composition comprising the one or more		
CC	polypeptides or their antibodies. The polynucleotide or the compound that		
CC	modulates its activity is useful for preparing a medicament for treating		
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction		

```
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published_pct_sequences.  
XX  
SQ Sequence 357 AA;  
  
Query Match          3.4%; Score 88; DB 7; Length 357;  
Best Local Similarity 21.1%; Pred.No. 53;  
Matches      83; Conservative   49; Mismatches    116; Indels     146; Gaps       22;  
  
QY      1 MDPKLGRMAASLLAVLLLLLLLGERGFESSPPSPALLEKVFQYIDLHQDEFVQTLEKWAIE 60  
        |::| :||| ||||| ::| :||| :||| :|||  
Db      1 MAPRRVRSLRGLPALLLLL--LFLGPWPAAS-----HGKYSR-----E 38  
  
QY      61 SDSVQPVP-RFRQEELFRMVAADTLQR LGARVASVDMG PQLPDQS LPIPPVILA ELG 119  
        ::||| :|||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db      39 KNQKPSPKRSEGEFRM-----EKLNQLWEK-----AQLHLPPVRLAE LH 80  
  
QY      120 SDPTKGTVCFYG HLDV QPAD-----RGDGWLTD-----PYVLTE--VD GKLY 159  
        :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db      81 AD-----LKIQERDELA WKKLKDGLD EDGEKEARLRNLNVILAK YGLDKGD 129  
  
QY      160 GRGATDN KGP VLAWIN AVSAFRA LEQDL PVNIKFI IEGME EAG--SVALEELVE KEK-DR 216  
        |::| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db      130 ARQVT SNS-----LSGTQED GLDDPRLE KLWHKA KTSG 162  
  
QY      217 FFGVDIV IVIS DN LWISO RKPAITYCTGR NSY-FMV EVKC RDQDFH SGTF-----G 266  
        ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db      163 KFS GEEL---DKL W----REFLHKHEKV HEYN VLVLET LSRT EEIHN VISPSDSL DI KG 214  
  
QY      267 GILHEPMD LVALLG SL-----VDSSGH-----ILVPGIY D-----EVVPLTEE EI 307  
        :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db      215 SVLHSRH TELKEK LR SINQG LD RL RRVSHQGYST EA EFEE PRVIDLWD LAQA SANLT DKEL 274  
  
QY      308 NTYKAIHDLEEYRN-S SRVEKF LFDTK EEILMH 340  
        ::||| :||| :||| :||| :||| :||| :||| :|||  
Db      275 EAFR-----EELKHFE AKIE KHNYQKOLEIAH 302  
  
RESULT 830  
ADD44963  
ID ADD44963 standard; protein; 357 AA.  
XX  
AC ADD44963;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P30533, SEQ ID NO 10394.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX
```





Db 1 MAPRRVRSFLRGLPALLLLLL---LPLGPWPAAS-----HGKYSR-----E 38

Qy 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119

Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQRHLPPVRLAELH 80

Qy 120 SDPTKGTVCFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159

Db 81 AD-----LKIQRDELAWKKLKDGLDEGEKEARLIRNLNVILAKYGLDGKKD 129

Qy 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG--SVALEELVEKEK-DR 216

Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLWHKAKTSG 162

Qy 217 FFSGVDYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266

Db 163 KFSGEEL---DKLW---REFLHHKEKVHEYNVLTLSRTEIHNENVISPSDLSDIKG 214

Qy 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVPPLTEEEI 307

Db 215 SVLHSRHTELKEKLR SINQGLDRLRRVSHQGYSTEAEEFPRVIDLWDLAQSANLTDKEL 274

Qy 308 NTYKAIHLDLEEYRN-SSRVEKFLFDTKEEILMH 340

Db 275 EAFR-----EELKHFEAKIEKHNYQKQLEIAH 302

RESULT 832

ADD46492

ID ADD46492 standard; protein; 357 AA.

XX

AC ADD46492;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P30533, SEQ ID NO 12173.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

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PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; P30533.

XX

PT New composition comprising two or more isolated polypeptides, useful for

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XX

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CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 357 AA;

Query Match 3.4%; Score 88; DB 7; Length 357;

Best Local Similarity 21.1%; Pred. No. 53;

Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

Qy 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60

Db 1 MAPRRVRSFLRGLPALLLLLL---LFLGPWPAAS-----HGKYSR-----E 38

Qy 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119

Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQRHLPPVRLAELH 80

Qy 120 SDPTKGTVCFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159

Db 81 AD-----LKIQRDELAWKKLKDGLDEGEKEARLIRNLNVILAKYGLDGKKD 129

Qy 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG--SVALEELVEKEK-DR 216

Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLWHKAKTSG 162

Qy 217 FFSGVDYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266

Db 163 KFSGEEL---DKLW---REFLHHKEKVHEYNVLTLSRTEIHNENVISPSDLSDIKG 214

Qy 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVPPLTEEEI 307

Db 215 SVLHSRHTELKEKLR SINQGLDRLRRVSHQGYSTEAEEFPRVIDLWDLAQSANLTDKEL 274

Qy 308 NTYKAIHLDLEEYRN-SSRVEKFLFDTKEEILMH 340

Db 275 EAFR-----EELKHFEAKIEKHNYQKQLEIAH 302

RESULT 833

ADJ75361

ID ADJ75361 standard; protein; 357 AA.

XX

AC ADJ75361;

XX

DT 20-MAY-2004 (first entry)

XX

DE Marker gene related amino acid sequence SEQ ID NO:613.

XX

KW bronchial asthma; chronic obstructive pulmonary disease;

KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

XX gene therapy; marker.

OS Homo sapiens.

XX

PN EP1394274-A2.

XX 03-MAR-2004.

PD

XX

PF 04-AUG-2003; 2003EP-00254857.

XX

PR 06-AUG-2002; 2002JP-00229312.

XX

PR 20-MAR-2003; 2003JP-00077212.

XX

PA (GENO-) GENOX RES INC.

XX

PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;

XX

DR WPI; 2004-193155/19.

XX

PT Testing for bronchial asthma or chronic obstructive pulmonary disease by

PT comparing the expression level of a marker gene in a biological sample

PT from a subject with the expression level of the gene in a sample from a

PT healthy subject.

XX

PS Example 11; SEQ ID NO 613; 241pp; English.

XX

CC The present invention describes a method of testing for bronchial asthma

CC or chronic obstructive pulmonary disease. The method comprises

CC determining the expression level of a marker gene in a biological sample

CC from a subject, comparing the expression level determined with the

CC expression level of the marker gene in a biological sample from a healthy

CC subject, and judging whether the subject has bronchial asthma or chronic

CC obstructive pulmonary disease. The marker gene comprises: (a) a group of

CC genes (S1) whose expression levels increase when respiratory epithelial

CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)

CC whose expression levels decrease when respiratory epithelial cells are

CC stimulated with interleukin-13. Also described: (1) a reagent (I) for

CC testing for bronchial asthma or chronic obstructive pulmonary disease;

CC (2) a kit for screening for a candidate compound for a therapeutic agent

CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

CC an animal model for bronchial asthma or chronic obstructive pulmonary

CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a

CC method for producing an animal model for bronchial asthma or chronic

CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial

CC asthma or chronic obstructive pulmonary disease, comprising the compound,

CC a marker gene or an antisense nucleic acid corresponding to a portion of

CC the marker gene, a ribozyme, a polynucleotide that suppresses the

CC expression of the gene through an RNAi effect or an antibody recognising

CC a protein encoded by a marker gene; and (7) a DNA chip for testing for

CC bronchial asthma or a chronic obstructive pulmonary disease, on which a

CC probe has been immobilised to assay a marker gene. (I) has respiratory

CC and antiasthmatic activities, and can be used in gene therapy. The method

CC is useful for testing for or screening for a therapeutic agent for

CC bronchial asthma or chronic obstructive pulmonary disease. The present

CC sequence is used in the exemplification of the present invention.

XX

SQ Sequence 357 AA;

Query Match 3.4%; Score 88; DB 8; Length 357;

Best Local Similarity 21.1%; Pred. No. 53;

Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60

DB 1 MAPRRVRSFRLGLPALLLLL---LFLGPWPAAS-----HGKYSR-----E 38

QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQPLPDGSLPIPPVILAEIG 119

DB 39 KNQPKPSPKRESGEBFRM-----EKLNLWEK-----AQLHLPPVRLAEHL 80

QY 120 SDPTKGTVCFYGHLDVQPAD-----RGDGLWLT-----PYVLTE--VDGKLY 159

DB 81 AD-----LKIQRDELAWKLLDGLDGEKEARLIRNLNVILAKYGLDGKDK 129

QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIFKPIEGMEEAG--SVALEELVEKEK-DR 216

DB 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLVHAKTSG 162

QY 217 FFSGVYIVISDNLWISQRKPAITYGTRGSY-FWVEVKCRDQDFHSGTF-----G 266

DB 163 KFSGEEL---DKLW----REFLHHKEKVHEYNVLLETLSRTEEHENVISPSDLSDIKG 214

QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307

DB 215 SVLHSRHTELKEKLSINQGLDLRLRRVSHQGYSTEAEEPRVIDLWDLAQSANLTDKEL 274

QY 308 NTYKAHLDLEEYRN-SSRVEKFLFDTKEEILMH 340

DB 275 EAFR-----BELKHEAKIEKHNHYQKQLEIAH 302

RESULT 834

ADQ91471

ID ADQ91471 standard; protein; 357 AA.

XX

AC ADQ91471;

XX

DT 23-SEP-2004 (first entry)

XX

DE Amino acid sequence of a receptor-associated peptide (RAP).

XX

KW neurotrophin; neural growth factor; NGF;

KW brain derived neurotrophic factor; BDNF; neurotrophin-3; NT-3; NT-4/5;

KW Vps1Op-domain receptor; SorLA; Sortilin; SorCS1; SorCS-2; SorCS-3;

KW neurotrophin related disease; inflammatory pain; pancreas disease;

KW kidney disorder; lung disorder; cardiovascular disorder; tumour;

KW psychiatric disorder; neuronal disorder; Alzheimer's disease;

KW parkinson's disease; Huntington's chorea; stroke; ALS;

KW peripheral neuropathy; necrosis; neuron loss; nerve damage;

KW kidney dysfunction; injury; aberrant sprouting; epilepsy; schizophrenia;

KW peripheral neuropathy; distal sensorimotor neuropathy;

KW autonomic neuropathy; gastrointestinal tract; urinary bladder atony;

KW post-polio syndrome; AIDS-associated neuropathy; hereditary neuropathy;

KW Charcot-Marie-Tooth disease; Refsum's disease; Abetalipoproteinemia;

KW Tangier disease; Krabbe's disease; Metachromatic leukodystrophy;

KW Fabry's disease; Dejerine-Sottas syndrome; depression; mania;

KW Down's syndrome; receptor-associated peptide; RAP.

XX

OS Unidentified.

XX

PN WO2004056385-A2.

XX

PD 08-JUL-2004.

XX

PF 19-DEC-2003; 2003WO-DK000919.

XX

PR 20-DEC-2002; 2002DK-00001977.

XX

PA (UYAA-) UNIV AARHUS.

XX

PI Nykjaer A, Petersen CM;

XX

DR WPI; 2004-500263/47.

XX

PT Modulating the activity of a (pro-)neurotrophin in a cell or an organism,

PT useful for treating e.g. inflammatory disorders, comprises administering

PT an agent that inhibits binding of (pro-)neurotrophin with Vps1 Op-domain

PT receptor.

XX

PS Disclosure; SEQ ID NO 12; 66pp; English.

XX

CC The specification describes a method for modulating the activity of

CC neurotrophins, such as neural growth factor (NGF), brain derived

CC neurotrophic factor (BDNF), neurotrophin-3 (NT-3), and NT-4/5. This

CC modulation is carried out by interfering with binding between a

CC neurotrophin and a receptor of the Vps1Op-domain receptor family.

CC Alternatively, expression of the receptor of the Vps1Op-domain receptor

CC family is modulated. Such receptors are selected from SorLA, Sortilin,

CC SorCS1, SorCS-2, or SorCS-3. The soluble receptor is useful in the

CC preparation of a medicament or a diagnostic agent for diagnosing

CC neurotrophin related diseases. Agents which modulate the activity of



CC neurotrophins are useful for treating diseases or disorders, including  
CC inflammatory pain, diseases or disorders of pancreas, kidney disorders,  
CC lung disorders, cardiovascular disorders, various types of tumours,  
CC psychiatric disorders or neuronal disorders, Alzheimer's disease,  
CC Parkinson's disease, Huntington's chorea, stroke, ALS, peripheral  
CC neuropathies, necrosis or loss of neurons, nerve damage to trauma, kidney  
CC dysfunction, injury, and the toxic effects of chemotherapeutics used to  
CC treat cancer and AIDS, aberrant sprouting in epilepsy, schizophrenia,  
CC pancreas or lung injury and/or dysfunction, injury and/or dysfunction of  
CC the central and/or peripheral nervous systems, peripheral neuropathy,  
CC distal sensorimotor neuropathy, or autonomic neuropathies, such as  
CC reduced motility of the gastrointestinal tract or atony of the urinary  
CC bladder, post-polio syndrome or AIDS-associated neuropathy; hereditary  
CC neuropathies, such as Charcot-Marie-Tooth disease, Refsum's disease,  
CC Abetalipoproteinemia, Tangier disease, Krabbe's disease, Metachromatic  
CC leukodystrophy, Fabry's disease, and Dejerine-Sottas syndrome,  
CC depression, mania or Down's syndrome. The present represents a receptor-  
CC associated peptide (RAP). Peptides derived from RAP may be used as agents  
CC in the method of the invention to modulate neurotrophin activity.

XX  
SQ Sequence 357 AA;

Query Match 3.4%; Score 88; DB 8; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLLLGERGMFSSPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLLL--LFLGPWPAAS-----HGKYSR-----E 38  
QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQLPDGQSLPIPPVILAE 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQLHLPPVRLAE 80  
QY 120 SDPTKGTVCYFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLKDGLDEGEKEARLIRNLNLVILAKYGLDGK 129  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLVHAKTSG 162  
QY 217 FFGVDYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL---DKLW----REFLHKKEKVHEYNVLLETLSRTEEIHENVISPSDLSIKG 214  
QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307  
Db 215 SVLHSRHTELKEKLSINQGLDRLRRVSHQGYSTEAFEEPRVIDLWDLAQSANLTDKEL 274  
QY 308 NTYKAHLDLEEYRN-SSRVEKFLDFTKKEILMH 340  
Db 275 EAFR-----EELKHFEAKIEKHNHYQKQLEIAH 302

RESULT 835  
ADP23135  
ID ADP23135 standard; protein; 357 AA.

XX ADP23135;

AC ADP23135;

XX 18-NOV-2004 (first entry)

DT PRO polypeptide SEQ ID NO:229.

DE PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
XX osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;  
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

PN

PD

XX 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

PR (GETH ) GENENTECH INC.

PA Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
PI Wu TD;

XX WPI; 2004-419628/39.

DR N-PSDB; ADP23134.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.

XX Claim 7; SEQ ID NO 229; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence represents a PRO protein  
CC of the invention.

XX Sequence 357 AA;

Query Match 3.4%; Score 88; DB 8; Length 357;  
Best Local Similarity 21.1%; Pred. No. 53;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLLLGERGMFSSPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLLL--LFLGPWPAAS-----HGKYSR-----E 38  
QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQLPDGQSLPIPPVILAE 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQLHLPPVRLAE 80  
QY 120 SDPTKGTVCYFYGHLDVQPAD-----RGDGWLTD-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLKDGLDEGEKEARLIRNLNLVILAKYGLDGK 129  
QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLVHAKTSG 162  
QY 217 FFGVDYIVISDNLWISQRKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266

Db 163 KFSGEEL-----DKLM-----REFLHKKEKVHEYNVLLLETLSRTEETHENVISPSDLSDIKG 214

QY 267 GILHEPMADLVALIGSL-----VDSSGH-----ILVPGIYD-----EVVPLTEEEI 307

Db 215 SVLHSRHTELKEKLR SINQGLDRLRRVSHQGYSTEA EFEEPRVIDLWDLAQSANLTDKEL 274

QY 308 NTYKAIHLDLBEYRN-SSRVEKFLFDTKEEILMH 340

Db 275 EAFR-----BELKHFEAKIEKHNHYQKOLEIAH 302

RESULT 836

ADA35354

ID ADA35354 standard; protein; 364 AA.

XX

AC ADA35354;

XX

DT 20-NOV-2003 (first entry)

XX

DE Acinetobacter baumannii protein #2515.

XX

KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;

KW plant biocontrol agent.

XX

OS Acinetobacter baumannii.

XX

PN US6562958-B1.

XX

PD 13-MAY-2003.

XX

PF 04-JUN-1999; 99US-00328352.

XX

PR 09-JUN-1998; 98US-0088701P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Breton G, Bush D;

XX

DR WPI; 2003-576092/54.

DR N-PSDB; ADA31228.

XX

PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents

PT for diagnosing a bacterial disease, as components of antibacterial

PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for

PT plants.

XX

PS Example; SEQ ID NO 6641; 328pp; English.

XX

CC The invention relates to isolated Acinetobacter baumannii nucleic acids.

CC The A. baumannii nucleic acids and polypeptides are useful as reagents

CC for diagnosing a bacterial disease, as components of antibacterial

CC vaccines, as targets for antibacterial drugs, to detect the presence of

CC A. baumannii and other Acinetobacter species in a sample, in screening

CC compounds for the ability to interfere with the A. baumannii life cycle

CC or to inhibit A. baumannii infection, and as biocontrol agents for

CC plants. The present sequence represents the amino acid sequence of an A.

CC baumannii protein.

XX

SQ Sequence 364 AA;

Query Match 3.4%; Score 88; DB 6; Length 364;

Best Local Similarity 15.6%; Pred. No. 54;

Matches 59; Conservative 58; Mismatches 102; Indels 160; Gaps 15;

QY 203 SVALEELVEKEDRFFSGVDY-----IVISDNLWISQKPAITYGTRG 245

Db 2 SIDISELLKPINDSLCCGEDYSFNSFEHFIKARTQDDLLDQGDWVAERKQA----- 54

QY 246 NSYFMVEVKCRDQDFHSGTGGILHEPMADLVALIGSLVDSSGHI-----LVPGI----- 295

Db 55 -----DWDFVAKSVSTLLIEKTKD-IRLLTWVIEAWTHLNGFEGMKGITLTHT 102

QY 296 -----YDEVVPLTEEE-----INT---YKAIHLD----- 316

Db 103 MLNQYWQDIHPITIEDDDLQRIQLLQGLINQLPMLLKKVPLTNTAPYNNLDDYDNFLYHE 162

QY 317 -----LEEYRNS---SRVEKF---LFDTK-----EELMHLMWR 343

Db 163 NIRRKQTEEYESQSGPSELEQFQAIFNTSKTFQYSNYQEFNSVLTEWNVLKQTLDLHMG 222

QY 344 YPSLSIHGIEGAFD-----EPGKTVIPGRVIG-- 371

Db 223 LDSPSFAAIDSAFETIHSTLRKIYKAEAFGTGLAPSQEQAAVITTPSMENQVPVQIVSDQ 282

QY 372 -KFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSN-----KMVVSMTLGLHPWIANID 423

Db 283 PMFQPQAQTHLANREQAMKVLQEIADYFQANEPHSPVSYMLQKTIKWSQMPLHEWLAQVI 342

QY 424 DTQYLAAKRAIRTVFGTEP 442

Db 343 KDEH--PLQMVQEMLGVQP 359

RESULT 837

ABM69223

ID ABM69223 standard; protein; 399 AA.

XX

AC ABM69223;

XX

DT 20-NOV-2003 (first entry)

XX

DE Photorhabdus luminescens protein sequence #2320.

XX

KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

KW detection; food; gene expression; plant; animal; microorganism; toxin;

KW antibiotic; biopesticide; virulence factor; disease model; plague;

KW whooping cough.

XX

OS Photorhabdus luminescens.

XX

PN WO200294867-A2.

XX

PD 28-NOV-2002.

XX

PF 07-FEB-2002; 2002WO-IB003040.

XX

PR 07-FEB-2001; 2001FR-00001659.

XX

PA (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;

XX

DR WPI; 2003-148459/14.

XX

PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,

PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX

PS Claim 2; SEQ ID NO 2320; 1205pp; French.

XX

CC The invention relates to the isolation of genes and their encoded

CC proteins from Photorhabdus luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of P. luminescens

CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the

CC polypeptides encoded by the genes are used for detection/identification

CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

CC carry a gene-containing vector are used to select compounds that

CC modulate, regulate, induce or inhibit expression of the genes in plants,

CC animals or microorganisms other than P. luminescens and are able to alter

CC response or sensitivity to toxins and antibiotics produced by P.

CC luminescens. Cells transformed to express the genes are useful for

CC recombinant production of the proteins, particularly toxins and

CC antibacterials useful as insecticides, bactericides and fungicides. The

CC genes, proteins, vectors containing the genes and Ab are also useful





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PR 22-JUL-1997; 97US-0053344P.
PR 22-JUL-1997; 97US-0053377P.
PR 03-SEP-1997; 97US-0057483P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
XX
PI Choi GH, Erwin AL, Hanson MS, Lathigra R;
XX
XX WPI; 1999-189980/16.
DR N-PSDB; AAX61503.
XX
PT New isolated Borrelia burgdorferi nucleic acids - used to develop
PT products for the diagnosis, prevention and treatment of diseases caused
PT by Borrelia, particularly Lyme disease.
XX
PS Claim 12; Page 71; 275pp; English.
XX
CC This sequence represents a Borrelia burgdorferi (Bb) protein of the
CC invention, which is suitable for use in a vaccine. The Bb polypeptides
CC can be used in vaccines for eliciting protective antibodies to members of
CC the Borrelia genus, particularly for the use against Lyme disease in
CC humans and animals. They can be used for preventing or attenuating an
CC infection caused by a member of the Borrelia genus. The products can also
CC be used for detection of members of the Borrelia genus
XX
SQ Sequence 505 AA;

Query Match 3.4%; Score 88; DB 2; Length 505;
Best Local Similarity 20.0%; Pred. No. 90;
Matches 104; Conservative 83; Mismatches 185; Indels 148; Gaps 26;

QY 33 ALLEKVFQYIDLHQDEFV-----QTLKEWVAIESDSVQVPRFRQ-----ELFR 76
Db 11 ALLSKDELIPFYKFLFLFFFTLLACSKVSKDFIVFNKD-VKTSRIDNPNSNVLEVNK 69

QY 77 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE-----LGSDP--T 123
Db 70 MEDFFGDIIDLKGYKILSV---QENLNLDVYFEQVVLQAQNFNLNAYLFIIGFDPKIK 125

QY 124 KGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAW---INAVSA 179
Db 126 AGTILFKTQIDIDPKNSYNWYLED--ITGDYDFNIVIOGFLKDKSVLYVFQKSVLNDVSS 183

QY 180 FRALEQDLPNIKFIIEGMEEAGSVALEELVEKEKDRF-FSGVDYIVISDNLWISQRKPA 238
Db 184 YRPIFFD-KVNGTVLIN--KYARSSAYEE--NRSRESYPISLEKYEKVGEDLIISKIE-- 236

QY 239 IYTGTRGNSVEMVEVKCRDQDFHSGTGGILHEPMAADLVALLGSLVDSSGHILVPGIYDE 298
Db 237 -----KYEYSNVQGR-----YCLSSVSEKVGKI-DNNIYKT 266

QY 299 VVPLTEEEINTYKAIH---LDLEEYRNSRVEK-----FLFDTKEEILMHLWRYPSLSIH 350
Db 267 LKNLSKDEV--YKFLHGVMYDVHDY-NKMHVKDIDEVLFLSFERQSSEINLFRKNSQEVA 323

QY 351 GIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVS 410
Db 324 KIE-YISKPAYNT-----LNVSA-----KSLFS 345

QY 411 MTLGLHPWIANDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPL 470
Db 346 DLIVYNFWIKIVD-----KENIEIKIDTSTNSYDMSGFSGTGKFPDE---NVLNVKK 394

QY 471 GAVD-----DGEHSQNEKINRWN-----YIEGTKLFAAFF 500
Db 395 GSSDIYFIPSGNVYVKDKIYDFSYPHLTVIDENKIYYGIF 434

RESULT 840
AAY57085
ID AAY57085 standard; protein; 563 AA.
XX
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```
AC AAY57085;
XX
DT 28-FEB-2000 (first entry)
XX
DE Human rhodopsin kinase amino acid sequence.
XX
KW Neglected target tissue antigen; NTTA; autoimmunity; autoimmune response;
KW immunotherapeutic agent; insulin dependent diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
KW uveoretinitis; inflammatory response.
XX
OS Homo sapiens.
XX
PN WO9956763-Al.
XX
PD 11-NOV-1999.
XX
PF 07-MAY-1999; 99WO-US010250.
XX
PR 07-MAY-1998; 98US-0084636P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Kaufman DL, Tian J, Olcott A;
XX
DR WPI; 2000-052905/04.
XX
PT Administration of neglected target tissue antigens to modulate immune
PT responses.
XX
PS Disclosure; Page 28; 79pp; English.
XX
CC Amino acid sequences AAY57063-Y57091 are examples of neglected target
CC tissue antigens NTTAs. NTTAs are antigens (whole antigens or fragments)
CC not involved in autoimmunity. These peptides and proteins are used in the
CC method of the invention which involves administering an NTTA as an
CC antigen based immunotherapeutic agent, to a host afflicted with an
CC autoimmune response associated with an autoimmune disease. The
CC immunotherapeutic agent is used to treat autoimmune diseases such as
CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory
CC immune responses. The NTTA induces regulatory tolerance by elicitation of
CC regulatory T cells among T cells recognizing the NTTA but not
CC participating in the immune response. The NTTA are capable of recognition
CC by substantial populations of uncommitted T cells which can be primed, or
CC biased, towards regulatory responses to provide effective treatment. The
CC NTTA are effective in regulating undesirable immune responses even when
CC target determinants used as agents promoting tolerance agents have failed
CC to induce an effective regulatory T cell response. NTTAs as agents
CC promoting tolerance are anticipated to be safer than use of target
CC determinants
XX
SQ Sequence 563 AA;

Query Match 3.4%; Score 88; DB 3; Length 563;
Best Local Similarity 22.7%; Pred. No. 1.1e+02;
Matches 48; Conservative 33; Mismatches 66; Indels 64; Gaps 9;

QY 11 SLLAVLLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSV---QPV 67
Db 8 TVVANSAFIAARGSFDSGSSQPSRDKKYLAKLKLPLPSKCESLRDSLSLEFESVCLEQPI 67

QY 68 PR--FRQ-----ELFRMMA---VAADTLQRLGAR----- 91
Db 68 GKXLFQQFLOSAEKHLPALELWKDIEDYDADNDLQPOKACTILAQYLDPOAKLFCSFELD 127

QY 92 ---VASVDMGPQQLPDGQSLPIPPVILAEELGSDPTK---GTVCF-----YGHLDVQPADR 140
Db 128 EGIVAKFKEGPVEIQDGLFQLQATLAHLGQAPFQFEYLGSLYFLRFLQWKWLEAQP--M 185

QY 141 GDGWLTDPPYVL-----TEVDGKLY 159
Db 186 GEDWFLDFRVLGKGFGFEVSACQMKATGKLY 216
```

RESULT 841  
ADG12800  
ID ADG12800 standard; protein; 563 AA.  
XX AC  
XX ADG12800;  
DT 26-FEB-2004 (first entry)  
XX  
DE Human rhodopsin kinase GRK1 amino acid sequence SEQ ID NO:23.  
XX  
KW G protein coupled receptor; GPCR;  
KW G protein coupled receptor internalisation; arrestin;  
KW G protein coupled receptor kinase; GRK; modified GRK; cardiant;  
KW cardiovascular; hypotensive; antiarteriosclerotic; nephrotropic;  
KW antidiabetic; antiasthmatic; respiratory; antiinflammatory; antiallergic;  
KW antirheumatic; antiarthritic; gastrointestinal; antidepressant;  
KW analgesic; anorectic; antiparkinsonian; nootropic; neuroprotective;  
KW immunosuppressive; cytostatic; G protein antagonist;  
KW aberrant GPCR desensitisation; angina pectoris; hypertension;  
KW myocardial infarction; arrhythmia; congestive heart failure;  
KW atherosclerosis; renal failure; diabetes; asthma; chronic bronchitis;  
KW rhinitis; allergy; rheumatoid arthritis; inflammatory bowel disease;  
KW gastric ulcer; pain; obesity; depression; obsessive-compulsive disorder;  
KW Parkinson's disease; Alzheimer's disease; multiple sclerosis; cancer;  
human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003097795-A2.  
XX  
PD 27-NOV-2003.  
XX  
PF 12-MAY-2003; 2003WO-US014581.  
XX  
PR 13-MAY-2002; 2002US-0379986P.  
PR 07-AUG-2002; 2002US-0401698P.  
XX  
PA (NORA-) NORAK BIOSCI INC.  
XX  
XX Oakley RH, Hudson CC;  
PI  
XX  
DR WPI; 2004-022856/02.  
DR N-PSDB; ADG12801.  
XX  
PT Identifying a compound which alters GPCR internalization by monitoring  
PT affinity for arrestin, useful for treating disorders such as  
PT hypertension, myocardial infarction, atherosclerosis, diabetes, asthma,  
PT allergies and cancer.  
XX  
PS Disclosure; SEQ ID NO 23; 127pp; English.  
XX  
CC The present invention describes a method for identifying a compound (I)  
CC which alters G protein coupled receptor (GPCR) internalisation. The  
CC method comprises providing a cell comprising a GPCR, an arrestin, and a  
CC modified G protein coupled receptor kinase (GRK), exposing the cell to  
CC the compound, determining the cellular distribution of the GPCR,  
CC arrestin, or modified GRK, and monitoring a difference between the  
CC distribution of the GPCR, arrestin, or modified GRK in the cell in the  
CC presence and absence of the compound. The GPCR in the method described  
CC above is at least partially internalised in an agonist-independent manner  
CC upon expression of the GRK. (I) has cardiant, cardiovascular,  
CC hypotensive, antiarteriosclerotic, nephrotropic, antidiabetic,  
CC antiasthmatic, respiratory, antiinflammatory, antiallergic,  
CC antirheumatic, antiarthritic, gastrointestinal, antidepressant,  
CC analgesic, anorectic, antiparkinsonian, nootropic, neuroprotective,  
CC immunosuppressive and cytostatic activities, and can be used as a G  
CC protein antagonist. The methods and compositions of the present invention  
CC are useful for treating disorders associated with aberrant GPCR  
CC desensitisation, such as angina pectoris, essential hypertension,  
CC myocardial infarction, arrhythmias, congestive heart failure,  
CC atherosclerosis, renal failure, diabetes, asthma, chronic bronchitis,

CC rhinitis, allergies, rheumatoid arthritis, inflammatory bowel disease,  
CC gastric ulcers, pain, obesity, depression, obsessive-compulsive disorder,  
CC Parkinson's disease, Alzheimer's disease, multiple sclerosis and cancer.  
CC The present sequence is used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 563 AA;  
Query Match 3.4%; Score 88; DB 8; Length 563;  
Best Local Similarity 22.7%; Pred. No. 1.1e+02;  
Matches 48; Conservative 33; Mismatches 66; Indels 64; Gaps 9;  
QY 11 SLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSV---QPV 67  
Db 8 TVVANSAFIAARGSPDSSSQPSRDKKYLAKLKLPPLSKCESLRDSLSLEFESVCLEQPI 67  
QY 68 PR--FRQ-----ELFRMMA---VAADTLQRLGAR----- 91  
Db 68 GKKLFOQFLQSAEKHLPALELWKDIEDYDTADNDLQPKAQTILAQYLDPOAKLFCSF 127  
QY 92 ---VASVDMGPPQQLPDGQSLPIPPVILAEIGSDPTK---GTVCF-----YGHLDVQPADR 140  
Db 128 EGIVAKFKEGPEIQQDGLFQPLLOATLAHLGQAPFQEYLGSLYFLRFLQWKWLEAQP--M 185  
QY 141 GDGWLTPPYVL-----TEVDGKLY 159  
Db 186 GEDWFLDFRVLGKGFGGEVSACQMKATGKLY 216  
RESULT 842  
ABB55505  
ID ABB55505 standard; protein; 576 AA.  
XX  
AC ABB55505;  
XX  
DT 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX  
DE Lactococcus lactis protein ezrA.  
XX  
KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
XX  
OS Lactococcus lactis; IL1403.  
XX  
PN FR2807446-A1.  
XX  
PD 12-OCT-2001.  
XX  
PF 11-APR-2000; 2000FR-00004630.  
XX  
PR 11-APR-2000; 2000FR-00004630.  
XX  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
XX  
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
XX  
DR WPI; 2002-043418/06.  
XX  
PT New nucleotide sequence useful in the identification of Lactococcus  
PT lactis and related species.  
XX  
PS Claim 6; SEQ ID NO 2207; 2504pp; French.  
XX  
CC The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic  
CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at







Query Match 3.4%; Score 88; DB 8; Length 682;  
Best Local Similarity 21.1%; Pred. No. 1.4e+02;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLL--LFLGPWPAAS-----HGKYSR-----E 38

QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQLHLPPVRLAELH 80

QY 120 SDPTKGTVCFYGHLDVQPAD-----RGDGWLT-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLDGLDEGEKEARLIRNLNVLAKYGLDGKGD 129

QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDPRLEKLWHKAKTSG 162

QY 217 FFSGVYIVISDNLWISQRKPAITYGTRNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL-----DKLW-----REFLHHKEKVHEYNVLLETLSRTEEIHENVISPSDLSDIKG 214

QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVPPLTEEEI 307  
Db 215 SVLHSRHTELKEKLSINQGLDRLRRVSHQGYSTEAEFEPRVIDLWDLAQSANLTDKEL 274

QY 308 NTYKAITHLDLEEYRN-SSRVEKFLFDTTKEEILMH 340  
Db 275 EAFR-----EELKHFEAKIEKHNHYQKQLEIAH 302

RESULT 846  
ADQ39605  
ID ADQ39605 standard; protein; 682 AA.

XX  
AC ADQ39605;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1268.  
XX  
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
KW cardiant; gene therapy; human.  
XX Homo sapiens.  
XX WO2004058052-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-US040978.  
XX  
PR 20-DEC-2002; 2002US-0434778P.  
PR 10-MAR-2003; 2003US-0453135P.  
PR 30-APR-2003; 2003US-0466412P.  
PR 23-SEP-2003; 2003US-0504955P.  
XX  
PA (APPL-) APPLERA CORP.  
XX  
PI Cargill M, Devlin JJ, Iakoubova O;  
XX  
DR WPI; 2004-533949/51.  
DR N-PSDB; ADQ38777.  
XX  
PT Identifying an individual who has an altered risk for developing  
PT myocardial infarction by detecting a single nucleotide polymorphism in  
PT the individual's nucleic acids.  
XX  
PS Claim 10; SEQ ID NO 1268; 145pp; English.  
XX

CC The invention relates to a novel method for identifying an individual who  
CC has an altered risk for developing myocardial infarction. The method  
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
CC the nucleotide sequences given in the specification in the individual's  
CC nucleic acids, where the presence of the SNP is correlated with an  
CC altered risk for myocardial infarction in the individual. The invention  
CC further comprises: an isolated nucleic acid molecule comprising at least  
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
CC the specification or its complement and encoding any one of the amino  
CC acid sequences given in the specification; an isolated polypeptide  
CC comprising an amino acid sequence given in the specification; an antibody  
CC that specifically binds to the polypeptide or its antigen-binding  
CC fragment; an amplified polynucleotide containing an SNP given in the  
CC specification and which is between about 16 and 1000 nucleotides in  
CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
CC method for identifying an agent useful in treating or preventing  
CC myocardial infarction. The novel detection method has cardiant activity.  
CC The nucleic acids of the invention may be used in gene therapy. The  
CC method is useful in identifying an individual who has an increased or  
CC decreased risk for developing myocardial infarction and for preparing a  
CC composition for treating or preventing myocardial infarction. This  
CC sequence represents the protein of a human myocardial infarction-  
CC associated gene containing one or more SNP's of the invention. Note: This  
CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.

XX  
SQ Sequence 682 AA;

Query Match 3.4%; Score 88; DB 8; Length 682;  
Best Local Similarity 21.1%; Pred. No. 1.4e+02;  
Matches 83; Conservative 49; Mismatches 116; Indels 146; Gaps 22;

QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLL--LFLGPWPAAS-----HGKYSR-----E 38

QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQLHLPPVRLAELH 80

QY 120 SDPTKGTVCFYGHLDVQPAD-----RGDGWLT-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKKLDGLDEGEKEARLIRNLNVLAKYGLDGKGD 129

QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDPRLEKLWHKAKTSG 162

QY 217 FFSGVYIVISDNLWISQRKPAITYGTRNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL-----DKLW-----REFLHHKEKVHEYNVLLETLSRTEEIHENVISPSDLSDIKG 214

QY 267 GILHEPMADLVALLGSL-----VDSSGH-----ILVPGIYD-----EVPPLTEEEI 307  
Db 215 SVLHSRHTELKEKLSINQGLDRLRRVSHQGYSTEAEFEPRVIDLWDLAQSANLTDKEL 274

QY 308 NTYKAITHLDLEEYRN-SSRVEKFLFDTTKEEILMH 340  
Db 275 EAFR-----EELKHFEAKIEKHNHYQKQLEIAH 302

RESULT 847  
ABG25201  
ID ABG25201 standard; protein; 687 AA.  
XX  
AC ABG25201;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #25192.  
XX













Db 426 LIQGNRV 432

RESULT 853  
ADJ68276

ID ADJ68276 standard; protein; 779 AA.

XX

AC ADJ68276;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human heat mitochondrial protein as a therapeutic target SeqID82.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

XX WO2003087768-A2.

PN

XX

PD 23-OCT-2003.

XX

PF 04-APR-2003; 2003WO-US010870.

XX

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

PI

DR WPI; 2003-845369/78.

XX

PT Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX

PS Claim 1; SEQ ID NO 82; 180pp; English.

XX

CC This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, nootropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytostatic activities. This polypeptide sequence is a human heart

CC mitochondrial protein of the invention.

XX

SQ Sequence 779 AA;

QY 140 RGDGWLTDPPYVLTEVDGKLYGRGATD-----NKGPLVLAWINAVSAFRALEQDLPVNIKFI 194

Db 93 EREGRLRAAYNLVK-----RGITNLCVIGDGS-----LTGADTFRSEWSDL----- 134

QY 195 IEGMEEAGSVALEELVEKEK-----DRFFSGVDYIVISDNLW--ISQRKPAITYG 242

Db 135 LSDLOKAGKITDEEATKSSYLIVGLVGSIDNDFCGTDMTIGTDSALHRIMEIVDAIT-- 192

QY 243 TRGNSY---FMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVP----- 293

Db 193 TTAQSHQRTFVLEVWGR---HCG-----YLALVTSLSGADWVFIPECPDD 236

QY 294 -----GIYDE-VVPLTEEEINTYKAHLDLEEYRNSR 325

Db 237 DWEEHLRRLSETTRGSRNLNIIIVAEGAIDKNGKPITSEDIKNLV----- 282

QY 326 VEKFLFDTKKEIILMHLWRYPVPSLSIHGIEGAFD-----EPGKTVI-----PCRVI- 370

Db 283 VKRLGYDTRVTVLGHVQR-----GGTPSAFDRILGSRMGVEAVMALLEGTPDTPACVVS 336

QY 371 --GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMITGLHPWIANIDDTQYL 428

Db 337 LSGNQAVRL-PLMECVQVTKDVTKAMDE-----KKFDEALKLRGRSFMNWNVEVYKLL 387

QY 429 AAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGSEHSQNEKINRW 488

Db 388 AHVR-----PPVSKSGS-----HTVAVMNVGAPAAAGMNAAVRSTVRIG 425

QY 489 YIEGTKL 495

Db 426 LIQGNRV 432

RESULT 854

ABU07399

ID ABU07399 standard; protein; 780 AA.

XX AC ABU07399;

DT 28-JAN-2003 (first entry)

XX DE Protein differentially regulated in prostate cancer #2.

XX KW Prostate cancer; gene expression; differential regulation;

XX KW molecular marker; drug target; cancer detection; cancer diagnosis;

XX KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX OS Homo sapiens.

XX PN WO200281638-A2.

XX PD 17-OCT-2002.

XX PF 08-APR-2002; 2002WO-US010824.

XX PR 06-APR-2001; 2001US-0281731P.

XX PR 06-APR-2001; 2001US-0281732P.

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.

XX PI Sun Z, Jay G;

XX DR WPI; 2003-058520/05.

XX PT Novel genes which are differentially regulated in prostate cancer, useful

PT for diagnosing prostate cancer in prostate tissue sample and assessing

PT therapeutic or preventive intervention in prostate cancer patients.

PS Claim 1; Page 199-201; 416pp; English.

XX CC The invention describes genes (I) which are differentially regulated in

CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a



QY 89 GARVASVDMGPQQLPDG-----QSLPIPPVILAEIAGSDPTKGTVCYFGHLDVQPAD 139  
Db 45 GARVFFVHEGYQGLVDGGDHKEATWESVS-----MMLQLG-----GTV--IGSARCKDFR 93  
QY 140 RGDGWLTDPPYLTVEVDGKLYGRGATD-----NKGVPVLAWINAVSAFRALEQDLPPVNIKFI 194  
Db 94 EREGRLRAAYNLVK-----RGITNLCVIGDGS-----LTGADTFRSEWSDL----- 135  
QY 195 IEGMEEAGSVALEELVEKEK-----DRFFSGVDYIVISDNLW--ISQRKPAITYG 242  
Db 136 LSDLQKAGKITDEEATKSSYLNIIVGLVGSIDNDFCGTDMTIGTDSALHRIMEIVDAIT-- 193  
QY 243 TRGNSY---FMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVP----- 293  
Db 194 TTAQSHQRTFVLEVMGR-----HCG-----YLALVTSLSCGADWVFPECPDD 237  
QY 294 -----GIYDE-VVPLTEEBEINTYKAIHLDLEEYRNSR 325  
Db 238 DWEEHLCRRLSETRTRGSRNLNIIIVAEGAIDKNGKPITSEDIKNLV----- 283  
QY 326 VEKFLFDTKEEILMHLWRYPSLSIHGEGAFD-----EPGKTVI-----PGRVI- 370  
Db 284 VKRLGYDTRVTVLGHVQR-----GGTPSAFDRILGSRMGVEAVMALLEGTPTDPACVVS 337  
QY 371 --GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYL 428  
Db 338 LSGNQAVRL-PLMECVQVTKDVTKAMDE-----KKFDEALKLRGRSFMNWVEVYKLL 388  
QY 429 AAKRAIRTVFGTEPDMIRDCSTIPIAKMFOEIVHKSVVLIPLGAVDGGEHSQNEKINRW 488  
Db 389 AHVR-----PPVSKSGS-----HTVAVMNVGAPAAAGMNAAVRSTVRIG 426  
QY 489 YIEGTXL 495  
Db 427 LIQGNRV 433

RESULT 856

ABB631178  
ID ABB631178 standard; protein; 1121 AA.  
XX  
AC ABB631178;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 16326.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
DR N-PSDB; ABL07281.  
XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX

PS Disclosure; SEQ ID NO 16326; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1121 AA;

Query Match 3.4%; Score 88; DB 4; Length 1121;  
Best Local Similarity 19.3%; Pred. No. 3.1e+02;  
Matches 97; Conservative 93; Mismatches 148; Indels 164; Gaps 29;  
QY 12 LLAVLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFR 71  
Db 279 LITVKYVVLQFETLKDSNKPILLATL-----KYLMTLQRNVASABCF TK--RFH 326  
QY 72 QELFRM---MAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVIL---AELGSDPTKG 125  
Db 327 EELLHLVLRMSVSSATVASMAKV-YITLSQRQ---HQEQEIEQHILETVYVYKIPQNPKN 382  
QY 126 TVC-----FYGH-----LDVQPADRGDGLTDPYVLT 152  
Db 383 ITYEQFRNELTRYLKTLYQFPPLQEFDFYARVLARNLLNLESSCL-ENFLNDDTIIE 441  
QY 153 EVDGKLY-----GRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALE 207  
Db 442 SEFQRLYVNIISRSVGATGN-----IQIHTTTSRALRDEQAALQLRL---NNTDPESPEMQ 493  
QY 208 ELVEKEKDRFFSGVDYIVISDNLWISQ---RKPAITYGTRGNSYFMVEVKCRDQDFHSGT 264  
Db 494 QLL---KEYAFS---YMRIHAVLMVNKLHVRVYVADIYETLAK--FVLEMTPLNENI---T 542  
QY 265 FGGILHEPMADLVALL-GSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNS 323  
Db 543 LYG--SESLANMLVLLHGDLDKSDGEMI-----DKVSGLTEE-----FDLP---T 582  
QY 324 SRVEKFLFDTKKEILMHLWRYPSLSIHGEGAFDEPGTKTVIPGRVIGKFSIRLVPH--- 380  
Db 583 NRWVKLLMKYK---MLHIYKDSNVNKKG-----SIALTAHLRL 617  
QY 381 --MNVSAVEKQVTRHLEDVFSK-----RNSSN-----KMVVSMTLGL 415  
Db 618 IDMNCSALDSWLLRYI--IFKESLSLLIKNMIRIRSEVTNSSQRNRLPLKYILNMVVNL 675  
QY 416 HPWIANIDDTQYLAAKRAIRTV 437  
Db 676 -----RLDEAQFSLSIKLLHVL 692

RESULT 857

ABU24033  
ID ABU24033 standard; protein; 1241 AA.  
XX  
AC ABU24033;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #9560.  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Clostridium acetobutylicum.  
OS  
XX WO200277183-A2.  
PN  
XX 03-OCT-2002.  
PD







Qy 230 LWTISQKPAITYG---TRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALLGSLVDS 286  
Db 256 ---TNQREAAASHGFGKTSNGS-FKVN-SCKD---HIG-----KS 286  
Qy 287 SGHILVPGIYDEVVPLTEEE-----INTVKAHLDLLEEYRNSRVEKFL 330  
Db 287 MPHVLDEDEVYETVVDTSEEDSFSLCPSKCRTKNLQKVRTSKTRKKIFHE-ANADECEKSK 345  
Qy 331 FDTKEEILMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVI---GKFSIRLVPHMNVSAV 386  
Db 346 NOVKE-----KYSFVS--EVEPNDTDPDLSNVANQKPFESGSDKISKEVVP--SLACE 394  
Qy 387 EKQVTRHLEDVFSKRNSSNMVMSMTLGLHPWIANI-----DDTQY--- 427  
Db 395 WSQLT--LSDLLDTENKRKKDFTLSENSL-PRISSLPKSEKPLNEETVVNKRDEEQHLES 451  
Qy 428 ----LAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLI 468  
Db 452 HTDCILAVKQAI-----SGTSPVASSFQGI-KKSIFRI 483

RESULT 860  
AAB47152  
ID AAB47152 standard; protein; 160 AA.  
XX  
AC AAB47152;

DT 04-JUN-2001 (first entry)

XX S. aureus kdtB.

XX kdtB; Staphylococcus aureus; phosphopantetheinyl adenyllyl transferase;  
KW PPAT; Ylbi; Bacillus subtilis; microbial disease; otitis media;  
KW bacterial tracheitis; thyroiditis; lung abscess; infective endocarditis;  
KW splenic abscess; cerebral abscess; conjunctivitis; toxic shock syndrome;  
KW impetigo; wound infection; septic arthritis.

XX Staphylococcus aureus.

XX WO200118249-A1.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000WO-US024478.

XX 10-SEP-1999; 99US-00393615.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Throup JP, Van Horn S;

XX WPI; 2001-235213/24.  
DR N-PSDB; AAC85583.

XX New Staphylococcus aureus kdtB polynucleotides and polypeptides, useful  
PT for screening antimicrobial compounds and for treating or diagnosing  
PT microbial diseases, e.g. lung or cerebral abscess, toxic shock syndrome  
PT or wound infections.

XX Claim 1; Page 34-35; 37pp; English.

XX This sequence is kdtB protein from Staphylococcus aureus which is a  
CC member of the phosphopantetheinyl adenyllyl transferase (PPAT) family.  
CC kdtB is related by amino acid homology to Ylbi from Bacillus subtilis.  
CC kdtB polypeptide and polynucleotide are useful for treating microbial  
CC diseases, especially diseases caused by Staphylococcus aureus, e.g.  
CC otitis media, bacterial tracheitis, thyroiditis, lung abscess, infective  
CC endocarditis, splenic abscess, cerebral abscess, conjunctivitis, toxic  
CC shock syndrome, impetigo, wound infection or septic arthritis. These are  
CC also useful as diagnostic reagents for diagnosing or staging of a  
CC disease, or for evaluating the response of an infectious organism to

CC drugs. The kdtB polypeptide and polynucleotide are useful for screening  
CC (ant)agonists of the kdtB polypeptide, as well as for screening compounds  
CC for antimicrobial activity  
XX  
SQ Sequence 160 AA;

Query Match 3.3%; Score 87.5; DB 4; Length 160;  
Best Local Similarity 20.6%; Pred. No. 17;  
Matches 28; Conservative 37; Mismatches 48; Indels 23; Gaps 8;

Qy 291 LVPGIYDEV---VPLTEEEINTYKAHLDLLEEYRNSRVEKFLFDTK-----EEILMHLW 342  
Db 7 VIPGSFDPITYGHLDITERSTDRFDEIHVCV--LKNKKEGTFSLEERMDLIEQSVKHL- 63

Qy 343 RYPSLSIHGIEGAF----DEPGTKTVIPG-RVIGKFSIRLVPHMNVSAVEKQVTRHLEDV 397  
Db 64 --PNVKVHQFSGLLVDYCEQVGAKTIIRGLRAVSDFEYEL----RLTSMNKKLNNEIETL 117

Qy 398 FSKRNSSNMVVSMTL 413

Db 118 Y-MMSSTNYSFISSSI 132

RESULT 861  
ABM73238  
ID ABM73238 standard; protein; 160 AA.  
XX  
AC ABM73238;

DT 20-NOV-2003 (first entry)

XX Staphylococcus aureus protein #2478.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;  
KW enzymatic assay; antibiotic target.

XX Staphylococcus aureus.

XX WO200294868-A2.

XX 28-NOV-2002.

XX 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Massignani V, Mora M, Scarselli M;

XX WPI; 2003-120786/11.  
DR N-PSDB; ACF74798.

XX New Staphylococcus aureus protein, useful as a vaccine for treating or  
PT preventing Staphylococcal infection, specifically an infection caused by  
PT S. aureus, e.g. sepsis.

XX Claim 1; SEQ ID NO 4956; 49pp; English.

XX The invention relates to novel genes and encoded proteins from  
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a  
CC nucleic acid encoding the protein, or an antibody to the protein, is  
CC useful as a pharmaceutical, particularly as a vaccine for treating or  
CC preventing infection due to Staphylococcus bacteria, specifically an  
CC infection caused by S. aureus. The composition is particularly useful for  
CC treating or preventing sepsis in a patient. The composition can also be  
CC used for diagnostics. The protein is also used in an assay for enzymatic  
CC studies and as a target for antibiotics. This sequence represents one of  
CC the novel S. aureus proteins of the invention

XX Sequence 160 AA;

Query Match 3.3%; Score 87.5; DB 6; Length 160;



Best Local Similarity 20.6%; Pred. No. 17;		Matches 28; Conservative 37; Mismatches 48; Indels 23; Gaps 8;	
QY	291	LVPGIYDEV---VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTK----EEILMHLW	342
Db	7	VIPGSFDPITYGHLDIIRSTDRFDEIHVCV--LKNSKKEGTFSLERMDLIEQSVKHL-	63
QY	343	RYPSLSIHGIEGAF---DEPGTKTVIPG-RVIGKFSIRLVPHMNVSAVEKQVTRHLEDV	397
Db	64	--PNVKVHQFSGLLVDYCEQVGAKTIIRGLRAVSDPEYEL---RLTSMNKKLNNEIETL	117
QY	398	FSKRNSSNMVVSMTL	413
Db	118	Y-MMSSTNYSFISSSI	132
RESULT 862			
AAE09049			
ID	AAE09049	standard; protein; 245 AA.	
XX			
AC	AAE09049;		
XX			
DT	15-NOV-2001	(first entry)	
XX			
DE	Equine influenza virus H3N8	PeicalNP-N-245 protein.	
XX			
KW	Equine influenza virus; ei; cold adaptation; temperature sensitivity;		
KW	vaccine; PeicalNP-N-245 protein.		
XX			
OS	Equine influenza virus H3N8.		
XX			
PN	WO200160849-A2.		
XX			
PD	23-AUG-2001.		
XX			
PF	16-FEB-2001; 2001WO-US005048.		
XX			
PR	16-FEB-2000; 2000US-00506286.		
XX			
PA	(UYPI-) UNIV PITTSBURGH.		
XX			
PI	Dowling PW, Youngner JS;		
XX			
DR	WPI; 2001-522584/57.		
XX			
PT	Novel isolated equine influenza virus (wild-type and cold-adapted)		
PT	proteins and viruses containing nucleic acid molecules encoding the		
PT	proteins, which are useful for protecting animals from influenza virus		
PT	infections.		
XX			
PS	Claim 5; Page 158; 172pp; English.		
XX			
CC	The patent discloses cold-adapted equine influenza viruses and		
CC	reassortant influenza A viruses comprising at least one genome segment of		
CC	such an equine influenza virus, wherein the equine influenza virus genome		
CC	segment confers at least one identifying phenotype of the cold-adapted		
CC	equine influenza virus, such as cold adaptation, temperature sensitivity,		
CC	dominant interference or attenuation. The viruses are useful for		
CC	protecting animals from diseases caused by influenza viruses. They are		
CC	also used as vaccines. The present sequence is equine influenza (ei)		
CC	virus H3N8 Peical (wild type) NP-N-245 protein		
XX			
SQ	Sequence 245 AA;		
Query Match			
Best Local Similarity 3.3%; Score 87.5; DB 4; Length 245;			
Matches 60; Conservative 46; Mismatches 106; Indels 77; Gaps 15;			
QY	228	DNLWISQRKPAITYTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSS	287
Db	6	DNHLSLDIKIMASQGTK-RSYEQMETDGERQN-----ATEIRASVGRMVVGI	51
QY	288	GHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFL---FDTKEEILMHLWRY	344
Db		52 GRFYVQ-----MCTELKLNDEHG-----RLIQNSMTIERMVLSAFDERN--KYLEEH	
97		345 PLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSS	
404		98 PS-----AGKDPKKTGGPIYRRKDGKWMRELILH-----DKEEIMR-----IWRQANNG	
141		405 NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDM--IRDGSTIP-----	
452		142 EDATAGLT-HMMIWHSNLNDTTYQTRALVRT--GMDPRMCSMMQGSTLPRRSGAAGAAV	
198		453 --IAKMFOEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAF	
499		199 KGVGTVMVMEILR----MIKRGINDR-----NFWRSENGRRTRIAY	
234		RESULT 863	
		ABU18369	
ID	ABU18369	standard; protein; 246 AA.	
XX			
AC	ABU18369;		
XX			
DT	19-JUN-2003	(first entry)	
XX			
DE	Protein encoded by Prokaryotic essential gene #3896.		
XX			
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.		
XX			
OS	Bacillus anthracis.		
XX			
PN	WO200277183-A2.		
XX			
PD	03-OCT-2002.		
XX			
PF	21-MAR-2002; 2002WO-US009107.		
XX			
PR	21-MAR-2001; 2001US-00815242.		
PR	06-SEP-2001; 2001US-00948993.		
PR	25-OCT-2001; 2001US-0342923P.		
PR	08-FEB-2002; 2002US-00072851.		
PR	06-MAR-2002; 2002US-0362699P.		
XX			
PA	(ELIT-) ELITRA PHARM INC.		
XX			
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;		
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;		
XX			
DR	WPI; 2003-029926/02.		
DR	N-PSDB; ACA22239.		
XX			
PT	New antisense nucleic acids, useful for identifying proteins or screening		
PT	for homologous nucleic acids required for cellular proliferation to		
PT	isolate candidate molecules for rational drug discovery programs.		
XX			
PS	Claim 25; SEQ ID NO 46293; 1766pp; English.		
XX			
CC	The invention relates to an isolated nucleic acid comprising any one of		
CC	the 6213 antisense sequences given in the specification where expression		
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:		
CC	(1) a vector comprising a promoter operably linked to the nucleic acid		
CC	encoding a polypeptide whose expression is inhibited by the antisense		
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated		
CC	polypeptide or its fragment whose expression is inhibited by the		
CC	antisense nucleic acid; (4) an antibody capable of specifically binding		
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular		
CC	proliferation or the activity of a gene in an operon required for		
CC	proliferation; (7) identifying a compound that influences the activity of		
CC	the gene product or that has an activity against a biological pathway		
CC	required for proliferation, or that inhibits cellular proliferation; (8)		
CC	identifying a gene required for cellular proliferation or the biological		
CC	pathway in which a proliferation-required gene or its gene product lies		
CC	or a gene on which the test compound that inhibits proliferation of an		
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a		









QY 166 -----NKG PVL-----AWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEEL- 209  
Db 172 PFYMAQGPIMLKTAGEIADGVLVNASN-----PKDEFAVPKIEEKAAGR-SLDEID 225  
QY 210 -----VEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVVEVKCRDQ--- 258  
Db 226 VAA YTCFSIDKDEDKAIEATKIVV-----AFIVMGSPDVVLERHG-----IDTEKAEQIAE 276  
QY 259 -----DFHSGTGGILHEPNMADLVALLG---SLVDSSGHILVPGIYDEVV--PLTEEEIN 308  
Db 277 AIGKGDF--GTAIGLVDEDMIEAFSIAGDPDPTVVVDKIEELLKAGVTQVVVVGSPIGPDK-- 332  
QY 309 TYKAIHL 315  
Db 333 -EKAIEL 338

RESULT 867  
ABG91539  
ID ABG91539 standard; protein; 362 AA.  
XX AC ABG91539;  
XX 18-NOV-2002 (first entry)  
XX Purine/pyrimidine triphosphate type nucleotidyltransferase #124.  
KW Nucleotidyltransferase; enzyme; active site engineering;  
KW alpha-D-glucopyranosyl phosphate thymidyltransferase; Ep;  
KW substrate specificity; nucleotide sugar;  
KW glycosylated bioactive natural product.  
XX  
OS Candida albicans.  
XX  
PN WO200248331-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 13-DEC-2001; 2001WO-US047953.  
XX  
PR 13-DEC-2000; 2000US-0254927P.  
XX  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX  
PI Thorson JS, Nikilov DB;  
XX  
XX WPI; 2002-608282/65.  
DR  
XX  
PT Nucleotidyltransferase mutated at one or more amino acids, useful in  
PT the synthesis of nucleotide sugars.  
XX  
PS Claim 3; Page; 182pp; English.  
XX

The invention relates to a Nucleotidyltransferase mutated at one or more amino acids selected from V173, G147, W224, N112, G175, D111, E162, T201, I200, E199, R195, L89, L89T, L109, Y146 or Y177 (with reference to the Salmonella enterica rmlA-encoded alpha-D-glucopyranosyl phosphate thymidyltransferase, Ep, enzyme appearing as ABG91798). The mutations alter the substrate specificity of the enzymes. The mutants and methods involving them are used in the synthesis of nucleotide sugars for altering nucleotidyltransferase substrate specificity. The nucleotidyltransferase exhibits different substrate specificity for GTP, CTP, TTP, UTP and ATP than a non-mutated nucleotidyltransferase. The mutant may also exhibit a high degree of sequence identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate thymidyltransferase (Ep) and can convert a wide variety of phosphates. The mutants can be exploited in the biosynthesis of glycosylated bioactive natural products of pharmacological use. The present sequence is a nucleotidyltransferase exhibiting a high degree of sequence identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate thymidyltransferase (Ep). Note: The present sequence is not displayed in the specification but was obtained from Genbank

SQ Sequence 362 AA;  
Query Match 3.3%; Score 87.5; DB 5; Length 362;  
Best Local Similarity 19.8%; Pred. No. 60;  
Matches 75; Conservative 68; Mismatches 129; Indels 107; Gaps 20;  
QY 148 PYVLTEVDGKLYRGATDNKGPVLAWIN-----AVSAFRALEQDLPVNIKFIIEGMEE-- 200  
Db 32 PMILHQIEA-LAAAGVTD-----IVLAVNYRPEVMVSTLKKYEEYGVSTFSVE--EEPL 84  
QY 201 --AGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVVEVKCRDQ 258  
Db 85 GTAGPLKLAEEVLKKDDSPFFVLNSDVICD-----YPFKEL-----A 121  
QY 259 DFH-----SGT-----FGGILHEP-----MADLVALLGSLVDSSGHILVP 293  
Db 122 DFHKAHGAAGTIVATKVDEPSKYGVIVHDRDTPNLIDRFVEKPVFVGNRINAGLYILNP 181  
QY 294 GIYD-----EVVPLTEEEINTYKAIHLDLEEY-RNSSRVEKFLEDTKEEILMHL 341  
Db 182 SVIDLIEMRPTSIEKETFPILVEQKQLYS----FDLEGYWMDVGQPKDFLSGTCLYLTSLS 238  
QY 342 WRYP-----SLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNV---SAVEKQVTRH 393  
Db 239 KKHPEKLCCKEYVHGGNVLIDP--TAKIHPSALIGP-NVTIGPNVVVGEGARIQRSVL-- 293  
QY 394 LEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDM-----IRDG 448  
Db 294 --LANSQVKDHAWVKSTIVGWNRSRIGKWARTEGV-----TVLGDDDVVEKNEIYVNGA 343  
QY 449 STIPIAKMFQEI VHKSVVL 467  
Db 344 KVLPHKSISSNVEKESIIM 362

RESULT 868  
ABP73386  
ID ABP73386 standard; protein; 362 AA.  
XX AC ABP73386;  
XX 30-JAN-2003 (first entry)  
XX Candida albicans essential protein SEQ ID NO 7223.  
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;  
KW signal transduction; DNA replication; cell division; growth;  
KW proliferation; Candida albicans; fungicide; antifungal.  
OS Candida albicans.  
XX WO200253728-A2.  
XX 11-JUL-2002.  
XX 26-DEC-2001; 2001WO-US049486.  
PR 29-DEC-2000; 2000US-0259128P.  
PR 20-FEB-2001; 2001US-00792024.  
PR 22-AUG-2001; 2001US-0314050P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;  
PI WPI; 2002-566694/60.  
DR N-PSDB; ABZ31936.  
XX Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.  
PS Claim 44; SEQ ID NO 7223; 167pp + Sequence Listing; English.





KW diterpene synthase; defence toxin; volatile defensive signal;  
KW pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.  
XX Streptococcus pyogenes.  
XX US2004072323-A1.  
XX 15-APR-2004.  
XX 07-JAN-2002; 2002US-00041018.  
XX 05-JAN-2001; 2001US-0259880P.  
XX (MATS/) MATSUDA S P T.  
XX (HART/) HART E A.  
XX Matsuda SPT, Hart EA;  
XX WPI; 2004-373921/35.  
XX New unicellular organisms comprising exogenous nucleic acids encoding a  
PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for  
PT producing diterpenes and diterpene precursors.  
XX Disclosure; SEQ ID NO 172; 38pp; English.  
XX The invention relates to a unicellular organism for producing a diterpene  
CC or diterpene precursor comprising an exogenous nucleic acid sequence  
CC encoding a geranylgeranyl pyrophosphate synthase under the control of a  
CC promoter operable in the organism, and an exogenous nucleic acid sequence  
CC encoding a diterpene synthase under the control of a promoter operable in  
CC the organism. The invention also relates to methods of producing a  
CC diterpene or diterpene precursor and a method of isolating a diterpene  
CC synthase comprising growing several cells in the presence of a  
CC polyaromatic resin to make a cell/resin mixture, where at least one of  
CC the cells further comprises at least one isolated and purified nucleic  
CC acid sequence of a yeast expression library, and the expression of the  
CC nucleic acid sequence is regulated by an inducible promoter under  
CC conditions where the expression is induced, filtering the cell/resin  
CC mixture, extracting the cell/resin mixture with alcohol to produce an  
CC organic eluent and analysing the organic eluent by a screening method  
CC including chromatography and/or spectroscopy, to identify the nucleic  
CC acid sequence encoding the diterpene synthase. The unicellular  
CC microorganism is useful as a diterpene or diterpene precursor producing  
CC system. Diterpenes, in plants, serve as defence toxins, volatile  
CC defensive signals, pollinator attractants and photoprotectants. This  
CC sequence represents an HMG-CoA reductase polypeptide used in the scope of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification but was obtained in electronic format from  
CC USPTO at seqdata.uspto.gov/sequence.html.  
XX SQ Sequence 425 AA;  
Query Match 3.3%; Score 87.5; DB 8; Length 425;  
Best Local Similarity 20.1%; Pred. No. 77;  
Matches 64; Conservative 34; Mismatches 90; Indels 131; Gaps 13;  
QY 75 FRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLD 134  
Db 168 FLIFYLTVDTQEAMGANMVT-MMEALVPDLTRLKSGHCLMAILSNVATESLVTTSCEIP 226  
QY 135 VQPADRGDG-----WLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 227 VRLDRDKTKSLQLAQKIELASRLAQVDPY-----RATTHNKG----- 264  
QY 180 FRALEQDLFVNKIFIEGMEAGSVALEELVEKEKDRFFSGVDYIVI-SDNLWISORKPA 238  
Db 265 -----IFNGIDAVVIATGNDWRAIERAGA 287  
QY 239 ITYGTRGNSYFMVEVKCRDQD-----FHSGTFF-----GILHEP-- 272  
Db 288 HAYASRNGSYQGLSQWHFDQDKQVLLGQMTLPMPIASKGSGIPLNPTVSTAHDLNQPDA 347

QY 273 --MADLVALLG-----SLVDS---SGH-----ILVPGIYDEVVP-----LTE 304  
Db 348 KTLAQLIASVGLAQNFAALKALTSSGIQAGHMKLHAKSLALLAGATQDEIAPLVNALLAD 407  
QY 305 EEINTYKAIHLDLEEYRNS 323  
Db 408 KPINLEKA-HFYLSQLRQS 425  
RESULT 871  
ADM98851  
ID ADM98851 standard; protein; 425 AA.  
XX  
AC ADM98851;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE HMG-CoA reductase polypeptide #104.  
XX  
KW Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor;  
KW diterpene synthase; defence toxin; volatile defensive signal;  
KW pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.  
XX  
OS Streptococcus pyogenes.  
XX  
PN US2004072323-A1.  
XX  
PD 15-APR-2004.  
XX  
PF 07-JAN-2002; 2002US-00041018.  
XX  
PR 05-JAN-2001; 2001US-0259880P.  
XX  
PA (MATS/) MATSUDA S P T.  
PA (HART/) HART E A.  
XX  
PI Matsuda SPT, Hart EA;  
XX  
DR WPI; 2004-373921/35.  
XX  
PT New unicellular organisms comprising exogenous nucleic acids encoding a  
PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for  
PT producing diterpenes and diterpene precursors.  
XX Disclosure; SEQ ID NO 271; 38pp; English.  
XX The invention relates to a unicellular organism for producing a diterpene  
CC or diterpene precursor comprising an exogenous nucleic acid sequence  
CC encoding a geranylgeranyl pyrophosphate synthase under the control of a  
CC promoter operable in the organism, and an exogenous nucleic acid sequence  
CC encoding a diterpene synthase under the control of a promoter operable in  
CC the organism. The invention also relates to methods of producing a  
CC diterpene or diterpene precursor and a method of isolating a diterpene  
CC synthase comprising growing several cells in the presence of a  
CC polyaromatic resin to make a cell/resin mixture, where at least one of  
CC the cells further comprises at least one isolated and purified nucleic  
CC acid sequence of a yeast expression library, and the expression of the  
CC nucleic acid sequence is regulated by an inducible promoter under  
CC conditions where the expression is induced, filtering the cell/resin  
CC mixture, extracting the cell/resin mixture with alcohol to produce an  
CC organic eluent and analysing the organic eluent by a screening method  
CC including chromatography and/or spectroscopy, to identify the nucleic  
CC acid sequence encoding the diterpene synthase. The unicellular  
CC microorganism is useful as a diterpene or diterpene precursor producing  
CC system. Diterpenes, in plants, serve as defence toxins, volatile  
CC defensive signals, pollinator attractants and photoprotectants. This  
CC sequence represents an HMG-CoA reductase polypeptide used in the scope of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification but was obtained in electronic format from  
CC USPTO at seqdata.uspto.gov/sequence.html.  
XX SQ Sequence 425 AA;







PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match
Best Local Similarity 3.3%; Score 87.5; DB 3; Length 455;
Matches 75; Conservative 49; Mismatches 78; Indels 119; Gaps 21;

QY 175 NAVSAFRAL-EQDLFPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWIS 233
Db 93 NRVASFRPVREEECORMMDKIYKAADQSGTVDLSLL-----LSFTNCVVCRCQ----- 140

QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFCGILHEPMADLVALLGSLVDSSGHILVP 293
Db 141 -----AFGKRYNEY-GTEMK-----RFIDILYETQ----ALLGTLFFSD---LFP 177

QY 294 --GIYDEVVPLTE-----EEINTYKAIHLD--LEEYRNSRVEKFLFDTKKEEILMHLWR 343
Db 178 YFGFLDNLTGSLARLKKAFAKELDTYLQELLDETLDPNRPKQETESFI-----DLLMQIYK 232

QY 344 YPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 403
Db 233 -----DQP-----FSIKFT-HENVKAM-----ILDIVVPGTDT 259

QY 404 SNKMVV-SMTLGLHPWIANIDDTQYL-----AAKRA---IRTVFG-----TEPDMIRDGS 449
Db 260 AAADVWVWAMT-----YLIKYPEAMKKAQDEVRSVIGDKGVYSEED----- 299

QY 450 TIPIAKMFQEIHKSVVLIPL 470
Db 300 -IPNLPYLKAVIKESLRLEPV 319

RESULT 874
ADN48102
ID ADN48102 standard; protein; 480 AA.
XX
AC ADN48102;
XX
DT 01-JUL-2004 (first entry)
XX
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1980.
XX
KW gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.
XX
OS Thermococcus kodakaraensis.
XX
PN WO2004022736-A1.
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XX
PD 18-MAR-2004.
XX
PF 29-AUG-2003; 2003WO-IB003597.
XX
PR 30-AUG-2002; 2002JP-00319011.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Imanaka T, Atomi H;
XX
DR WPI; 2004-257583/24.
XX
PT Method for disrupting targeted gene in genome of organism particularly
PT thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
XX
PS Claim 9; SEQ ID NO 1980; 598pp; Japanese.
XX
CC This invention relates to a novel method for targeting disruption of an
CC arbitrary gene in a genome of an organism which comprises providing the
CC whole sequential data of the genome of such organism, selecting at least
CC 1 arbitrary region in the sequence, providing a vector that contains a
CC sequence homologous with the selected region and a marker gene,
CC transformation, and homologous recombination. The genome is preferably
CC the genome of a hyperthermostable archaeobacterium, particularly
CC Thermococcus kodakaraensis KOD1. The method is for targeting the
CC disruption of a gene in the genome of an organism, which is applicable in
CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC disruption of a gene at an arbitrary position in a genome can be achieved
CC efficiently and reliably. The present sequence is that of a protein
CC encoded by the genome of Thermococcus kodakaraensis which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 480 AA;

Query Match
Best Local Similarity 3.3%; Score 87.5; DB 8; Length 480;
Matches 52; Conservative 35; Mismatches 81; Indels 61; Gaps 13;

QY 257 QDFHSGTFCGILHEPMADLVALLGSLVDSSGHILVPGI---YDEVV---PLTEEEIN- 308
Db 243 DMEFYSRIF-----RVGLPSAVGOSANSFGFVWLTRIYGYGDVTYAAYTITRLVNF 295

QY 309 -----TYKAIHLDLEEYRNSRVEK-----FLFDTKEEILMHLWRYPSLSI 349
Db 296 ITSARGVSMAMGTMTIAQNIQAERYERAKRIAERAMVINFLIASSAILIIGLFRVPVFKV 355

QY 350 HGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNK-MV 408
Db 356 F-----LDDP--KVIAQSEYVLKYFLISVPFFN--GIFVVVTR-----TFSSAGHTKKSMV 402

QY 409 VSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF 457
Db 403 LSM---LRLWGFRI-PLSYVFGYVAAVTVFGLR-----VPLAELF 438

RESULT 875
AAY19807
ID AAY19807 standard; protein; 491 AA.
XX
AC AAY19807;
XX
DT 19-JUL-1999 (first entry)
XX
DE B. burgdorferi antigenic protein, t929.aa.
XX
KW Antigenic protein; vaccine; Lyme disease; infection; detection.
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XX SQ      Sequence 494 AA;
      Query Match      3.3%; Score 87.5; DB 6; Length 494;
      Best Local Similarity 18.0%; Pred. No. 97;
      Matches 74; Conservative 64; Mismatches 152; Indels 121; Gaps 14;

QY 170 VLWINAVSAFRALEQDLVPNIKFIIIEGMEEAGSVALEELVEKE----- 213
Db 5 ILAVEAVSNEKALPREK-----IFEALESALATATKKYEQEIDVRVEIDRKSGDFT 58
QY 214 -----KDRFFSGVDYI-----VISDNLWISQKPAITYGT 243
Db 59 FRRWLVEEVTOPTREITLEAARFEDESMNVGDYVEDQIESVTFDRITTTQAKQVIVQKV 118
QY 244 RGSYFMVEVKCRDQDFHSG-TFGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPL 302
Db 119 REAERAMVVDQFRE---HEGEIITGVVKKVNRDNITL-----DLGNNAEAVILREDMLP- 169
QY 303 TEEEINTYKAHLDLEEYRNSSRVEKFLFDTKKEIIMHLWR--YPSL--SIHGIEGAFDE 358
Db 170 -RENFRPGDRIRGVLYAVRPEARGLFVTRSKPEMLIELFRIEVP EIGEVELEIKAAARD 228
QY 359 PGTKTVIP-----GRVIG-----KFSIRLVP 379
Db 229 PGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIVLWDDNPAQFVINAMA 288
QY 380 HMNVSAVEKQVTRHLEDVFSK-----RNSSNKQVVVSMTLGLHPWTIANIDDTQ--YL 428
Db 289 PADVASIVVDEDKHTMDIAVEAGNLAQAIGNRQNVRLASQLSGWELNVMTVDDLQAKHQ 348
QY 429 AAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VW---LIPLGAVDD 475
Db 349 AEAHAAIDTFTKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLEIDGLDE 399

RESULT 877
ABB05768
ID ABB05768 standard; protein; 498 AA.
XX
AC ABB05768;
XX
DT 07-MAY-2002 (first entry)
XX
DE Influenza A/Udorn/72 (H3N2) Strain NP protein SEQ ID NO:10.
XX
KW Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
KW Influenza A virus; genome.
XX
OS Influenzavirus A.
XX
PN WO200200884-A2.
XX
PD 03-JAN-2002.
XX
PF 21-JUN-2001; 2001WO-US019826.
XX
PR 23-JUN-2000; 2000US-0213650P.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Galarza JM, Latham TE;
XX
DR WPI; 2002-139923/18.
DR N-PSDB; ABA93938.
XX
PT Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT polypeptide, useful in diagnosis and for generating new influenza A
PT variant strains.
XX
PS Disclosure; Page 68-70; 103pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) having the
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CC complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC strand, antigenomic message sense. ABA93934 to ABA93944 encode the
CC Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC from the present invention. (I) is useful for designing polymerase chain
CC reaction (PCR) primers for use in a PCR assay to detect the presence of
CC the corresponding virus segment in a sample or for designing and
CC selecting peptides for use in an enzyme linked immunosorbant assay to
CC detect the presence of the corresponding protein produced by that segment
CC in a sample, hence is useful in diagnosis and may be modified by mutation
CC to generate new influenza A variant strains. ABA94945 to ABA94039
CC represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC are used in an example from the present invention
XX
SQ      Sequence 498 AA;
      Query Match      3.3%; Score 87.5; DB 5; Length 498;
      Best Local Similarity 21.1%; Pred. No. 98;
      Matches 51; Conservative 41; Mismatches 87; Indels 63; Gaps 13;

QY 275 DLVALLGSLVDSSGHILVPGIYDEVVPLTBEETINTYKAHLDLEEYRNSSRVEKFL---F 331
Db 24 EIRASVGKMIDGIGRFYIQ-----MCTELKLSDYEG-----RLIQNSLTIERMVLSAF 71
QY 332 DTKEEILMHLWRYPSLSIHGIEGAFDEPGCTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVT 391
Db 72 DERRN--RYLEEHP-----AGKDPKKTGGPIYKRVDRKWMRELVLV-----DKEEI 116
QY 392 RHLEDVFSKRNSSNKQVVSMVTGLHPWTIANIDDTQYLAAKRAIRTVFGTEPDM--IRDGS 449
Db 117 RR---IWRQANNGGDDATAGLT-HMMIWHNSNLNDTTYQTRALVRT--GMDPRMCSLMQGS 170
QY 450 TIP-----IAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFA 497
Db 171 TLPRRSGAAGA AVKGVGTVMVMEILR---MIKRGINDR-----NEWRGENGKRTKG 217
QY 498 AF 499
Db 218 AY 219

RESULT 878
AAG11138
ID AAG11138 standard; protein; 499 AA.
XX
AC AAG11138;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9743.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.

PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match	3.3%	Score 87.5;	DB 3;	Length 499;
Best Local Similarity	23.4%;	Pred. No. 99;		
Matches 75;	Conservative 49;	Mismatches 78;	Indels 119;	Gaps 21;

[illegible]

RESULT 879  
ADN72839  
ID ADN72839 standard; protein: 499 AA.

ADN72839;	(first entry)
15-JUL-2004	

DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 734.  
XX  
KW plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;  
KW animal feed product; thale cress; cell wall biosynthesis;  
KW nitrogen metabolism; carbon metabolism.

OS *Arabidopsis thaliana*.

PN WO2004035798-A2.

PD 29-APR-2004.

XX

PF	20-OCT-2003; 2003WO-EP011658.
XX	
PR	18-OCT-2002; 2002EP-00079408.
XX	
PA	(CROP-) CROPDESIGN NV.
XX	
PI	Inze D, De Veylder L, Vlieghe K;
XX	
DR	WPI; 2004-348466/32.
DR	N-PSDB; ADN72838.

Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

PS Claim 1; SEQ ID NO 734; 134pp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up- or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the E2Fa/DPa transcription factor, given in an exemplification of the invention.

Sequence 499 AA;

Query Match	3.3%;	Score 87.5;	DB 8;	Length 499;
Best Local Similarity	23.4%;	Pred. No. 99;		
Matches	75; Conservative	49; Mismatches	78; Indels	119; Gaps
				21;

[illegible]

RESULT 880  
ADO15671  
ID ADO15





Db 303 MLEKPTDGREVVCHASAWDFYNGKDF-RIKQCTTVNLEDLVVAHHEMIGHIQYFMQYKDLP 361

QY 258 QDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD- 316

Db 362 VALREGANPG-FHEAIGDVLAL---SVSTPKHLHSLNLLSSEGGSDHDFNFKMWDK 417

QY 317 -----LEEYRNSSRVEKFLFD---TKEEILMHLW----RYPSL--SIHGIEGAFDE 358

Db 418 IAFIPFSYLVQDQWRW-----VFDGSITKENYNQEWWSRLKYQGLCPPVPRTQGD- 470

QY 359 PGTKTVIPG-----RVIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSSNKVVVSM 412

Db 471 PGAKFHIPSSVPYIRYFVFSFIQFHEALCQAAGHTGPLHKCDIYQSKAQRLATAMK 530

QY 413 LGL-HPW 418

Db 531 LGFSRPW 537

RESULT 882

ADM16517

ID ADM16517 standard; protein; 589 AA.

XX

AC ADM16517;

XX

DT 17-JUN-2004 (first entry)

XX

DE Mutant ACE (delta36NJ) amino acid sequence, seq id 2.

XX

KW Hypotensive; enzyme inhibitor; crystal; angiotensin converting enzyme;

KW peptidyl dipeptidase A; EC.3.15.1; ACE; lisinopril; hypertension;

KW protein co-ordinate data; human; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO2004024765-A1.

XX

PD 25-MAR-2004.

XX

PF 12-SEP-2003; 2003WO-GB003966.

XX

PR 12-SEP-2002; 2002GB-00021169.

XX

PA (UYBA-) UNIV BATH.

PA (UYCA-) UNIV CAPE TOWN.

PA (ACHA/) ACHARYA R.

PA (STUR/) STURROCK E.

XX

PI Acharya R, Sturrock E;

XX

DR WPI; 2004-283034/26.

XX

PT Crystals of Angiotensin converting enzyme, useful for identifying

PT hypotensive therapies.

XX

PS Claim 4; SEQ ID NO 2; 291pp; English.

XX

CC The invention relates to a crystal (I) of an Angiotensin converting

CC enzyme (peptidyl dipeptidase A, EC.3.15.1) (ACE) protein. Also disclosed

CC is a method for preparing (II) the ACE crystal (I). The ACE crystal may

CC be used to screen for modulators, especially inhibitors, e.g. lisinopril,

CC of ACE activity which may be used for the treatment of e.g. hypertension.

CC The current sequence represents the mutant ACE amino acid sequence

CC designated delta36NJ.

XX

SQ Sequence 589 AA;

Query Match 3.3%; Score 87.5; DB 8; Length 589;

Best Local Similarity 20.8%; Pred. No. 1.3e+02;

Matches 89; Conservative 57; Mismatches 196; Indels 85; Gaps 21;

QY 33 ALLEKVFQYIDL-----HQDEFVQTLKENVAIESDSVQVPRFRQELFRMMAVAADTLQR 87

Db 156 AILQFYPKYVELINQAARLNGYVDAGDSW-----RSMYETPSLEQDLERLFQBLQPLYLN 210

QY 88 LGA---RVASVDMGPQQLP-DGQSLPIPPVIL-----AELGSDPTKGTVCFYG--HLDVQP 137

Db 211 LHAYVRRALHRHYGAQHINLEG---PIPAHLGNMWAQTSNIYDLVVPFAPSAPMDTTE 267

QY 138 ADRGDGWLTPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEG 197

Db 268 AMLKQGW-TPRRMFKOADDFFTSLGL-----LPVPPEFWNKS 303

QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD 257

Db 304 MLEKPTDGREVVCHASAWDFYNGKDF-RIKQCTTVNLEDLVVAHHEMIGHIQYFMQYKDLP 362

QY 258 QDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD- 316

Db 363 VALREGANPG-FHEAIGDVLAL---SVSTPKHLHSLNLLSSEGGSDHDFNFKMWDK 418

QY 317 -----LEEYRNSSRVEKFLFD---TKEEILMHLW----RYPSL--SIHGIEGAFDE 358

Db 419 IAFIPFSYLVQDQWRW-----VFDGSITKENYNQEWWSRLKYQGLCPPVPRTQGD- 471

QY 359 PGTKTVIPG-----RVIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSSNKVVVSM 412

Db 472 PGAKFHIPSSVPYIRYFVFSFIQFHEALCQAAGHTGPLHKCDIYQSKAQRLATAMK 531

QY 413 LGL-HPW 418

Db 532 LGFSRPW 538

RESULT 883

ABB92271

ID ABB92271 standard; protein; 678 AA.

XX

AC ABB92271;

XX

DT 31-MAY-2002 (first entry)

XX

DE Herbicidally active polypeptide SEQ ID NO 1482.

XX

KW Herbicidal; plant; agriculture; herbicide.

XX

OS Arabidopsis thaliana.

XX

PN WO200210210-A2.

XX

PD 07-FEB-2002.

XX

PF 28-AUG-2001; 2001WO-EP009892.

XX

PR 28-AUG-2001; 2001WO-EP009892.

PA (FARB ) BAYER AG.

XX

PI Tietjen K, Weidler M;

XX

DR WPI; 2002-269010/31.

XX

PT Identifying plant target proteins for herbicidally active compounds,

PT comprising aligning and comparing nucleic acid or amino acid sequences

PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms.

XX

PS Claim 5; SEQ ID NO 1482; 261pp + Sequence Listing; English.

XX

CC The invention relates to identifying target proteins (ABB90790-ABB94016)

CC for herbicidally active compounds, comprising aligning and comparing

CC nucleic acid or amino acid sequences from plant with nucleic acid or

CC amino acid sequences from non-plant organisms using suitable search

CC parameters, where plant sequences having an E-value greater by a factor

CC of 3 than the E-value of most similar non-plant sequences are selected.









XX Blackshear PJ, Zeldin DC, Graves JP, Stumpo DJ;  
XX WPI; 2003-854031/79.  
XX New RFX4v3 polypeptide, useful in preparing a composition for diagnosing  
PT or treating congenital hydrocephalus.  
XX  
PS Claim 3; SEQ ID NO 6; 76pp; English.  
XX  
CC The present sequence is the protein sequence of mouse RFX4 v3, a novel  
CC splice variant of the regulatory factor X 4 (RFX4) member of the winged  
CC helix transcription factor family. The human RFX4 v3 polypeptide ADF18691  
CC inhibits the phenotypic expression of congenital hydrocephalus. When one  
CC allele is defective, there is universal congenital hydrocephalus with  
CC aqeductal stenosis, probably secondary to agenesis of the subcommissural  
CC organ. The defect appears to be compatible with life, and in some cases  
CC normal fertility. This hydrocephalus exhibits an autosomal dominant  
CC inheritance pattern. When 2 alleles are defective, there is severe  
CC disruption of brain formation and prenatal or perinatal death. The  
CC RFX4 v3 transcript is novel in that it contains a mixture of exons from 2  
CC previously identified transcripts as well as a completely novel exon that  
CC encodes the N-terminus of the protein. The invention provides human,  
CC mouse and zebrafish RFX4 v3 proteins and nucleic acids, as well as  
CC transgenic animals with altered RFX4 v3 genes, and assays for the  
CC detection of RFX4 v3 and RFX4 v3 polymorphisms associated with disease  
CC states. Also provided are methods of determining a subject's risk of  
CC developing congenital hydrocephalus, methods of screening for drugs that  
CC inhibit or potentiate RFX4 v3 action, and methods of using RFX4 v3  
CC nucleic acid or polypeptide to treat congenital hydrocephalus.  
XX  
SQ Sequence 737 AA;  
  
Query Match 3.3%; Score 87.5; DB 7; Length 737;  
Best Local Similarity 19.2%; Pred. No. 1.8e+02;  
Matches 69; Conservative 57; Mismatches 120; Indels 113; Gaps 18;  
  
QY 188 PNVIKFIIEGMEEAGSVALE-----ELVEKEKDRFFSGVDYIVISDNLWISQRKPA 238  
Db 59 PATLQWLEENYEIAEGVICPRISALYMHYLDFCERKNDTPVNAASFGLI-----IRQQFPQ 113  
QY 239 IT-----YGTGRNS---YFMVEVKCRDQDF-----HSGTFGGILHEPM 273  
Db 114 LTTRRLGTGRGQSKHYHYGIKAVKSSQYDVMYSKGAWVSETGKREVTQTVAYSR 173  
QY 274 ADLVALLGSLVDSSGHILVPGIYDEVVP--LTTEEINTYKAHLDLEEYRNSR-----V 326  
Db 174 SKLGTLLPDF-----PNVKDLNLPASLPBEKVSTF-----IMVYRTHCQRILDTV 218  
QY 327 EKFLFDTKEILMHLWR-----YPSLSIHGIEGAFDE-----PGTKTVIP 366  
Db 219 IRANFDEVQSFLLHFQGMPPHMLPVLGSSTVNVIVGVCDSILYKAISGVLMPETVLQALP 278  
QY 367 G---RVIGKFSIRL-----VPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTL 413  
Db 279 DSLTQVIRKFAQLDEWLKVALHDLPE-NLRNIKFELSRFSQILRRQTSLNHLCOASRT 337  
QY 414 GLH-----PWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVH 462  
Db 338 VIHSADITFQMLEDW-RNVDLSS--ITKQTLTYM-----EDSRDEHRRLLIQLYQEFDH 388  
  
RESULT 889  
ADN27040  
ID ADN27040 standard; protein; 764 AA.  
XX  
AC ADN27040;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #9693.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
CC New recombinant DNA construct comprising a promoter positioned to provide  
CC for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 9693; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 764 AA;

Query Match 3.3%; Score 87.5; DB 8; Length 764;  
Best Local Similarity 18.7%; Pred. No. 1.9e+02;  
Matches 112; Conservative 90; Mismatches 175; Indels 221; Gaps 34;  
  
QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYI---DLHQ----DEFVQ-- 51  
Db 232 VDFRNSNTAVAFADWIPLL-----PTDNALMDAMAYVIVSENLDQAFLDQYVQGF 284  
QY 52 -----TLKEWVAIESDSVQPVFRFRQELFRMMAVAADTLQRLGARVASV--- 95  
Db 285 DEEHMPEGVPAHESLVSYLFGKDGVEKTPWEAEAIK---VPAETIRRIAREYATTKPA 341  
QY 96 ----DMGPQQLPDGQSLPIPPVILAEGLGSDPTKGTVCFYGHLDVQPADRGDW----- 144



Db 342 ALIQWGPQRHSCGERTALGATMLASI-----TGNVGLG-----GWAGGYIGL 385

Qy 145 -----LTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPN----- 190

Db 386 SRKGCVGLEDVNPY-----PGAI-----PTLSWVDI-----ECPEKVTPAEGLLG 427

Qy 191 -----IKFIIEGMEEAGSVALEE-----LVEKEKDRFFSGVDYIVISDNLWISQ 234

Db 428 VDKLNSPIKML---LNLAGDFIANQNPDIRTIRVLEDE-----SLVEFIVSDLFMTPS 479

Qy 235 RK-----PAITYGTRGN-----SYFMVEVKCRDQDFHSGTFGGILHEPMDLVALL 280

Db 480 ARYADILLPGNTFFERYNIGATWNGDYFILSQKIVDNYYESRS-----EYDWLAEVADKL 535

Qy 281 GS-----LVDSSGCHILVPGIYDEVVPLTEEEINTYKAHLD----- 316

Db 536 GAKDVFTGCKTEEEWVRWIVDET-----RAKYPETLSWEELEKVGISKFHYDGPRVAFQD 590

Qy 317 -LEEYRN-----SSRVEKF---LFTKKEEILMHLWRYPYSLSIH--GIEGAFDEPGTKTV 364

Db 591 QIEDPVNPFPTSPGKIELFSKTLVD-----MHNPEIPAIPVYVPAWEGPEDE----- 638

Qy 365 IPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS--NKMVVSMTLGLHPWIANI 422

Db 639 ----LTEKYPLQLIGWTK-----ARDNSTFYNNPWLQAMVQEVWINPM 679

Qy 423 DDTQYLAAKRAIRTVFGTEPDMIRD-GSTIPIAKMFQEIHKSVVLIPLGA--VDDGE 477

Db 680 D-----AKPRNI--VTGDRVKVFENDRGTTMLQARVTSRVI-PGVIAAPTGSWFPTPDGK 729

RESULT 890

ABU29875

ID ABU29875 standard; protein; 786 AA.

AC ABU29875;

XX 19-JUN-2003 (first entry)

DT Protein encoded by Prokaryotic essential gene #15402.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Enterococcus faecium.

XX WO200277183-A2.

PN 03-OCT-2002.

PD 21-MAR-2002; 2002WO-US009107.

PF 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA33745.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 57799; 1766pp; English.

PS The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

Qy Sequence 786 AA;

Query Match 3.3%; Score 87.5; DB 6; Length 786;

Best Local Similarity 19.0%; Pred. No. 2e+02;

Matches 63; Conservative 47; Mismatches 91; Indels 131; Gaps 15;

Qy 187 LPVNIKFIIEGMEEAGSVA-----LLELVEKEKDRFFSGVDYIVISDNL 230

Db 129 IPVLSRRLKEAIDEDGRVTDASPELKSIRQNRSEQAVREQLDGIVRGKNAKYLSDAI 188

Qy 231 WISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMDLVALLGSLVDSSGHI 290

Db 189 -ITMR-----NDRYVIPVK---QEYR-GVFGVVDQSA-----SGQT 221

Qy 291 LVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIH 350

Db 222 LF-----IEPKQVVDLN-----NRLRQYQIAERNEI----- 247

Qy 351 GIEGAFDEPGTKTVIPGRVIGKFSIRLVPHM-----NVSAVEKQVTRHLEDVFSKRNSN 405

Db 248 -----QRILSELSAELVPHRQEIHNNAVYVIGKM-----DLNNAKARFG 285

Qy 406 KMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIV---- 461

Db 286 KEVKAIVPG-----ISEDNHVVLKQARHPLIDQEKVVSND---ITIGKDYQAIKITGP 335

Qy 462 ---HKSVVLIPLG-----AVDDGEHSQ 480

Db 336 NTGGKTITLKTLLQLMQAGLPPIPAGEESQ 367

RESULT 891

AAU34969

ID AAU34969 standard; protein; 788 AA.

XX AC AAU34969;

XX 14-FEB-2002 (first entry)

DE Enterococcus faecalis cellular proliferation protein #256.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.  
Enterococcus faecalis.  
WO200170955-A2.  
27-SEP-2001.  
21-MAR-2001; 2001WO-US009180.  
21-MAR-2000; 2000US-0191078P.  
23-MAY-2000; 2000US-0206848P.  
26-MAY-2000; 2000US-0207727P.  
23-OCT-2000; 2000US-0242578P.  
27-NOV-2000; 2000US-0253625P.  
22-DEC-2000; 2000US-0257931P.  
16-FEB-2001; 2001US-0269308P.  
(ELIT-) ELITRA PHARM INC.  
Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
Yamamoto RT, Xu HH;  
WPI; 2001-611495/70.  
N-PSTB; AAS52828.  
  
New polynucleotides for the identification and development of  
antibiotics, comprise sequences of antisense nucleic acids.

Example 3; SEQ ID NO 10562; 51pp; English.

The invention relates to antisense inhibitors of genes essential to  
prokaryotic cellular proliferation, their use in identifying the genes,  
their use in the discovery of novel antibiotics, the essential genes  
themselves and the encoded proteins. The prokaryotes used are Escherichia  
coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
useful for the identification of potential new targets for antibiotic  
development. The antisense nucleic acids can also be used to identify  
proteins used in proliferation, to express these proteins, and to obtain  
antibodies capable of binding to the expressed proteins. The proteins can  
be used to screen compounds in rational drug discovery programmes. The  
antisense nucleic acid sequence is also useful to screen for homologous  
nucleic acids which are required for cell proliferation in a wide variety  
of organisms. The present sequence represents an essential prokaryotic  
cellular proliferation protein. Note: The sequence data for this patent  
did not form part of the printed specification, but was obtained in  
electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

Sequence 788 AA;

Query Match                  3.3%; Score 87.5; DB 4; Length 788;  
Best Local Similarity        19.8%; Pred. No. 2e+02;  
Matches      96; Conservative     72; Mismatches    179; Indels    137; Gaps    24

QY    31 PPALLEKFQYIDLHQDEF-VQTLEKWEVAIESDSVQPVRFRQELFRMMVAADTLQRIG 89  
| | : : : : : : : : : : : : : : : : : :  
Db    36 PIADENKIQAWLNETQDGLKVQLRGGI-----PIPK-----LENIQ 72  
| | : : : : : : : : : : : : : : : : : :

QY    90 ARVASVDMGPQQLPDGQSLLPPPVILAE LGS--DPTKGTVCFYGHLDVPQPAD--RGDGWL 145  
: : : : : : : : : : : : : : : : : :  
Db    73 PHMKRIEIGAD-----LNGVELAQGRVLSTTSELTRFFDELSENEVDFERLYMWR 123  
: : : : : : : : : : : : : : : : : :

QY    146 TDPLYLTVEVGKLYGRGATDNKPVLAWINAVSAFRALEODLPVNIKFIIEGMEEAGSVA 205  
|| || : : : : : : : : : : : : : : : : : :  
Db    124 EQLEVLPENRQL--KQAIDDDGVYTD--EASPALKAIRQ-----NIR-----R 163  
| | : : : : : : : : : : : : : : : : : :

QY    206 LEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYCTRGNYSFMVEVKCRDQDFHSGTF 265  
| : : : : : : : : : : : : : : : : : :  
Db    164 SEQTIREELDSIIRGKNARYLSDAL-----VTMRNERVYPVK---QEY-KNIF 208  
| : : : : : : : : : : : : : : : : : :

QY    266 GGILHEPMADLVALLGSLDVSSCHILVPGIYDEVVPLTEETINTYKAIHLDLEEYRNSSR 325

Db	209	GGVVDQSA-----SGQTLF-----IEPKQILEMNN-----RLRQQQIAERNE	244
Qy	326	VEKFLDFTKEEILMHLWRYPSLSIHG--IEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV	383
Db	247	ITRILAELSAELV-----PYRREITHNAYVIGKLDFFINAKA-----RLGKELKAVVPEISQ	297
Qy	384	S--AVEKQVTRHLED-----VFSSKRNSNKMVVVSMTLGLHPWIAN--	421
Db	298	ANHVVFKQARHPLLDPEKAVANDIVIGEEYQAIKITGPNPTGGKTTILKTGLLLQLMGQAG	357
Qy	422	-----IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP-----IAKMFQEIIVHKS VWLI-PLG	471
Db	358	LPIPVEEESKMGIFTEVFADIGDEQSI EQSLSTFSSHMTNIVSVLKKVDHQSLVLFDELG	417
Qy	472	AVDD	475
Db	418	AGTD	421
RESULT 892			
ID	ADC97107		
XX	ADC97107	standard; protein; 789 AA.	
AC	ADC97107;		
XX	01-JAN-2004	(first entry)	
XX	E. faecium	protein sequence SEQ ID 6734.	
DE	Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.		
KW	Enterococcus faecium.		
OS	US6583275-B1.		
XX	24-JUN-2003.		
PN	30-JUN-1998;	98US-00107532.	
XX	02-JUL-1997;	97US-0051571P.	
PR	14-MAY-1998;	98US-0085598P.	
XX	(GENO-) GENOME THERAPEUTICS CORP.		
PA	Doucette-Stamm LA, Bush D;		
XX	WPI; 2003-799836/75.		
PI	N-PSDB; ADC93453.		
DR	New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection.		
DR	Example 1; SEQ ID NO 6734; 243pp; English.		
XX	The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to a transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids are useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans - derived peptides or antisense polypeptides. Pharmaceutical compositions		

CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.

XX Sequence 789 AA;

Query Match 3.3%; Score 87.5; DB 7; Length 789;  
Best Local Similarity 19.0%; Pred. No. 2e+02;  
Matches 63; Conservative 47; Mismatches 91; Indels 131; Gaps 15;

Qy 187 LPVNIKPIIEGMEAGSVA-----LEELVEKKDRFFSGVDYIVISDNL 230  
Db 132 IPVLSRLKEAIDEDGRVTDASPCLKSIRQNIRSEQAVREQLDGIVRGKNAYLSDAI 191  
Qy 231 WISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHI 290  
Db 192 -ITMR-----NDRYVIPVK---QEYR-GVFGGVVHDQSA-----SGQT 224  
Qy 291 LVPGIYDEVVPLTEEEINTYKAIHLDEEYRNSSSRVEKFLFDTKKEIIMHLMWRYPSLSIH 350  
Db 225 LF-----IEPKQVVDLN-----NRLRQYQIAERNEI----- 250  
Qy 351 GIEGAFDEPGTKTIVIPGRVICKFSIRLVPHM-----NVSAVEKQVTRHLEDVFSKRNSN 405  
Db 251 -----ORILSELSAELVPHRQEIIHNAYVICKM-----DLNNAKAREG 288  
Qy 406 KMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVEGTEPDMIRDGSTITPIAKMFOEIV---- 461  
Db 289 KEVKAIVPG-----ISEDNHVVLKQARHPLIDQEKVVNSD---ITIGKDYQAIIVITGP 338  
Qy 462 ---HKSVVLIPLG-----AVDDGEHSQ 480  
Db 339 NTGGKTIITLKTLLQLMQAGLPPIPAGEESQ 370

RESULT 893  
ABM67553

ID ABM67553 standard; protein; 930 AA.

XX AC ABM67553;

DT 20-NOV-2003 (first entry)

XX Photorhabdus luminescens protein sequence #650.

DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.

XX Photorhabdus luminescens.

OS WO200294867-A2.

XX 28-NOV-2002.

PF 07-FEB-2002; 2002WO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

XX (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A,  
PI Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 650; 1205pp; French.

CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins

XX SQ Sequence 930 AA;

Query Match 3.3%; Score 87.5; DB 6; Length 930;  
Best Local Similarity 21.5%; Pred. No. 2.6e+02;  
Matches 103; Conservative 58; Mismatches 177; Indels 141; Gaps 26;

Qy 11 SLLAVLLLLLERGMFSS-----PSPPPALLEKVFQYIDLHQDEFVQTLKE---WVAIES 61  
Db 33 SNLTVMIRLSHRFILMSADIATIQAPIPLSPADFSSEDLRYPVVKQHLEEFQLWL---- 88  
Qy 62 DSVQVPVPRFRQELFRMVAADTLQRLGARVASVDMGPGQLPDGQSL-PIPPVILAE LGS 120  
Db 89 -----EHA FK-AGISAEAL--ISARSDYIDQLQLWYAYRFDKISSLSLIAVGG 135  
Qy 121 DPTKGTVCYFYGHLDVQPADRGWGLTDPYVLTEVDGKLYGCGATDNKGPVLAW---INAV 177  
Db 136 -----YGRRELHPLSDIDLILSEQPLTPPQANVGQFIT-----LLWDIRLEVG 180  
Qy 178 SAFRALEQDLPVNIKFIIEGMEAGSVALEELVEKEKDRFFSGVDYIYI-----SDNL 230  
Db 181 HSVRTLEEC-----LEGLSDL--TIATNLIE--SRLICGDSISIFLRLQRHTFSDGF 228  
Qy 231 WISQKPAITYGTRGNSYF---MVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVD-- 285  
Db 229 WPS-----TEFFDAKIVEQHERHQRYHSTSYN---LEP--DIKSSPGGLRDIH 271  
Qy 286 -----SSGHILVPGIYDEVVP---LTEEEINTYK-----AIHLDLEEYRNSSRV 326  
Db 272 TLLWVARRHFGATSI-DEMVDGFLTAERNEELNECQSFRLWRIRFALHLVVRNYDN---- 326  
Qy 327 EKFLPDTKBEIIMHLMWRYPSLSIHGIEGAFDEPGTKV-----IPGRV--IGKFSIRLVP 379  
Db 327 -RLLFDRQFSIAQLL-----GYHGERNQPVVERMMKDFYRMTRRVSELNMLQLQFD 376  
Qy 380 HMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVE 438  
Db 377 EAILALETNEKSRSLDSEFQLRGO-----LIDLIDETLFIKEPAAIMRMF 421

RESULT 894  
AAR29770

ID AAR29770 standard; protein; 954 AA.

XX AC AAR29770;

XX 27-APR-1993 (first entry)

DE Porcine PAM-8.

XX peptidyl-glycine alpha-amidating monooxygenase; pig; pro-hormone.











CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1052 AA;  
  
Query Match 3.3%; Score 87.5; DB 7; Length 1052;  
Best Local Similarity 19.6%; Pred. No. 3.1e+02;  
Matches 85; Conservative 68; Mismatches 163; Indels 117; Gaps 21;  
  
Qy 28 PSPPP---ALLEKVFQYIDLHQDEFVQTLKEWVA--IESDSVQVPVPRFRQELFRMMAVAA 82  
Db 645 PNCPTLYSLMTKCWAYDPSRRPRFTE-LKAQLSTILEEKAQOERMESRRQATVSW 703  
  
Qy 83 DTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKTCFYGHLDVQ--PADR 140  
Db 704 DS-----GGDEAPPKPSRPGYPSPRSSEGFYPSQHMVQTNHYQVSGYPGSH 751  
  
Qy 141 GDGWLTPYVLTVEVDGKLY-GRGA-----TD--NKGP--VLAW-----INAVSAFRALEQD 186  
Db 752 G-----ITAMAGSIYPGQASLLDQTDSDWNHRPQEIAMWQPNVEDSTVLDLRGIGQV 802  
  
Qy 187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ----RKPAITYG 242  
Db 803 LPTHL-----MEER---LIRQQQEMEEDQRWLEKEERFLKPDVRLSRGSDIDREDGSLQG 853  
  
Qy 243 TRGNSYFMVEVKCRD-----QDFHSGTFGGILHEPMADLVALLGSLVDSSGHI 290  
Db 854 PIGNQHIYQPVGKPDPAAPPKPPRPGAPGHLGS-----LASLSSPADS----- 897  
  
Qy 291 LVPGIYDEVVPLTEEEINTYKAHLDLEE---YRNSRVEKFLDFTKEEI-----LMH 340  
Db 898 -----YNEGKVLQPOEISPPPTANLDRSNDKVYENVTVGLVKAVIEMSSKIOPAPPEEYVP 952  
  
Qy 341 LWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP---HMNVSAVEKQVTRHLEDV 397  
Db 953 MVKEVGLALRTLTLATVDE-----TIPLLPASTHREIEMAQKLLNSDLGEL 997  
  
Qy 398 FSKRNSNKMVVS 410  
Db 998 INKMKLAQQYVMT 1010  
  
RESULT 899  
ADF45056  
ID ADF45056 standard; protein; 1052 AA.  
XX  
AC ADF45056;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human kinase FAK1.  
KW Human; protein kinase; enzyme; inhibitor; FAK1.  
XX  
OS Homo sapiens.  
XX  
PN WO2003081210-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 20-MAR-2003; 2003WO-US008725.  
XX  
PR 21-MAR-2002; 2002US-0366892P.  
XX  
PA (SUNE-) SUNESIS PHARM INC.  
XX  
PI Prescott JC, Braisted A;  
XX  
XX WPI; 2003-865136/80.  
XX  
PT Identifying ligand binding to inactive conformation of target protein

PT kinase (T) comprises contacting the conformation modified (T) which  
PT contains reactive group at binding site, with ligands and detecting  
PT kinase-ligand conjugate formation.  
XX  
PS Disclosure; SEQ ID NO 25; 260pp; English.  
XX  
CC The present invention relates to a method for identifying a ligand (L),  
CC which binds to an inactive conformation of target protein kinase (T). The  
CC method involves contacting inactive conformation of (T), which contains  
CC or is modified to contain a reactive group at or near a binding site of  
CC interest, with one or more ligand candidates capable of covalently  
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).  
CC The method is useful for identifying protein kinase inhibitors that  
CC preferentially bind to inactive conformation of a target protein kinase.  
CC The present sequence is a protein kinase which may be modified via an  
CC amino acid substitution, for use in the method of the invention.  
XX  
SQ Sequence 1052 AA;  
  
Query Match 3.3%; Score 87.5; DB 7; Length 1052;  
Best Local Similarity 19.6%; Pred. No. 3.1e+02;  
Matches 85; Conservative 68; Mismatches 163; Indels 117; Gaps 21;  
  
Qy 28 PSPPP---ALLEKVFQYIDLHQDEFVQTLKEWVA--IESDSVQVPVPRFRQELFRMMAVAA 82  
Db 645 PNCPTLYSLMTKCWAYDPSRRPRFTE-LKAQLSTILEEKAQOERMESRRQATVSW 703  
  
Qy 83 DTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKTCFYGHLDVQ--PADR 140  
Db 704 DS-----GGDEAPPKPSRPGYPSPRSSEGFYPSQHMVQTNHYQVSGYPGSH 751  
  
Qy 141 GDGWLTPYVLTVEVDGKLY-GRGA-----TD--NKGP--VLAW-----INAVSAFRALEQD 186  
Db 752 G-----ITAMAGSIYPGQASLLDQTDSDWNHRPQEIAMWQPNVEDSTVLDLRGIGQV 802  
  
Qy 187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ----RKPAITYG 242  
Db 803 LPTHL-----MEER---LIRQQQEMEEDQRWLEKEERFLKPDVRLSRGSDIDREDGSLQG 853  
  
Qy 243 TRGNSYFMVEVKCRD-----QDFHSGTFGGILHEPMADLVALLGSLVDSSGHI 290  
Db 854 PIGNQHIYQPVGKPDPAAPPKPPRPGAPGHLGS-----LASLSSPADS----- 897  
  
Qy 291 LVPGIYDEVVPLTEEEINTYKAHLDLEE---YRNSRVEKFLDFTKEEI-----LMH 340  
Db 898 -----YNEGKVLQPOEISPPPTANLDRSNDKVYENVTVGLVKAVIEMSSKIOPAPPEEYVP 952  
  
Qy 341 LWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP---HMNVSAVEKQVTRHLEDV 397  
Db 953 MVKEVGLALRTLTLATVDE-----TIPLLPASTHREIEMAQKLLNSDLGEL 997  
  
Qy 398 FSKRNSNKMVVS 410  
Db 998 INKMKLAQQYVMT 1010  
  
RESULT 900  
ADL97784  
ID ADL97784 standard; protein; 1052 AA.  
XX  
AC ADL97784;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human focal adhesion kinase YK454R mutant protein.  
KW focal adhesion kinase; FAK; gene expression; mifepristone.  
XX  
OS Homo sapiens.  
XX  
PN WO2004027018-A2.  
XX  
PD 01-APR-2004.

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XX 08-SEP-2003; 2003WO-IB003968.
XX PF
XX ID
PR 19-SEP-2002; 2002US-0412078P.
XX PA
XX (PF12 ) PFIZER PROD INC.
XX PI
XX Roberts WG, Whalen PM, Ung EJT;
XX WPI; 2004-295396/27.
DR N-PSDB; ADL97788.
XX
XX Identifying cell-active inhibitors of focal adhesion kinase (FAK), by
PT adding inducing agent to mammalian cells, adding test compound, capturing
PT expressed FAK, and detecting phosphorylation of FAK.
XX
XX Example; SEQ ID NO 3; 48pp; English.
XX
XX The invention relates to a method of identifying (M1) cell-active
CC inhibitors of focal adhesion kinase (FAK), by adding inducing agent to
CC mammalian cells to induce expression of a gene encoding FAK, where
CC mammalian cells are stably transfected with gene, and the gene is
CC expressed in presence of inducing agent, adding test compound, capturing
CC expressed FAK using FAK capture agent, and detecting phosphorylation of
CC FAK. (M1) is useful for identifying cell-active inhibitors of focal
CC adhesion kinase (claimed). (M1) allows induction of FAK in cells using an
CC inducible system, which allows for tight repression of gene expression
CC when not induced, resulting in viable cell clones. (M1) allows detection
CC of phosphorylated FAK which may be used to identify inhibitors of FAK
CC kinase activity. The assay allows for detection of total FAK protein,
CC total phosphorylated FAK protein, or FAK protein phosphorylated at a
CC given tyrosine at position 397. (M1) allows in vivo screening of FAK
CC inhibitors by feeding the animals with mifepristone. This sequence
CC corresponds to the wild type FAK protein.
XX
SQ Sequence 1052 AA;
Query Match 3.3%; Score 87.5; DB 8; Length 1052;
Best Local Similarity 19.6%; Pred. No. 3.1e+02;
Matches 85; Conservative 68; Mismatches 163; Indels 117; Gaps 21;
QY 28 PSEPP--ALLEKVFQYIDLHQDEFVQTLKEWVA--IESDSVQVPVPRFQELFRMMAVAA 82
Db 645 PNCPTLYSLMTKCWAYDPSRRPRFTE-LKAQLSTILEEKAQOERMRMESRRQATVSW 703
QY 83 DTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPTKGTVCYFVGHLDVQ--PADR 140
Db 704 DS-----GGSEAPPKPSRPGYSPRSSEGFYSPQHMVQTNHYQVSGYPGSH 751
QY 141 GDGWLTDPTYVLTEVDGKLY-GRGA----TD--NKGP--VLAW-----INAVSAFRALEQD 186
Db 752 G-----ITAMAGSIYPGQASLLDQTDTSWNHRPQEIAMWQPNVEDSTVLDLRGIGQV 802
QY 187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ----RKPAITYG 242
Db 803 LPTHLL-----MEER---LIRQQQEMEEDQWLKEKEERFLKPDVRLSRGSDREDGSLQG 853
QY 243 TRGNSYFMVEVKCRD-----QDFHSGTFCGILHEPMADLVALLGSLVDSSGHI 290
Db 854 PIGNQHIYQPVGKPDPAAPPKPPRPGAPGHLGS-----LASLSPADS---- 897
QY 291 LVPGIYDEVVPLTEEEINTYKAHLDLEE---YRNSRVEKFLFDTKEEI-----LMH 340
Db 898 -----YNEGKVLQPOEISPPPTANLDRSNDKVYENVTVGLKAVIEMSSKIQPAPPEEYVP 952
QY 341 LWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP---HMNVSAVEKQVTRHLEDV 397
Db 953 MVKEVGLALRTLATVDE-----TIPLLPASTHREIEMAQKLNSDLGEL 997
QY 398 FSKRNSNKMVVS 410
Db 998 INKMKLAQQYVMT 1010
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RESULT 901
ADL97783
ID ADL97783 standard; protein; 1052 AA.
XX
XX AC ADL97783;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human focal adhesion kinase Y397F mutant protein.
DE
XX focal adhesion kinase; FAK; gene expression; mifepristone.
XX
XX Homo sapiens.
OS
XX
XX WO2004027018-A2.
PN
XX
XX 01-APR-2004.
PD
XX
XX 08-SEP-2003; 2003WO-IB003968.
PF
XX
XX 19-SEP-2002; 2002US-0412078P.
PR
XX
XX (PF12 ) PFIZER PROD INC.
PA
XX
XX Roberts WG, Whalen PM, Ung EJT;
PI
XX WPI; 2004-295396/27.
XX N-PSDB; ADL97787.
XX
XX Identifying cell-active inhibitors of focal adhesion kinase (FAK), by
PT adding inducing agent to mammalian cells, adding test compound, capturing
PT expressed FAK, and detecting phosphorylation of FAK.
XX
XX Example; SEQ ID NO 2; 48pp; English.
XX
XX The invention relates to a method of identifying (M1) cell-active
CC inhibitors of focal adhesion kinase (FAK), by adding inducing agent to
CC mammalian cells to induce expression of a gene encoding FAK, where
CC mammalian cells are stably transfected with gene, and the gene is
CC expressed in presence of inducing agent, adding test compound, capturing
CC expressed FAK using FAK capture agent, and detecting phosphorylation of
CC FAK. (M1) is useful for identifying cell-active inhibitors of focal
CC adhesion kinase (claimed). (M1) allows induction of FAK in cells using an
CC inducible system, which allows for tight repression of gene expression
CC when not induced, resulting in viable cell clones. (M1) allows detection
CC of phosphorylated FAK which may be used to identify inhibitors of FAK
CC kinase activity. The assay allows for detection of total FAK protein,
CC total phosphorylated FAK protein, or FAK protein phosphorylated at a
CC given tyrosine at position 397. (M1) allows in vivo screening of FAK
CC inhibitors by feeding the animals with mifepristone. This sequence
CC corresponds to the wild type FAK protein.
XX
SQ Sequence 1052 AA;
```

```
Query Match 3.3%; Score 87.5; DB 8; Length 1052;
Best Local Similarity 19.6%; Pred. No. 3.1e+02;
Matches 85; Conservative 68; Mismatches 163; Indels 117; Gaps 21;
QY 28 PSEPP--ALLEKVFQYIDLHQDEFVQTLKEWVA--IESDSVQVPVPRFQELFRMMAVAA 82
Db 645 PNCPTLYSLMTKCWAYDPSRRPRFTE-LKAQLSTILEEKAQOERMRMESRRQATVSW 703
QY 83 DTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPTKGTVCYFVGHLDVQ--PADR 140
Db 704 DS-----GGSEAPPKPSRPGYSPRSSEGFYSPQHMVQTNHYQVSGYPGSH 751
QY 141 GDGWLTDPTYVLTEVDGKLY-GRGA----TD--NKGP--VLAW-----INAVSAFRALEQD 186
Db 752 G-----ITAMAGSIYPGQASLLDQTDTSWNHRPQEIAMWQPNVEDSTVLDLRGIGQV 802
QY 187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ----RKPAITYG 242
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Db 803 LPTHL-----MEER---LIRQQQEMEEDQRLWLEKEERFLKPDVRLSRGSDIDREDGSLQG 853  
QY 243 TRGNSYFMVEVKCRD-----QDFHSGTFFGGILHEPMDLVALLGSLVDSSGHI 290  
Db 854 PIGNQHIYQPVGKPDPAAPPKPPRPGAPGHLGS-----LASLSSPADS----- 897  
QY 291 LVPGIYDEVVPLTEEEINTYKAIHLDLEE---YRNSRVEKFLFDTKKEI-----LMH 340  
Db 898 -----YNEGVLQPOEISPPPTANLDRSNDKVYENVVTGLVKAVIEMSSKIQAPPEEYVP 952  
QY 341 LWRYPSLSIHGEGAFDEPGTKTIVIPGRVIGKFSIRLVP---HMNVSAVEKQVTRHLEDV 397  
Db 953 MVKEVGLALRTLTLATVDE-----TIPLLPASTHREIEMAQKLLNSDLGEL 997  
QY 398 FSKRNSNKMVVS 410  
Db 998 INKMQLAQQYVMT 1010

RESULT 902

ADL97782  
ID ADL97782 standard; protein; 1052 AA.

XX AC ADL97782;

XX DT 17-JUN-2004 (first entry)

XX DE Human focal adhesion kinase wild type protein.

XX KW focal adhesion kinase; FAK; gene expression; mifepristone.

XX OS Homo sapiens.

XX PN WO2004027018-A2.

XX PD 01-APR-2004.

XX PF 08-SEP-2003; 2003WO-IB003968.

XX PR 19-SEP-2002; 2002US-0412078P.

XX PA (PFIZ ) PFIZER PROD INC.

XX PI Roberts WG, Whalen PM, Ung EJT;

XX DR WPI; 2004-295396/27.

DR N-PSDB; ADL97786.

XX PT Identifying cell-active inhibitors of focal adhesion kinase (FAK), by  
PT adding inducing agent to mammalian cells, adding test compound, capturing  
PT expressed FAK, and detecting phosphorylation of FAK.

XX PS Example; SEQ ID NO 1; 48pp; English.

XX CC The invention relates to a method of identifying (M1) cell-active  
CC inhibitors of focal adhesion kinase (FAK), by adding inducing agent to  
CC mammalian cells to induce expression of a gene encoding FAK, where  
CC mammalian cells are stably transfected with gene, and the gene is  
CC expressed in presence of inducing agent, adding test compound, capturing  
CC expressed FAK using FAK capture agent, and detecting phosphorylation of  
CC FAK. (M1) is useful for identifying cell-active inhibitors of focal  
CC adhesion kinase (claimed). (M1) allows induction of FAK in cells using an  
CC inducible system, which allows for tight repression of gene expression  
CC when not induced, resulting in viable cell clones. (M1) allows detection  
CC of phosphorylated FAK which may be used to identify inhibitors of FAK  
CC kinase activity. The assay allows for detection of total FAK protein,  
CC total phosphorylated FAK protein, or FAK protein phosphorylated at a  
CC given tyrosine at position 397. (M1) allows in vivo screening of FAK  
CC inhibitors by feeding the animals with mifepristone. This sequence  
CC corresponds to the wild type FAK protein.

XX SQ Sequence 1052 AA;

Query Match 3.3%; Score 87.5; DB 8; Length 1052;  
Best Local Similarity 19.6%; Pred. No. 3.le+02;  
Matches 85; Conservative 68; Mismatches 163; Indels 117; Gaps 21;  
QY 28 PSPPP---ALLEKVFQYIDLHQDEFVQTLKEWVA--IESDSVQVPVPRFRQELFRMMAVAA 82  
Db 645 PNCPTLYSLMTKCWAYDPSRRPRFTE-LKAQLSTILEEKAQOEERMESRRQATVSW 703  
QY 83 DTLQRLGARVASVDMGPQQLPDGQSLPIPPPVILAEIGSDPTKGTVCFYGHLDVQ--PADR 140  
Db 704 DS-----GGDEAPPKPSRPGYSPRSSEGYPSPQHMVQTNHYQVSGYPGSH 751  
QY 141 GDGWLTDPPYVLTEVDGKLY-GRGA---TD--NKGP--VLAW-----INAVSAFRALEQD 186  
Db 752 G-----ITAMAGSIYPGQASLLDQTDSWNHRPQEIAMWQPNVEDSTVLDLRGIGQV 802  
QY 187 LPVNIKFIIEGMEEAGSVALHEELVEKEKDRFFSGVDYIVISDNLWISQ----RKPAITYG 242  
Db 803 LPTHL-----MEER---LIRQQQEMEEDQRLWLEKEERFLKPDVRLSRGSDIDREDGSLQG 853  
QY 243 TRGNSYFMVEVKCRD-----QDFHSGTFFGGILHEPMDLVALLGSLVDSSGHI 290  
Db 854 PIGNQHIYQPVGKPDPAAPPKPPRPGAPGHLGS-----LASLSSPADS----- 897  
QY 291 LVPGIYDEVVPLTEEEINTYKAIHLDLEE---YRNSRVEKFLFDTKKEI-----LMH 340  
Db 898 -----YNEGVLQPOEISPPPTANLDRSNDKVYENVVTGLVKAVIEMSSKIQAPPEEYVP 952  
QY 341 LWRYPSLSIHGEGAFDEPGTKTIVIPGRVIGKFSIRLVP---HMNVSAVEKQVTRHLEDV 397  
Db 953 MVKEVGLALRTLTLATVDE-----TIPLLPASTHREIEMAQKLLNSDLGEL 997  
QY 398 FSKRNSNKMVVS 410  
Db 998 INKMQLAQQYVMT 1010

RESULT 903

ADS00186  
ID ADS00186 standard; protein; 1052 AA.

XX AC ADS00186;

XX DT 16-DEC-2004 (first entry)

XX DE Human focal adhesion kinase, FAK.

XX KW Human; focal adhesion kinase; FAK; enzyme; antisense therapy;

XX KW cell migration; neovascularisation; breast cancer; colon cancer;

XX KW mouth cancer; skin cancer; angiogenic disorder;

XX KW retinal neovascularisation; melanoma; embryonic development dysfunction;  
XX KW 5-fluorouracil.

XX OS Homo sapiens.

XX PN US2004192628-A1.

XX PD 30-SEP-2004.

XX PF 22-AUG-2003; 2003US-00646569.

XX PR 19-AUG-1999; 99US-00377310.

PR 13-JUL-2000; 2000WO-US018999.

PR 09-JAN-2001; 2001US-00757100.

XX PA (MONI/) MONIA' B P.

PA (GAAR/) GAARDE W A.

PA (NERO/) NERO P S.

XX PI Monia BP, Gaarde WA, Nero PS;

XX DR WPI; 2004-689880/67.

DR N-PSDB; ADS00185.





CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1168 AA;  
  
Query Match 3.3%; Score 87.5; DB 4; Length 1168;  
Best Local Similarity 19.1%; Pred. No. 3.7e+02;  
Matches 89; Conservative 72; Mismatches 165; Indels 139; Gaps 24;  
  
Qy 34 LLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAV 80  
Db 731 LLSKDIQYKDLGLLLIVDEEQRFGRHKEIKTKKNVDVLTLTATPIPRTH----- 782  
Qy 81 AADTLQRLGARVASVDMGFPQQLPDGQSLPPIPPVILAB-----LGSDFTKGTVCFYGH 132  
Db 783 ----MSMLGVR---DLSVIETPPENRFPVQTVYLEQNMSFIKEALERELSRDGOVFYLY 834  
Qy 133 LDVQ----PADRGDGLTDPYVLTEDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL 188  
Db 835 NKVQSIYEKREQLQMLMPDANIAV-AHQQMSE--DLEETMLSFINN-----EYDIL 883  
Qy 189 VNIKFIIIEGMEAGSVALBELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTR-GNS 247  
Db 884 VTTIETGTVDVPNA---NTLIIEDADRF--GLSOLY-----QLRGRVGRSSRIGYA 930  
Qy 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMADL-VALLGSLVDSSGHILVPGI-Y 296  
Db 931 YFLHPANKVLTETAEDRLQAIKEFTELGSGFKIAMRDNLIRGAGNLLGKQHQHGFIDTVGF 990  
Qy 297 DEVVPLTEEEINTYKAI-----HLD-----LEEYRNSSRVEK 328  
Db 991 DLYSQMLEEAVNEKRGIKEPESEVPEVEVDNLNDAYLPTHEYIANEQAKIEIYKKLRKTET 1050  
Qy 329 F--LFDTKKEEILMHLWRYP-----SLSIHGIEGAFDEPGTKTVI--PGRVIGKFS 374  
Db 1051 FDQIIDIKDELIDRFNDYPVEVARLLDIVEIKVHALHSGI-----TLIKDKGKIID--- 1101  
  
RESULT 906  
ABU16113  
ID ABU16113 standard; protein; 1168 AA.  
XX  
AC ABU16113;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #1640.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX

Db 884 VTTTIETGVDVPNA---NTLIIEDADRF--GLSOLY-----QLRGRVGRSSRIGYA 930  
Qy 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMADL-VALLGSLVDSSGHILVPGI-Y 296  
Db 931 YFLHPANKVLTETAEDRLQAIKEFTELGSGFKIAMRDNLIRGAGNLLGKQHQHGFIDTVGF 990  
Qy 297 DEVVPLTEEEINTYKAI-----HLD-----LEEYRNSSRVEK 328  
Db 991 DLYSQMLEEAVNEKRGIKEPESEVPEVEVDNLNDAYLPTHEYIANEQAKIEIYKKLRKTET 1050  
Qy 329 F--LFDTKKEEILMHLWRYP-----SLSIHGIEGAFDEPGTKTVI--PGRVIGKFS 374  
Db 1051 FDQIIDIKDELIDRFNDYPVEVARLLDIVEIKVHALHSGI-----TLIKDKGKIID--- 1101  
  
Qy 375 IRLVPHMNVSAVEK-----QVTRHLEDVFSKRNSSNKMVVSMT 412  
Db 1102 ----IHLSVKATENIDGEVLFKATQPLGRMTKMGVQNNAMTITLT 1142  
  
RESULT 905  
AAU36558  
ID AAU36558 standard; protein; 1168 AA.  
XX  
AC AAU36558;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Staphylococcus aureus cellular proliferation protein #728.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US009180.  
PR 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS54417.  
XX  
PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 12151; 511pp; English.  
XX  
CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.  
N-PSDB; ACA19983.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 44037; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

Sequence 1168 AA;

Db	991	DLYSQMLEEAVNEKRGIKEPESEVPEVVDLNLDAYLPTEYIANEQAKIEIYKKLRKTET	1050
QY	329	F--LFDTKKEILMHLWRYP-----SLSIHGIEGAFDEPGTKTVI--PGRVIGKFS	374
Db	1051	FDQIIDIKDELIDRFNDYPVEVARLLDIVEIKVHALHSGI-----TLIKDKGKIID---	1101
QY	375	IRLVPHMNVSAVEK-----QVTRHLEDVFSKRNSSNKMVVSMVT	412
Db	1102	----IHLSVKATENIDGEVLFKATQPLGRMTMKVGVQNNAMTITLT	1142
RESULT 907			
ABM71924			
ID	ABM71924	standard; protein; 1168 AA.	
XX	AC	ABM71924;	
XX	DT	20-NOV-2003 (first entry)	
XX	DE	Staphylococcus aureus protein #1164.	
XX	KW	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;	
KW	KW	enzymatic assay; antibiotic target.	
XX	OS	Staphylococcus aureus.	
XX	PN	WO200294868-A2.	
XX	PD	28-NOV-2002.	
XX	PF	27-MAR-2002; 2002WO-IB002637.	
XX	PR	27-MAR-2001; 2001GB-00007661.	
XX	PA	(CHIR-) CHIRON SPA.	
PI	PI	Masignani V, Mora M, Scarselli M;	
XX	DR	WPI; 2003-120786/11.	
DR	DR	N-PSDB; ACF73484.	
XX	PT	New Staphylococcus aureus protein, useful as a vaccine for treating or	
PT	PT	preventing Staphylococcal infection, specifically an infection caused by	
XX	XX	S. aureus, e.g. sepsis.	
PS	PS	Claim 1; SEQ ID NO 2328; 49pp; English.	
XX	CC	The invention relates to novel genes and encoded proteins from	
CC	CC	Staphylococcus aureus. A composition comprising the S. aureus protein, a	
CC	CC	nucleic acid encoding the protein, or an antibody to the protein, is	
CC	CC	useful as a pharmaceutical, particularly as a vaccine for treating or	
CC	CC	preventing infection due to Staphylococcus bacteria, specifically an	
CC	CC	infection caused by S. aureus. The composition is particularly useful for	
CC	CC	treating or preventing sepsis in a patient. The composition can also be	
CC	CC	used for diagnostics. The protein is also used in an assay for enzymatic	
CC	CC	studies and as a target for antibiotics. This sequence represents one of	
CC	XX	the novel S. aureus proteins of the invention	
SQ	SQ	Sequence 1168 AA;	



QY 133 LDVQ----PADRGDWLTPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP 188  
Dd 835 NKVQSIYEKREQLQMLMPDANIAV-AHQWTER--DLEETMLSFINN-----EYDIL 883  
QY 189 VNIKFIIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTR-GNS 247  
Dd 884 VTTTIIETGVDVNA---NTLIIEDADRF--GLSQLY-----QLRGRVGRSSRIGYA 930  
QY 248 YFM-----VEVKCRDQDFHSGT-FGGILHEPMADL-VALLGSLVDSSGHILVPGI-Y 296  
Dd 931 YFLHPANKVLTETAEDRLQAIKEFTELGSGFKIAMRDLNIRGAGNLLGKQQHGFIDTVGF 990  
QY 297 DEVVPLTEEEINTYKAI-----HLD-----LEEYRNSSRVEK 328  
Dd 991 DLYSQMLEEAVNEKRGIKEPESEVPEVEVDNLNDAYLPTHEYIANEQAKIEIYKLRKTET 1050  
QY 329 F--LFDTKKEILMHLWRYP-----SLSIHGIEGAFDEPGTKTVI--PGRVIGKFS 374  
Dd 1051 FDQIIDIKDELIDRFNDYPVEVARLLDIVEIKVHALHSGI-----TLIKDKGIID--- 1101  
QY 375 IRLVPHMNVSAVEK-----QVTRHLEDVPSKRNSSNKMVVSMT 412  
Dd 1102 ----IHLSVKATENIDGEVLFKATQPLGRTMKVGQVQNNAMTITLT 1142

RESULT 908  
ABP25823  
ID ABP25823 standard; protein; 1181 AA.  
XX  
AC ABP25823;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 822.  
XX  
KW Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;  
KW Group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;  
PI Tettelin H;  
XX  
DR WPI; 2002-352536/38.  
DR N-PSDB; ABN66454.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 3234-3235; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 1181 AA;  
  
Query Match 3.3%; Score 87.5; DB 5; Length 1181;  
Best Local Similarity 18.9%; Pred. No. 3.8e+02;  
Matches 98; Conservative 79; Mismatches 176; Indels 165; Gaps 27;  
  
Qy 47 DEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQL--PD 104  
Dd 604 DKPEVT----VTVHNKSKDP-----QELYQATVQTDKVD--GKLFA---LAPKALYETS 649  
Qy 105 GQSLPIP-----PVILAEAGSD---PTKGTVCYFYGHLDVQPADRGDWLTPDY--- 149  
Dd 650 WQKITIPANSSKQVTIPIDVSQFSKDLLAPMKNGYFLEGFVRFKQDPTKEELMSIPYIGF 709  
Qy 150 -----VLTEVDGKLYGRGATDN-----KGPVLAWINAVSAFRA--EQDLPV 189  
Dd 710 RGDFGNLSALEKPIYDSKDGSSYYHEANSDAKDQLDGLQFYALKNNFTALTTESNPWT 769  
Qy 190 NIKFIIIEGMEEGSVALEELVE-----KEKD-----RFFSGVDYIVISDNLWISQ 234  
Dd 770 IIKAVKEGVENIEDIESSEITETIFAGTFAKQDDSHYIHRHANGKPYAAISP----- 824  
Qy 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPG 294  
Dd 825 -----GDGN-----RDYVQFGTF-----LRNAKNLVAEVLCKEKNVVWTS 860  
Qy 295 IYDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFLPDTKEEILMHLWRYPYPSLSIHGIEG 354  
Dd 861 -----EVTEQVVKNY---NNDLASTLGSTRFEKTRWDGDK-----DG 895  
Qy 355 AFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVS---- 410  
Dd 896 KVVANGTYT-----YRVRYTP---ISSGAKB--QHTDFDVIVDNTTPEVATSATFS 941  
Qy 411 -----MTLGLHPWIA-----NIDTQYLAAKRAIRTVFGTEPDMIRDGST 450  
Dd 942 TEDRRLLTASPKTSQPVYRERIAITYMDELDLPTTEYISPNEGTFTLPEEAETM-EGAT 1000  
Qy 451 IPIAKM--FQEIIVHK---SWVLIPLGAVDDGHSQNEK 483  
Dd 1001 VPL-KMSDFTYVVEDMAGNITYTPVTVKLLEGHSNKPEQ 1037  
  
RESULT 909  
ADR83967  
ID ADR83967 standard; protein; 1181 AA.  
XX  
AC ADR83967;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE S. pyogenes hyperimmune system reactive antigen Spy2010.  
XX  
KW hyperimmune serum reactive antigen; vaccine; anticaline.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO2004078907-A2.  
XX  
PD 16-SEP-2004.  
XX  
PF 02-MAR-2004; 2004WO-EP002087.



```
XX
SQ      Sequence 1234 AA;

Query Match          3.3%;  Score 87.5;  DB 6;  Length 1234;
Best Local Similarity 19.4%;  Pred. No. 4e+02;
Matches 107;  Conservative 76;  Mismatches 197;  Indels 171;  Gaps 26;

QY      53 LKEWVAIESDSVQVPVPRFR-----QELFRMM-----AVAADTLQRLGARVA 93
Db      388 LSDESAIELD-VRAAPSARGHQRDIDEIFAMLRAHIAATGGYAALVAPGTGTAHRVVERLS 446

QY      94 SVDMPGQQLPDQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTE 153
Db      447 ESDTPAGMLDPGQA-PKPGVGVVLQG--PLRDGVIIPG-----ANLVVITE 489

QY      154 VDGKLYGRGATDNKGPVLA--WINAVSAFRALEQDLPVN---IKFIIEGMEE-AGSVAL 206
Db      490 TD--LTGSRVSAAEGRKRLAAKRRNIVDPLALTAGDLVVDHQHGIGRFVEMVERTVGGARR 547

QY      207 EELV-----EKEKDRFFSGVDYIVISDNL--WISQRKPAITYGTRGNSYFMVEV 253
Db      548 EYLVLEYASAKRGGAKNTDKLYVPMDSL---DQLSRYVGGQAPALS-RLGGSDWANTKT 603

QY      254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI-----YDEVVPLTE--EE 306
Db      604 KAR-----RAVREIAGELVSLYAKRQASPGHAFSPDTPWQAELEDAFGFTETVDQ 653

QY      307 INTYKAIHLDLEVRNSSRV-----EKFLFDTKEEILM-----H 340
Db      654 LTAIEEVKADMEKPIPMDRVICDVGYGKTEIAVRAAFKAVQDGKQVAVLVPTTLLADQH 713

QY      341 LWRYP-----LSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPH-----MNV 383
Db      714 LQTFGERMSGFPVITKLSRFTDAESRAVIDGLADGSVDIVIGTHRLLOTGVRWKDGL 773

QY      384 SAVEKQV--TRHLEDVFSKRNSSNMVVSMT-----LGLH-----416
Db      774 VVUDEEQRFGEVHEKHISLRTHVDVLTMSATPIPTRTLEMSLAGIREMSTILTPPEERYP 833

QY      417 --PWIANIDDTQYLAAKRAIRTVEGTEPDMRDGSTIPI-----AKMFOEIVHKS 464
Db      834 VLTYVGPDDKQIAAALRR-----ELLRDGQAFYVHNRVSSIDAARVRELVP 884

QY      465 VVLIPLGAVDD 475
Db      885 RVVVAHQMP 895
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RESULT 911
ABU34752
ID      ABU34752 standard; protein; 1234 AA.
XX
AC      ABU34752;
XX
DT      19-JUN-2003 (first entry)
XX
DE      Protein encoded by Prokaryotic essential gene #20279.
XX
KW      Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS      Mycobacterium bovis.
XX
PN      WO200277183-A2.
XX
PD      03-OCT-2002.
XX
PF      21-MAR-2002; 2002WO-US009107.
XX
PR      21-MAR-2001; 2001US-00815242.
PR      06-SEP-2001; 2001US-00948993.
PR      25-OCT-2001; 2001US-0342923P.
PR      08-FEB-2002; 2002US-00072851.
PR      06-MAR-2002; 2002US-0362699P.
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XX
PA      (ELIT-) ELITRA PHARM INC.
XX
PI      Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI      Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR      WPI; 2003-029926/02.
DR      N-PSDB; ACA38622.
XX
PT      New antisense nucleic acids, useful for identifying proteins or screening
PT      for homologous nucleic acids required for cellular proliferation to
PT      isolate candidate molecules for rational drug discovery programs.
XX
PS      Claim 25; SEQ ID NO 62676; 1766pp; English.
XX
CC      The invention relates to an isolated nucleic acid comprising any one of
CC      the 6213 antisense sequences given in the specification where expression
CC      of the nucleic acid inhibits proliferation of a cell. Also included are:
CC      (1) a vector comprising a promoter operably linked to the nucleic acid
CC      encoding a polypeptide whose expression is inhibited by the antisense
CC      nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC      polypeptide or its fragment whose expression is inhibited by the
CC      antisense nucleic acid; (4) an antibody capable of specifically binding
CC      the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC      proliferation or the activity of a gene in an operon required for
CC      proliferation; (7) identifying a compound that influences the activity of
CC      the gene product or that has an activity against a biological pathway; (8)
CC      required for proliferation, or that inhibits cellular proliferation; (8)
CC      identifying a gene required for cellular proliferation or the biological
CC      pathway in which a proliferation-required gene or its gene product lies
CC      or a gene on which the test compound that inhibits proliferation of an
CC      organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC      compound's activity; (11) a culture comprising strains in which the gene
CC      product is overexpressed or underexpressed; (12) determining the extent
CC      to which each of the strains is present in a culture or collection of
CC      strains; or (13) identifying the target of a compound that inhibits the
CC      proliferation of an organism. The antisense nucleic acids are useful for
CC      identifying proteins or screening for homologous nucleic acids required
CC      for cellular proliferation to isolate candidate molecules for rational
CC      drug discovery programs, or for screening homologous nucleic acids
CC      required for proliferation in cells other than S. aureus, S. typhimurium,
CC      K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC      the target prokaryotic essential genes. Note: The sequence data for this
CC      patent did not form part of the printed specification, but was obtained
CC      in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 1234 AA;
```

```
Query Match          3.3%;  Score 87.5;  DB 6;  Length 1234;
Best Local Similarity 19.4%;  Pred. No. 4e+02;
Matches 107;  Conservative 76;  Mismatches 197;  Indels 171;  Gaps 26;

QY      53 LKEWVAIESDSVQVPVPRFR-----QELFRMM-----AVAADTLQRLGARVA 93
Db      388 LSDESAIELD-VRAAPSARGHQRDIDEIFAMLRAHIAATGGYAALVAPGTGTAHRVVERLS 446

QY      94 SVDMPGQQLPDQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTE 153
Db      447 ESDTPAGMLDPGQA-PKPGVGVVLQG--PLRDGVIIPG-----ANLVVITE 489

QY      154 VDGKLYGRGATDNKGPVLA--WINAVSAFRALEQDLPVN---IKFIIEGMEE-AGSVAL 206
Db      490 TD--LTGSRVSAAEGRKRLAAKRRNIVDPLALTAGDLVVDHQHGIGRFVEMVERTVGGARR 547

QY      207 EELV-----EKEKDRFFSGVDYIVISDNL--WISQRKPAITYGTRGNSYFMVEV 253
Db      548 EYLVLEYASAKRGGAKNTDKLYVPMDSL---DQLSRYVGGQAPALS-RLGGSDWANTKT 603

QY      254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI-----YDEVVPLTE--EE 306
Db      604 KAR-----RAVREIAGELVSLYAKRQASPGHAFSPDTPWQAELEDAFGFTETVDQ 653
```



QY 307 INTYKAHLDLLEYRNSRV-----EKFLFDTKEEILM-----H 340  
D 654 LTAIEEVKADMEKPIPMDRVICGDVGKTEIAVRAAFKAVQDGKQVAVLPTTLLADQH 713  
QY 341 LMRVPS-----LSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPH-----MNV 383  
D 714 LQTFGERMSGFPVTIKGLSRFTDAESRAVIDGLADGSDIVIGTHRLLLQTGVRWKDLGL 773  
QY 384 SAVEKQV---TRHLEDVFSKRNSSNMVVSMT-----LGLH----- 416  
D 774 VVDEEQRFGVEHKEHKSRLRTHVDVLTMSATPIPRTEMLSLAGIREMSTILTPPEERYP 833  
QY 417 --PWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPI-----AKMFQEIIVHKS 464  
D 834 VLTXYGPHDDKQIAAALRR-----ELLRDGQAFYVHNRVSSIDAARVRELVPPEA 884  
QY 465 VVLIPLGAVDD 475  
D 885 RVVVAHGQMPPE 895  
RESULT 912  
AAO20501  
ID AAO20501 standard; protein; 1265 AA.  
XX  
AC AAO20501;  
XX  
DT 27-JUN-2002 (first entry)  
XX  
DE Protein of APP related human homologue hCP51674.  
XX  
KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;  
KW amyloid precursor protein; tissue-specific expression control; human APP;  
KW APP pathway modulator; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 38 /label= unknown  
FT /note= "Encoded by TGN"  
FT  
FT Misc-difference 39 /label= unknown  
FT /note= "Encoded by CNA"  
XX  
PN WO200226820-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 01-OCT-2001; 2001WO-EP011345.  
XX  
PR 29-SEP-2000; 2000US-0236893P.  
PR 14-JUN-2001; 2001US-0298309P.  
XX  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;  
PI Reinhardt MWHM, Zusman S;  
XX  
DR WPI; 2002-315796/35.  
DR N-PSDB; AAK99395.  
XX  
PT New transgenic fly, containing DNA encoding an Abeta portion of human  
PT APP, useful for identifying agents which modulate the APP pathway and  
PT which can be used to treat Alzheimer's disease.  
XX  
PS Example 4; Page 94-97; 129pp; English.  
XX  
CC The invention relates to a transgenic fly whose genome comprises DNA  
CC encoding a polypeptide having the Abeta portion of human amyloid  
CC precursor protein (APP), fused to a signal sequence. The DNA sequence  
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in

CC the specification. The DNA sequence is operably linked to a tissue-  
CC specific expression control sequence. Expression of the sequence gives  
CC the fly an altered phenotype. The purpose of the invention is for  
CC identifying agents that inhibit or promote the expression and/or function  
CC of genes or encoded polypeptides which modify the APP pathway. The agent  
CC is a compound, triple helix DNA, antisense oligonucleotide, double  
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
CC to treat conditions such as Alzheimer's disease. The agent can be used as  
CC an APP pathway modulator or in gene therapy. This sequence represents the  
CC protein of the APP related human homologue hCP51674  
XX  
SQ Sequence 1265 AA;

Query Match 3.3%; Score 87.5; DB 5; Length 1265;  
Best Local Similarity 20.8%; Pred. No. 4.2e+02;  
Matches 89; Conservative 57; Mismatches 196; Indels 85; Gaps 21;

QY 33 ALLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQVPFRFRQELFRMMVAADTLQR 87  
D 756 AILQFYPKYVELINQAARLNGYVDAGDSW-----RSMYETPSLEQDLERLFQELQPLYLN 810  
QY 88 LGA---RVASVDMGPPQLP-DGQSLPIPPVIL---AELGSDPTKGTVCFYG--HLDVQP 137  
D 811 LHAYVRRALHRHYGAQHINLEG--PIPAHLGNMWAQTWSNIYDLVVPFSPSMDTTE 867  
QY 138 ADRGDGWLTPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEG 197  
D 868 AMLKQGW-TPRRMFKEADDFFTSLGL-----LPVPPEFWNKS 903  
QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD 257  
D 904 MLEKPTDGREVVVCHASAWDFYNGKDF-RIKQCTTVNLEDLVVAHHEMIGHIQYFMQYKDLP 962  
QY 258 QDFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD- 316  
D 963 VALREGANPG-FHEAIGDVLAL---SVSTPKHLHSLNLLSSEGGSDHDFLMMKVALDK 1018  
QY 317 -----LEEYRNSRRVEKFLFD---TKBEILMHLW---RYPSL--SIHGIEGAFDE 358  
D 1019 IAFIPFSYLVQDWRWR-----VFDGSITKENYNQEWWSLRKYQGLCPPVPTQGD- 1071  
QY 359 PGTKTVIPG-----RVIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSSNMVVSMT 412  
D 1072 PGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKAGQRLATAMK 1131  
QY 413 LGL-HPW 418  
D 1132 LGFSRPW 1138

RESULT 913  
AAR04111  
ID AAR04111 standard; peptide; 1306 AA.  
XX

AC AAR04111;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-SEP-1990 (first entry)  
XX  
DE Human angiotensin converting enzyme (ACE).  
XX human angiotensin converting enzyme; hypertension; bradykinin.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Protein 30.1277  
FT /label= mature ACE  
FT /note= "derived from pre-ACE by removal of signal  
FT peptide"  
FT Modified-site 38.38  
FT /label= putative N-glycosylation site  
FT Modified-site 54.56.







Db 1004 VALREGANPG-FHEAIGDVLAL---SVSTPKHLHSLNLLSSEGGSDHDFINFLMKMALDK 1059  
QY 317 -----LEEYRNSSRVEKFLFD---TKEEILMHLW-----RYPSL--SIHGIEGAFDE 358  
Db 1060 IAFIPFSYLVQDQWRW-----VFDGSITKENYNQEWWSRLKLYQGLCPPVPRTQGDFFD- 1112  
QY 359 PGTKTVIPG-----RVIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSSNKVMVVSMT 412  
Db 1113 PGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQRLATAMK 1172  
QY 413 LGL-HPW 418  
Db 1173 LGFSRPW 1179  
RESULT 916  
AAE36412  
ID AAE36412 standard; protein; 1306 AA.  
XX AAE36412;  
AC AAE36412;  
XX 07-AUG-2003 (first entry)  
DT Human ACE reference protein (GI 4503273).  
XX Thrombospondin 2; THBS2; angiotensin converting enzyme; polymorphism;  
KW ACE-1; beta-fibrinogen; FGB; peripheral vascular disease; ischaemia;  
KW vascular disease; myocardial infarction; pulmonary embolism; stroke;  
KW atherosclerosis; coronary artery disease; venous thromboembolism; human.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO2003020118-A2.  
PN 13-MAR-2003.  
XX 04-SEP-2002; 2002WO-US028113.  
PF 05-SEP-2001; 2001US-0317178P.  
PR 16-OCT-2001; 2001US-0329958P.  
PR 14-DEC-2001; 2001US-00017724.  
XX (VITI-) VITIVITY INC.  
PA McCarthy J;  
PI WPI; 2003-300816/29.  
DR Identifying polymorphisms in thrombospondin 2, angiotensin converting  
PT enzyme and/or beta-fibrinogen genes in nucleic acid sample of subject, by  
PT contacting the nucleic acid with a complementary probe or primer.  
XX Disclosure; Fig 4; 194pp; English.  
PS The invention relates to a method for determining the identity of one or  
XX more allelic variants of a polymorphic region of a thrombospondin 2  
CC (THBS2), angiotensin converting enzyme (ACE)-1 and/or beta-fibrinogen  
CC (FGB) genes in a nucleic acid obtained from a subject. The method  
CC involves contacting the nucleic acid with a complementary probe or  
CC primer. The method is useful for diagnosing or aiding in the diagnosis of  
CC vascular disease or disorder in a subject e.g. myocardial infarction,  
CC coronary artery disease, atherosclerosis, ischaemia, stroke, peripheral  
CC vascular disease, venous thromboembolism and pulmonary embolism. The  
CC present sequence is human ACE reference protein. Note: This sequence is  
CC said to be encoded by SEQ ID NO: 3 (AAD55116). However this does not  
CC appear to be the case  
XX SQ Sequence 1306 AA;

Query Match 3.3%; Score 87.5; DB 6; Length 1306;  
Best Local Similarity 20.8%; Pred. No. 4.4e+02;  
Matches 89; Conservative 57; Mismatches 196; Indels 85; Gaps 21;

QY 33 ALLEKVFQYIDL-----HQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQR 87  
Db 797 AILQFYPKYVELINQAARLNGYVDAGDSW-----RSMYETPSLEQDLERLFOELQPLYLN 851  
QY 88 LGA---RVASVDMGPQQLP-DQQSLPIPPVIL-----AELGSDPTKGTVCFYG--HLDVQP 137  
Db 852 LHAYVRRALHRHYGAQHINLEG--PIPAHLGNMMACTWSNIYDLVVPFAPSMDTTE 908  
QY 138 ADRGDGWLTDYPVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEG 197  
Db 909 AMLKQGW-TPRRMFKEADFFTSLGL-----LPVPPEFWNKS 944  
QY 198 MEEAGSVALEELVEKEKDRFPFSGVDYIVISDNLWISQRPKPAITYGTRGNSYFVMEVKCRD 257  
Db 945 MLEKPTDGREVVCHASAWDFYNGKDF-RIKQCTTVNLEDLVVAHHEMGIQYFMQYKDLP 1003  
QY 258 QDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD- 316  
Db 1004 VALREGANPG-FHEAIGDVLAL---SVSTPKHLHSLNLLSSEGGSDHDFINFLMKMALDK 1059  
QY 317 -----LEEYRNSSRVEKFLFD---TKEEILMHLW-----RYPSL--SIHGIEGAFDE 358  
Db 1060 IAFIPFSYLVQDQWRW-----VFDGSITKENYNQEWWSRLKLYQGLCPPVPRTQGDFFD- 1112  
QY 359 PGTKTVIPG-----RVIGKFSIRLVPHMNV-SAVEKQVTRHLEDVFSKRNSSNKVMVVSMT 412  
Db 1113 PGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQRLATAMK 1172  
QY 413 LGL-HPW 418  
Db 1173 LGFSRPW 1179  
RESULT 917  
ADL95400  
ID ADL95400 standard; protein; 1306 AA.  
XX AC ADL95400;  
XX 20-MAY-2004 (first entry)  
DT Human endothelial angiotensin converting enzyme (huACE).  
XX bioactivity; angiotensin converting enzyme-2; ACE-2; human; enzyme; ACET;  
KW endothelial ACE; endothelial angiotensin converting enzyme.  
XX Homo sapiens.  
OS US6610497-B1.  
XX 26-AUG-2003.  
XX 29-SEP-1999; 99US-00407427.  
XX 11-DEC-1997; 97US-00989299.  
PR 30-SEP-1998; 98US-00163648.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Acton SL, Robison KE, Hsieh FY;  
PI WPI; 2003-895335/82.  
XX Identification of compound that modulates bioactivity of angiotensin  
PT converting enzymes-2 polypeptide, by detecting modulation of the  
PT bioactivity of polypeptide that is contacted with test compound as  
PT compared to control.  
XX Example; SEQ ID NO 7; 91pp; English.  
PS The invention describes a compound that modulates bioactivity of an  
CC angiotensin converting enzyme-2 (ACE-2) polypeptide. The compound is











The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct\\_sequences](http://ftp.wipo.int/pub/published/pct_sequences)

Sequence 6685 AA;

Query Match 3.3%; Score 87.5; DB 4; Length 6685;  
Best Local Similarity 20.2%; Pred. No. 5.5e+03;  
Matches 79; Conservative 53; Mismatches 131; Indels 129; Gaps 20;

**Qy**            118 LGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKG PVLAINAV 177  
| : | | | | | | | | : : | : | : |  
**Db**            2919 LQAETTAGT-----VTPTAIGDS-----ILNITGDLIHLASSDVRAPORSELGAE 2963

```

Qy 178 SAFRALEQD-----LPVNIKFIIIEGMEEGSAVLEELVE 211
    | | : | | | | | | | | | | | | | | | | | | |
Db 2964 SPLRMVASQAYNLTSALMRILTRSRVLNEEPAFSRAPANLSDVQ-----LVFLVD 3014

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Qy	212	KEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVE-----VKC-RDQDF-	260
		: : : : :	
Db	3015	SNPFLF---GYI---SNYTVSTKVASMAFQTQACAQIPIERLASERAITYKVPVNSDWA	3067

Qy	261	---	HS	G	F	G	I	L	H	E	P	M	A	D	L	V	A	L	G	S	L	V	D	S	-----	G	H	I	L	V	P	G	I	Y	D	E	V	V	P	L	T	E	E	I	307						
				:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:								
Db	3068	ARG	H	R	S	S	A	N	S	V	V	V	Q	P	Q	A	S	V	G	A	V	--	T	L	D	S	S	N	P	V	A	V	L	H	L	Q	N	Y	T	L	D	G	R	Y	-----	L	S	E	E	P	3119

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Qy ( 308 NTYKAIHLDL---EYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPCTKV 364
      | :|: | | | | | : :|: | | | :
Db 3120 EPYLAVYLHSERPNERNCASRR-----IRPESLQAGHRRPYTFFI 3161

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Qy	365	IPGR--VIGKFSIRLVPHMNVSAVEKQVTRH--LEDVFESKRNSNKMVVSMTLGLHPWIA  420
Db	3162	SPGTRDPVGSYRLNLSSHFWSALEVSGLYTSLCQFSEED-----VVWRTEGLLP---  3213

Qy	421	NIDDTQLAAKRAIR--TVFGTE----	PDMIR	446
		:::		
Db	3214	-LEETSPQAVCLTRHLTAEGASLFMP	PSHVR	3244

RESULT 924  
ABB66811  
ID ABB66811 standard; protein; 6815 AA.

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 27225.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS *Drosophila melanogaster*.

PN WO200171042-A2.

Db 2068 LIEIKETYEENKPEGDIEITTTTELVPESPDASDDQPVIVVQIKKKKKPVKDDLDKYIQQ 2127

XX  
PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

XX  
000000-000000, 000000 TO 000000

XXXXXXXXXXXX

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL10914.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from *Drosophila* and for elucidating cell signaling and cell-cell  
PT interactions.

PS Disclosure; SEQ ID NO 27225; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct](http://ftp.wipo.int/pub/published/pct) sequences

Sequence 6815 AA;  
SQ

Query Match	3.3%;	Score 87.5;	DB 4;	Length 6815;
Best Local Similarity	18.4%;	Pred. No. 5.7e+03;		
Matches 104;	Conservative	85;	Mismatches 200;	Indels 175;
				Gaps 28;

Qy	31	PPALLEKVFQYIDLHQDEFVQ---	TLKENVAIESDSQVPVPRFRQELFRMAVAA--	DTL 85
Dz	1652	PITVIEVTTQETETDDEKFPDEVTLKE---	IDHENAEEAP--KEQVFEITEYTKAIDEPL	1706

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Qy      86  QRLGARVASVDMGPQQ--LPDQGQSLPIPP-----VILAEGLSDPTKGTVCF 129
      :      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db     1707 SEVTV-VEITDEQPQEEVLPAQEKKPIKKQKXKLKPEDVNTYVVKVLEEL-TEPTQ-----1759

```

QY 130 YGHLDVQPADRGDWLTDPYV-----LTEVDG-----KLYGRGATDNKGP--- 169

Db 1760 ---FETIPEDADD--KPQPVIEDISENVQVQVILIEDGTPKQVEIKKKVSPKHPKEQV 1814

Qy	170	-----VLAWINAVS-AFRALEQDL-----PVNIK-----PIIEGME	200
		:    :    :    :    :	
Db	1815	FEITETRPSDEPLAETVITELTEEGLNKDVIPOEKKTVKKPKLKPEDIQSVYRVLEE	1874

Qy	201	-----AGSVALEELVEKEDRFFSGVDYIVISDNLWISQRKPAITYG 242
		: :   :   :   : : :
Db	1875	FNEQPWASTEKPIIEDIAESIEIVPTTEEDG-----ITKEVEVKKKVSRKQG 1923

Qy	243	TRGNSYFMVEVKCRDQDFHSGTGGILHPEMADLVALGSLVDSSGHILVPGIYDEVVPL	302
		: : :       : :     : :	
Db	1924	TKNQVFEIETKTSDEPLAE-VTILELSGDKS-----QEVTIL	1960

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QY 303 TEEINTYKAITHLDLEEYRNSRVEKFLFDTKEEILMHLWRYP SL--SINGIEGAFDEPG 360
      :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
Db 1661 PKEKKPIKKTIKLKPED-----VESYVNVNLEEF C-----EPQSFESPEPTEGEAHETK 2009

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QY 361 TKTVIPGRVIGKF--SIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPW 418
Db 2010 TKTKKPKPIVKAPENVILIEEMAPETVIENIVEIGEEVKQVTKTKL--KKKEGPKEY 2067

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```
QY      419 IANIDDTQYLAAKRAIRTVFGTE-----PDMIRDGSTIPIAKM-----FQE 459
          : | : | |           : ||       || | | | | | | | | | | | | | | | |
Db      2068 LIEIKETVEENKPEGDIEITTTTELVPESPDASDDQPVIIVQKIKKKKPKVDDLKYIQ 2127
```







Db 143 --SLFKGLRETLNRNLEL---GLTQ-GSFA---FIHKDFDVKETFN-----L 181  
QY 233 SQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILV 292  
Db 182 SKR-----YF--DTECVPMNFRNA-----SQAKRLMNHYYINKETRGI 217  
QY 293 PGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFL--FDT--KEEILMHLWRYPSSL 348  
Db 218 PKLDFEINPET-----KLILVDYILFKG-----KWLTPFDPVFTEVDTFHLDKYKTIK 265  
QY 349 IHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMV 408  
Db 266 VPMMYGA-----GKFA-----STFDKNFRCHVLKLPYQGNATMLVV 301  
QY 409 VSMTLGLH-----PWIANID-----DTQY-----LAAKRAIRTVF 438  
Db 302 LMEKMGDHLALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIIRIF 361  
QY 439 GTEPDMIR---DGSTIPIAKMFQEIIV 461  
Db 362 SPFADLSELSATGRNLQVSRVLQRTV 387

RESULT 929  
AAB74668  
ID AAB74668 standard; protein; 444 AA.

XX AAB74668;  
DT 12-JUN-2001 (first entry)  
XX Human protease and protease inhibitor PPIM-1.  
KW Human; protease; protease inhibitor; protease and protease inhibitor;  
KW PPIM; identification; diagnosis; anti-human immunodeficiency virus; HIV;  
KW antidiabetic; immunostimulant; immunomodulator; antiinflammatory;  
KW antithyroid; immunosuppressive; nephrotropic; antigit; thyromimetic;  
KW cytostatic; antibacterial; fungicide; virucide; hepatotropic; antiarteriosclerotic;  
KW antiatherosclerotic; antipsoriatic; virucide; hepatotropic; gene therapy;  
KW autoimmune combined immunodeficiency disease; AIDS; DiGeorge's syndrome;  
KW Cushing's disease; Addison's disease; autoimmune thyroiditis; gout;  
KW Grave's disease; Hashimoto's thyroiditis; Good pasture's syndrome; infection;  
KW Werner's syndrome; cell proliferative disorder; Sjogren's disease; cancer;  
KW atherosclerosis; cirrhosis; hepatitis; psoriasis.

XX Homo sapiens.  
OS  
XX  
PN WO200110903-A2.  
XX  
PD 15-FEB-2001.  
XX  
PF 09-AUG-2000; 2000WO-US021878.  
XX  
PR 09-AUG-1999; 99US-0147986P.  
PR 21-OCT-1999; 99US-0160807P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yue H, Lal P, Tang YT, Bandman O, Baughn MR, Azimzai Y, Lu DAM;  
PI Yang J;  
XX  
DR WPI; 2001-202760/20.  
DR N-PSDB; AAF81714.  
XX  
PT New protease (inhibitors) useful for diagnosis and treatment of  
PT autoimmune/inflammatory disorders such as acquired immunodeficiency  
PT syndrome, Cushing's disease, Addison's disease and cell proliferative  
PT disorders such as cancer.  
XX  
PS Claim 1; Page 91-92; 134pp; English.

XX AAF81714 to AAF81740 encode the human proteases and protease inhibitors  
CC (PPIMs) given in AAB74668 to AAB74694. The PPIMs can have activities such  
CC as: anti-human immunodeficiency virus (HIV); antidiabetic; antithyroid;  
CC immunostimulant; immunomodulator; antiinflammatory; immunosuppressive;  
CC nephrotropic; antigit; thyromimetic; cytostatic; antibacterial;  
CC fungicide; protozoacide; antiarteriosclerotic; antiatherosclerotic;  
CC virucide; antipsoriatic; and hepatotropic. PPIM polynucleotide and  
CC protein sequences can be used in the diagnosis, treatment and prevention  
CC of autoimmune/inflammatory disorders such as AIDS, DiGeorge's syndrome,  
CC severe combined immunodeficiency disease (SCID), Chediak-Higashi  
CC syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis,  
CC Crohn's disease, diabetes mellitus, Good pasture's syndrome, gout,  
CC Grave's disease, Hashimoto's thyroiditis, Sjogren's syndrome, Werner's  
CC syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic  
CC infections and cell proliferative disorder such as arteriosclerosis,  
CC atherosclerosis, cirrhosis, hepatitis, psoriasis and cancer. PPIM  
CC polynucleotide sequences can be used in somatic or germline gene therapy  
CC and in diagnosis of diseases. They can also be used in generating  
CC hybridisation probes useful in mapping the naturally occurring genomic  
CC sequences and in molecular biology techniques  
XX  
SQ Sequence 444 AA;

Query Match 3.3%; Score 87; DB 4; Length 444;  
Best Local Similarity 18.6%; Pred. No. 92;  
Matches 94; Conservative 79; Mismatches 151; Indels 182; Gaps 27;

QY 12 LLAVLL--LLLRGMFSSPSP--PALLEKVFQYI-----DLHQDFVQTLKEW 56  
Db 8 LLSVLLAQVWLVPGLPSPQSPETPAPQNQTSRVVQAPREEEEDQEASEEKEEAKAW 67  
QY 57 -VAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQLPDGQSLPDPVIL 115  
Db 68 LMASRQQLAKETSNFGFSLLRKISMRHD-----GNMVFS-----PFGMSLAMTGLML 114  
QY 116 AELGSDPTKGTVCIFYGHLVDVQPADRGDWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWIN 175  
Db 115 GATG--PTE-----TQIKRGLHLQALKPTKPGLLP--- 142  
QY 176 AVSAFRALEQDLPVNIKFIIEGMEAGSVALEELVEKE--KDRFFSGVDYIVISDNLWI 232  
Db 143 --SLFKGLRETLNRNLEL---GLSQ-GSFA---FIHKDFDVKETFN-----L 181  
QY 233 SQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILV 292  
Db 182 SKR-----YF--DTECVPMNFRNA-----SQAKRLMNHYYINKETRGI 217  
QY 293 PGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFL--FDT--KEEILMHLWRYPSSL 348  
Db 218 PKLDFEINPET-----KLILVDYILFKG-----KWLTPFDPVFTEVDTFHLDKYKTIK 265  
QY 349 IHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMV 408  
Db 266 VPMMYGA-----GKFA-----STFDKNFRCHVLKLPYQGNATMLVV 301  
QY 409 VSMTLGLH-----PWIANID-----DTQY-----LAAKRAIRTVF 438  
Db 302 LMEKMGDHLALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIIRIF 361  
QY 439 GTEPDMIR---DGSTIPIAKMFQEIIV 461  
Db 362 SPFADLSELSATGRNLQVSRVLQRTV 387

RESULT 930  
AAB10655  
ID AAB10655 standard; protein; 469 AA.  
XX  
AC AAB10655;  
XX  
DT 19-JAN-2001 (first entry)  
XX





Db 188 VAGSRG--YFLKGV-----LVFLEQALIQYALRTLGSRGYIPI 223

QY 293 -----PGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHL----- 341

Db 224 YTPFFMRKEVMOEVAQLSQFDEELYKVIGKSEKSDDNSYDEKYLIATSEQPIAALHRDE 283

QY 342 WRYPs---LSIHGIEGAF-----DEPGTKTVIPGRVIGKFSIRLVPHMNVs--AVE 387

Db 284 WLRPEDLPKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQF-VYSSPHDNKSWEMFE 342

QY 388 KOVTR-----HLEDVFSKRNSSNMVVSMTLGLHPW-----IANIDDT 425

Db 343 EMITTABEFYQSLGIPYHIVNVS---GSLNHAASKKLDLEAWPFGSGAFRELVSCTSNCT 399

QY 426 QYLAAKRAIR 435

Db 400 DYQARRLRIR 409

RESULT 932

ABM04796

ID ABM04796 standard; protein; 514 AA.

XX AC ABM04796;

XX DT 22-SEP-2003 (first entry)

XX DE Human seryl t-RNA synthetase.

XX KW spinal cord; neuropathic pain; central sensitisation pain; pain;

XX KW analgesic; gene therapy.

XX OS Homo sapiens.

XX PN EP1284298-A2.

XX PD 19-FEB-2003.

XX PF 26-JUL-2002; 2002EP-00255229.

XX PR 27-JUL-2001; 2001GB-00018354.

XX PR 07-FEB-2002; 2002GB-00002883.

XX PA (WARN ) WARNER LAMBERT CO.

XX PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX DR WPI; 2003-543489/52.

XX DR N-PSDB; ACF25338.

XX PT Use of an isolated gene sequence in the screening of compounds for

XX PT diagnosing or treating pain.

XX PS Claim 1; Page 71-73; 188pp; English.

XX CC The invention relates to a novel isolated gene sequence that is

XX CC downregulated in the spinal cord of a mammal in response to mechanically

XX CC distinct first and second models of neuropathic or central sensitisation

XX CC pain, useful in the screening of compounds for diagnosing or treating

XX CC pain. A protein encoded by a gene of the invention has analgesic

XX CC activity. A polynucleotide of the invention may have a use in gene

XX CC therapy. The gene sequence is useful for preparing a composition for

XX CC diagnosing or treating pain. The present sequence represents a protein

XX CC encoded by a gene of the invention

SQ Sequence 514 AA;

Query Match 3.3%; Score 87; DB 6; Length 514;

Best Local Similarity 21.6%; Pred. No. 1.2e+02;

Matches 67; Conservative 41; Mismatches 102; Indels 100; Gaps 15;

QY 196 EGMEEAGS-----VALEELVEKEKDRF-----FSGVDYIVISDNLWISQRKPAI 239

Db 130 ENLREIGNLLHPSVPISNDEDDVDNKNVERINGDCCTVRKKYSHVDLVVMVDG--FEGEXGAV 187

QY 240 TYGTRGNSYFMVEVKCRDQDPHSGTGGILHEPMADLVALLGSLVD-----SSGHILV 292

Db 188 VAGSRG--YFLKGV-----LVFLEQALIQYALRTLGSRGYIPI 223

QY 293 -----PGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHL----- 341

Db 224 YTPFFMRKEVMOEVAQLSQFDEELYKVIGKSEKSDDNSYDEKYLIATSEQPIAALHRDE 283

QY 342 WRYPs---LSIHGIEGAF-----DEPGTKTVIPGRVIGKFSIRLVPHMNVs--AVE 387

Db 284 WLRPEDLPKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQF-VYSSPHDNKSWEMFE 342

QY 388 KOVTR-----HLEDVFSKRNSSNMVVSMTLGLHPW-----IANIDDT 425

Db 343 EMITTABEFYQSLGIPYHIVNVS---GSLNHAASKKLDLEAWPFGSGAFRELVSCTSNCT 399

QY 426 QYLAAKRAIR 435

Db 400 DYQARRLRIR 409

RESULT 933

ADF77073

ID ADF77073 standard; protein; 514 AA.

XX AC ADF77073;

XX DT 26-FEB-2004 (first entry)

XX DE Seryl-tRNA synthetase.

XX KW seryl-tRNA synthetase; angiogenesis; cancer; diabetic retinopathy;

XX KW glaucoma; age-related macular degeneration; stroke; infertility;

XX KW heart disease; ulcer; scleroderma; chromosome 1p13.3-p13.1.

XX OS Homo sapiens.

XX PN WO2003094862-A2.

XX PD 20-NOV-2003.

XX PF 13-MAY-2003; 2003WO-US015357.

XX PR 13-MAY-2002; 2002US-0380566P.

XX PA (RIGE-) RIGEL PHARM INC.

XX PI Lorens J, Xu W;

XX DR WPI; 2004-022691/02.

XX DR N-PSDB; ADF77072.

XX DR GENBANK; NP\_006504.

XX PT Identifying compounds that modulate angiogenesis, useful for treating

XX PT e.g. cancer or stroke, comprises contacting the compound with a seryl-

XX PT tRNA synthetase polypeptide and determining the effect of the compound on

XX PT the polypeptide.

XX PS Claim 1; Fig 2; 55pp; English.

XX CC This sequence represents a seryl-tRNA synthetase polypeptide which was

XX CC first cloned from human brain. The seryl-tRNA synthetase polypeptide may

XX CC be used in the method of the invention for identifying a compound that

XX CC modulates angiogenesis. The method comprises contacting the compound with

XX CC a seryl-tRNA synthetase polypeptide, and determining the functional

XX CC effect of the compound upon seryl-tRNA synthetase polypeptide. The method

XX CC is useful in identifying agents that modulate angiogenesis or in

XX CC modulating angiogenesis in a subject for treating pathological states

XX CC such as cancer, diabetic retinopathy, glaucoma, age-related macular

XX CC degeneration, stroke, infertility, heart disease, ulcers or scleroderma.

[illegible]

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention



XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
PI WPI; 2001-639362/73.  
XX N-PSDB; AAS65632.  
DR  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 20; SEQ ID NO 31804; 103pp; English.  
PS  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activities. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 545 AA;

Query Match  
Best Local Similarity 3.3%; Score 87; DB 4; Length 545;  
Matches 95; Conservative 61; Mismatches 167; Indels 198; Gaps 24;

QY 56 WVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQLPDGQSLPIPPVIL 115  
Db 113 WWAVGS---EPCP-----AGRLRLGKELSTAAAGP----- 140

QY 116 AELGSDPTKGTGFCYGHLDVQPADRGDWL-----TDP-----YVLT----- 152  
Db 141 ---GGDDSNNSCCRGR-----DSNLVVFIMKVHLPATSPRAKKIMVITVSGHFSL 188

QY 153 -----EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP--VNIKFIIEGMEEGSVA 205  
Db 189 GSFTKTVIGKESDR-----VNSLSQLKLNLPNTNPRF--TRREEKGEKG 234

QY 206 LEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTF 265  
Db 235 AQERIDSLRRTGVTHEKQTAVSVENFIAELLPDKITNTEKCLKMLKAKARE----- 288

QY 266 GGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSR 325  
Db 289 ---LHEECRSLRRDQL-----EERSVMEDEMN-----EMKREGK 322

QY 326 VEKFLDFTKEEILMHLWRY---PSLSIHGIEGAFDEPGTK--TVIPGRVIGKFSIRLVPH 380  
Db 323 FREKRIKRNEQSLQEIWDYVKRPNRLTGVPESDCGENTKLENTLQDIQENFP-NLARQ 381

QY 381 MNVSAVEKQ-----VTRHLEDVFSKRNSNMKV-----VSMTLG 414  
Db 382 ANIQIQEIQMPORYSSRRATPRHIIIRFTKVEMKEKMLRAAREKGRVTHKGPMLRLTAD 441

QY 415 L-----HPW--IANI-----DDTQYLAAKRAIRTVFGTEPD 443  
Db 442 LSAETLQARREWGPIFNILKEKNFQPRISYPAKLSFVSEGEIKYFTDKQMLRDFVTRPA 501  
QY 444 M-IRDGSTIPIAKMFQEIYVHKSVVLLIPLGAVDDGCHSQNEK 483  
Db 502 LKAAEGST-----KHGKEQLVPAAA-----KSCQNVK 528

RESULT 936  
AAG16038  
ID AAG16038 standard; protein; 571 AA.  
XX  
AC AAG16038;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16524.  
XX  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.



Db 260 DLVSDFLPPSKGELAY-----ALDEVLGFLRNAVGSVFFSTMEDGKIVKGLAGVPDKG 312

QY 169 PVLAWINAVSAFRALEQDL-PVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDY-IVI 226

Db 313 PVL----LVGYHMLMGLELGPMSAFI-----KEKNILFRGMAHPVLY 351

QY 227 SDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGS---- 282

Db 352 SDN----DPAKAFDYG-----DWIKVFGAYPVT 375

QY 283 -----LVDSSGHILV-PGIYDEVVPLTBBEINTYKAHLDLEEVRNSSRVEKFLFDTKE 335

Db 376 ATNLFKLLDSKSHVLLFPG-----GAREALHNRGEQY-----KLIWPEQQ 415

QY 336 EILMHLWRYPSSLHIGIEGAFDEPGTKTVLPGRVIGKFSI-----RLVPHMNVSA 385

Db 416 EFVRMAARF-----GA-----TIVPFGTVGEDDIAELVLDYNDLMKIPILNDYI 459

QY 386 VEQVTRHLEDVFSKRNSSNMVSMITGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMI 445

Db 460 TE--VTRDTKQ-FKLREESEGEVANQPLVPLGPKVPGRFYFLGKPIET--KGRPELV 514

QY 446 RD 447

Db 515 KD 516

RESULT 937

AAG48655

ID AAG48655 standard; protein; 571 AA.

XX

AC AAG48655;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 61465.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EPI033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 02-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 22-JUL-1999; 99US-0145085P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.





PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
PS Claim 5; SEQ ID NO 2049; 261pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 646 AA;  
  
Query Match 3.3%; Score 87; DB 5; Length 646;  
Best Local Similarity 19.0%; Pred. No. 1.6e+02;  
Matches 84; Conservative 68; Mismatches 142; Indels 148; Gaps 22;  
  
QY 28 P S P P P A L L E K V F Q Y I D L H Q D E -----F V Q T L K E W V ----- 57  
Db 263 P A P P P Q A S S T I ---I D Y R D E K S F Q G S N I A I I V P S V I N L I I F V L I F S W K R K Q S H T I I N 319  
  
QY 58 -A I E S D S V Q P V R F R Q E L F R M M A V A A D T L ---Q R L G -A R V A S V D M G P Q Q L P D G Q S L P I P P 112  
Db 320 D V F D S N N G Q S M L R F D ---L R M I V T A T N N F S L E N K L G Q G F G S V Y K G --I L P S G Q E I A V K R 374  
  
QY 113 V I L A E L G S D P T K G T V C F Y G H L D V Q P A D R G D G W L T D P Y V L T E V D G K L Y G R G A T D N K G P V L A 172  
Db 375 L -----R K G S -----G Q G G M E F K N E V L L 392  
  
QY 173 W I N A V S A F R A L E Q D L P V N I K F I I E G M E E A G S V A L E E L V E K E D R F F S G V D Y I V I S D N L W I 232  
Db 393 -----L T R L Q H R N L V K L L G F C N E K D E E ---I L V Y E F V P N -----S S L D H F I F D E ---- 433  
  
QY 233 S O R K P A I T Y T R G N S Y F M V E V K C R D Q D F -H S G T F G G I L H E P M -----A D L 276  
Db 434 -E K R R V L T W D V R ---Y T I I E G V A R G L L Y L H E D S Q L R I I H R D L K A S N I L L D A E M N P K V A D F 489  
  
QY 277 -V A L L G S L V D S S G H I -L V P G I Y D E V V P -----L T E E E I N T Y K A I H L D L E E Y R N S S R V 326  
Db 490 G M A R L F D M D E T R G Q T S R V V G T Y G Y M A P E Y A T Y G Q F S T K S D V Y S F G V M L L E M I S G S N K K L 549  
  
QY 327 E K F L F D T K E E I L M H L W R Y P S L S I H G E A F D E P G T K T V I P G R V T G K F S I R L V P H M N V S A V 386  
Db 550 E K E E E E E E L P A F V W K -----R W I E G R F A E I I D P L A A P S N N I S I N E V M K L I H I G L L C V 603  
  
QY 387 E K Q V T R H L E D V F S K R N S S N K M V 408  
Db 604 Q -----E D I -S K R P S I N S I L 617  
  
RESULT 939  
ADF04165  
ID ADF04165 standard; protein; 663 AA.  
XX  
AC ADF04165;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Bacterial polypeptide #278.  
XX  
KW Proteus mirabilis infection; bacterial infection; antibacterial;  
KW immunostimulant.  
XX  
OS Proteus mirabilis.  
XX  
PN US6605709-B1.  
XX  
PD 12-AUG-2003.

XX 05-APR-2000; 2000US-00543681.  
PF  
XX 09-APR-1999; 99US-0128706P.  
PR  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA  
XX Breton GL;  
XX  
PI WPI; 2003-895291/82.  
XX N-PSDB; ADE99992.  
DR  
DR  
XX New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.  
XX  
XX Disclosure; SEQ ID NO 4450; 870pp; English.  
PS  
XX The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis,  
CC method for evaluating a compound for the ability to bind a P. mirabilis  
CC polypeptide and a method for screening test compounds for anti-bacterial  
CC activity. The polypeptides and polynucleotides are useful as molecular  
CC targets for diagnosing, preventing and treating pathological conditions  
CC resulting from bacterial infection, as reagents for diagnosis of  
CC bacterial diseases, as components of antibacterial vaccines, as targets  
CC for antibacterial drugs or as bio-control agents for plants. This  
CC sequence represents a Proteus mirabilis polypeptide of the invention.  
XX  
SQ Sequence 663 AA;  
  
Query Match 3.3%; Score 87; DB 7; Length 663;  
Best Local Similarity 19.1%; Pred. No. 1.7e+02;  
Matches 92; Conservative 65; Mismatches 144; Indels 180; Gaps 23;  
  
QY 67 V P R F R Q E L F R M M A V A A D T L Q R I G A R V A S V D M G P Q Q L P D G Q S L P I P P V I L A E L G S D P T K G T 126  
Db 10 L P T F R K N M F Q D N P L L A Q L K Q Q L H A -----Q T P R V E G L -----V K G T 45  
  
QY 127 V C F Y G H L D V Q P A D R G D G W L T D P Y V L T E V D G -K L Y G R G A T D N K G P V L A W I N A V S A F R A L E Q 185  
Db 46 -----D K G F G F L -----E V D G Q K S Y -----F I P P P Q M K K V M H G 73  
  
QY 186 D L P V N I K F I I E G M E E A G S V A L E E L V E K E D R F F S G V D Y I V I S D N L W I S O R K P A I ----- 239  
Db 74 D ---R I I A A V H T N N D K E S A E P E E L V E P F L T R F V G R V Q K E G D N R L W I I P D H P L L K D A I P C 130  
  
QY 240 -----T Y G T R G N S Y F M V E V K --C R D Q D F H ----- 261  
Db 131 R P I K S L T H P F A D Q D W A V A E M R R H P L K G D K H F Q A E L T D F T D K D D H F A P W W V T L M R H Q L E R 190  
  
QY 262 -----S G T F G G I L H E --P M A D L V A L L G S L V D S S G H I L V P G I Y D E V V P L T E E E I N T Y K A I 313  
Db 191 N A P E V D S E T L --T L H D D L P R E D I T A L S F V T I D S A S -----T E D ----- 226  
  
QY 314 H L D L E E Y R N S S R V E K F L F D T K E E I L M H L W R Y P S L S I H ---G I E G A F D E P G T K --T V I P G R 368  
Db 227 -----M D D A L Y I R K E E -----N G Q L S L Y I A I A D P T A Y I Q P N S K L D T I A A Q R 267  
  
QY 369 V I G K F S I R L V P H M N V S A V E K Q V T R H L E D V F S K R N S S N K M V V S M T L G L H P W I A N I D D T Q Y L 428  
Db 268 A L T N Y ----L P G F N I P M L P R E L S ---D N L C S L R P N E K R P A L V C Q V G I M E D G A L T D E I H F Y 320  
  
QY 429 A A --K R A I R T V F G T E P D M I R D G S T I P I A K M F Q E I V H K S V V L I P L G A V D D G E H S Q N E K I N R 486  
Db 321 S A W V E S K A K L V Y D N I S D W L -E G E E T P W A P E -N E I V H E Q V M L L -----K E M S E K R H I 369  
  
QY 487 W 487  
Db 370 W 370

RESULT 940  
AAG48654  
ID AAG48654 standard; protein; 704 AA.  
XX  
AC AAG48654;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61464.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
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PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
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PR 25-FEB-1999; 99US-0121825P.  
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PR	23-AUG-1999;	99US-0149902P.						
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PR	25-AUG-1999;	99US-0150566P.						
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PR	27-AUG-1999;	99US-0151080P.						
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PR	01-SEP-1999;	99US-0151930P.	Db	593	TE--VTRDTKQ-FKLRESEGEVANQPLYLPGLIPKVPGRFYFLFGKPIET--	KGRPELV	647	
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PR	10-SEP-1999;	99US-0153070P.	Qy	446	RD	447		
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Query Match								
Best Local Similarity 3.3%; Score 87; DB 3; Length 704;								
Matches 75; Conservative 47; Mismatches 104; Indels 136; Gaps 20;								
Qy	117	ELGSD---PTKGTVCFYGHLDVQPADRGDGLTDP----	YVLTEVDGKLY-GRGATDNKG	168				
Db	393	DLVSDFLPPSKGELAY-----	ALDEVLGFLRNAVGSVFFSTMEDGKIVKGLAGVPDKG	445				
Qy	169	PVLAWINAVSAFRALEQDL-PVNIKFIIEGMEERAGSVALEELVEKEKDRFFSGVDY-IVI	226					
Db	446	PVL----LVGYHMLMGLGLGPMSEAFI-----	KEKNILFRGMAHPVLY	484				
Qy	227	SDNLWISQRKPAITYGTRGNSYFMVVEVKCRDQDFHSGTFGGILHEPMADLVALLGS----	282					

protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

Arabidopsis thaliana.

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PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.  
Query Match 3.3%; Score 87; DB 3; Length 704;  
Best Local Similarity 20.7%; Pred. No. 1.9e+02;  
Matches 75; Conservative 47; Mismatches 104; Indels 136; Gaps 20;  
QY 117 ELGSD---PRKGTVCFYGHLDVQPADRGDWLTDP---YVLTEVDGKLY-GRGATDNKG 168  
Db DLVSDFLPPSKGELAY-----ALDEVLGFLRNAVGSVFFSTMEDGKIVKGLAGVPDKG 445  
QY 169 PVLAWINAVSAFRALEQDL-PVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDY-IVI 226  
Db PVL-----LVGYHMLMGLGLGPMSEAFI-----KEKNILFRGMAHPVLY 484  
QY 227 SDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALLSG---- 282  
Db SDN-----DPAKAFDYG-----DWIKVFGAYPVT 508  
QY 283 -----LVDSSGHILV-PGIYDEVVPLTETEEINTYKAHLDLEEYRNSSRVEKFLFDTK 335  
Db ATNLFKLLDSKSHVLLFPG-----GAREALHNRGEQY-----KLIWPEQQ 548  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSI-----RLVPHMNVSA 385  
Db EFVRMAARF-----GA-----TIVPFGTVGEDDIAELVLDYNDLMKIPILNDYI 592  
QY 386 VEKQVTRHLEDVFSKRNSNMVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMI 445  
Db TE--VTRDTKQ-FKLREESEGEVANQPLYLPGLPKVPGRFFYLFGKPIET--KGRPELV 647  
QY 446 RD 447  
Db 648 KD 649  
RESULT 942  
ADS08232  
ID ADS08232 standard; protein; 705 AA.  
XX  
AC ADS08232;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Staphylococcus epidermis polypeptide seqid 7527.  
XX  
KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
KW recombinant expression vector; infection; computer readable medium;  
KW computer based system.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN US2004147734-A1.  
XX  
PD 29-JUL-2004.  
XX  
PF 01-DEC-2003; 2003US-00724972.  
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PR 08-NOV-1997; 97US-0064964P.  
PR 13-AUG-1998; 98US-00134001.  
PR 29-NOV-1999; 99US-00450969.  
XX  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
XX  
XX Doucette-Stamm L, Bush D;  
PI  
XX  
DR WPI; 2004-580138/56.  
DR N-PSDB; ADS04460.  
XX  
XX New isolated polypeptide and encoding nucleic acid derived from  
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
PT treating an S. epidermidis bacterial infection.

XX Claim 17; SEQ ID NO 7527; 741pp; English.  
PS  
XX  
CC The invention describes an isolated nucleic acid comprising a nucleotide  
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
CC given in the specification. Also described are: a recombinant expression  
CC vector; a cell comprising a recombinant expression vector of (1);  
CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection, comprising a nucleic acid cited above and a carrier; treating  
CC a subject for S. epidermidis infection; a recombinant or substantially  
CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
CC sample; a computer readable medium having recorded in it the nucleotide  
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
CC system for identifying fragments of the Staphylococcus genome of  
CC commercial importance; a computer based system for identifying fragments  
CC of the Staphylococcus plasmids of commercial importance; identifying  
CC commercially important nucleic acid fragments of the Staphylococcus  
CC genome and/or plasmids; and identifying an expression modulating fragment  
CC of the Staphylococcus genome and/or plasmids. The methods and  
CC compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of an Staphylococcal epidermidis bacterial  
CC infection. This is the amino acid sequence of a S. epidermis protein of  
CC the invention.  
XX  
SQ Sequence 705 AA;  
Query Match 3.3%; Score 87; DB 8; Length 705;  
Best Local Similarity 20.8%; Pred. No. 1.9e+02;  
Matches 71; Conservative 47; Mismatches 128; Indels 96; Gaps 15;  
QY 157 KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIK-----FIIEG----MEEA 201  
Db 230 KFYKVSATINKD-----EQEVKTELKNKFPDSEDELHEFLFENDITDLTQK 274  
QY 202 GSVA-----LEELVEKEKDRF-FSGVDYIVISDNLWISQRKPAITYGTR 244  
Db GLVTDIEKEIGYTMPPKFYDLSALQEDMNDKYKISAKRTLEIAQTLY--EKKLITYPRT 331  
QY 245 GNSYFMVEVK---CRDQDFHSGTGGILHEPMDLVALLSGLVDSSGHILVPGIYDEVVP 301  
Db DSRYTEDEKEMLLENIDYLKEITKINLNNELTNNSLINPSKIEDHYAILITGNDFNKVD 391  
QY 302 LTEEEINTYKAI-----HLDLEEYRNSS---RVEKFLFDTKKEEILMHLWRYPSLSIHG 351  
Db LKEEEINVYKSILQNVAAMFMMDKEQYETTITIEIAVKKLMFEVKGKII----- 438  
QY 352 IEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLE-DVFSKRNSNMVVS 410  
Db -----QDNGFKALLNKQ---KTSEETIPNF-----EKNEEVDIELDLLEKETTPPKRYTE 485  
QY 411 MTGLGHPWIANIDDTQYLAAKRAIRTVFG-----TEPDMIRD 447  
Db KTL-LKAMANPIETLEDEGLSKTLKEVKGGLGTPATRADIIEN 526  
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ID AAG16036 standard; protein; 726 AA.  
XX  
AC AAG16036;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16522.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;



KW termination sequence.  
XX Arabidopsis thaliana.  
OS  
XX  
PN EP10333405-A2.  
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PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-00301439.  
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PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match

Best local Similarity 3.3%; Score 87; DB 3; Length 726;

Mismatches 75; Conservative 47; Mismatches 104; Indels 136; Gaps 20;

QY	117	ELGSD---	PTKGVCFYGHLDVQPADRGDWLTDP----	YVLTEVDGKLY-GRGATDNKG	168
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QY	169	PVLAWINAVSAFRALEQDL-PVNIKFII	EGNEEAGSVALEELVEKEKDRFFSGVDY-IVI	226	
Db	468	PVL-----	LVGYHMLMGLLELGPMSFAFI-----	KEKNILFRGMAHPVLY	506
QY	227	SDNLWISQRKPAITYGTRGNSYFMVEV	KCRDQDFHSGTGGILHEPNMADLVALLGS----	282	
Db	507	SDN-----	DPAKAFDYG-----	DWIKVFGAYPVT	530
QY	283	-----	LVDSSGHILV-PGIYDEVVPLTEEEINTYKA	IHLDLLEYRNSRVEKFLFDTKE	335
Db	531	ATNLFKLLDSKSHVLLFPG-----	GAREALHNRGEQY-----	KLIWPEQQ	570
QY	336	EILMHLWRYPSPLSIHGIEGAFDEPGTKT	VIPIGRVIGKFSI-----	RLVPHMNVSA	385
Db	571	EFVRMAARF-----	GA-----	TIVPFGTVGEDDIAELVLDYNDLMKIPILNDYI	614
QY	386	VEKQVTRHLEDVFSKRNSSNMVSMITGL	HPWIANIDDTQYLAAKRAIRTVFGTEPDMI	445	
Db	615	TE--VTRDTKQ-FKLRESEGEVANQPL	PLPGLIPKVPGRFYFLFGKPIET--KGRPELV	669	

QY	446	RD 447
Db	:	!
	670	KD 671
RESULT 944		
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ID	AAG48653 standard; protein; 726 AA.	
XX	AC AAG48653;	
XX	DT 18-OCT-2000 (first entry)	
XX	DE Arabidopsis thaliana protein fragment SBQ ID NO: 61463.	
XX	KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
XX	OS Arabidopsis thaliana.	
XX	PN EP1033405-A2.	
XX	PD 06-SEP-2000.	
XX	PF 25-FEB-2000; 2000EP-00301439.	
PR	25-FEB-1999;	99US-0121825P.
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PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.
PR	16-JUN-1999;	99US-0139453P.
PR	17-JUN-1999;	99US-0139492P.









PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.

PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-016192P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 3.3%; Score 87; DB 3; Length 856;  
Best Local Similarity 20.2%; Pred. No. 2.5e+02;  
Matches 67; Conservative 61; Mismatches 150; Indels 54; Gaps 15;



Db 119 VVKELSKCDVVVTESLVQLVRRFSGWNQ-AYGFFIWANSQTGYVHSGHTYNAMVDVLG 177  
QY 254 KCRDQDFHSGTGGILHBPMDLVALGSLVDSSGHIL----VPGIYDEVVPLTEEEINT 309  
Db 178 KCRNFDLMWELVNEMNKNEESKLVTL----DTMSKVRRRLAKSGKYNKAVDAFLEMEKS 232  
QY 310 YKAJHLDLEEYRN--SSRVEKFLFDTKEEILMLHW-----RYPSLSIHGIEGA--FDE 358  
Db 233 Y-GVKTDTIAMNSLMDALVKENSIEHAHEVFLKFLDTIKPDARTFNILIHGFCARKFDD 291  
QY 359 PGTKTVIPGRVIGKFSIRLVPHMNVSAVE-----KQVTRHLEDVFSKRNSSNKMVVS 410  
Db 292 --ARAMDLMKVTEFTPDVVTY--TSFVEAYCKEGDFFRRVNEMLEEM--RENGCNPNVVT 345  
QY 411 MTLGLHPWIANIDDTQVLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPL 470  
Db 346 YTIVMHS-----LGKSKQVAEALGVYERKMKEKG-CVPDAKFYSSLIH---ILSKT 391  
QY 471 GAVDDG---EHSQNEKINRWNYIEGTKLFAA 498  
Db 392 GRFKDAAEIFEDMTNQVRRDVLVYNTMISAA 423

RESULT 948  
AAU37030  
ID AAU37030 standard; protein; 876 AA.  
XX  
AC AAU37030;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Staphylococcus aureus cellular proliferation protein #1200.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US009180.  
XX  
PR 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS54889.  
XX  
PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 12623; 511pp; English.  
XX

CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 876 AA;

Query Match 3.3%; Score 87; DB 4; Length 876;  
Best Local Similarity 18.4%; Pred. No. 2.6e+02;  
Matches 98; Conservative 62; Mismatches 146; Indels 228; Gaps 26;  
QY 31 PPALLEKVFQYI-----DLHQDEFVQTLKEWVAIESDSVQVPRFRQELF 75  
Db 80 PPELSEQ-FPYIRQLLDAYHIKRYELDNYEADDIIGTLSK---EADKAG-----F 125  
QY 76 RMMVAAD-----TLQRLGARVASVD-----MGPOQLPDGQSL--- 108  
Db 126 QTIITGDRDLTQLATDNVTIYYTKGVTDVDHYTPDFAEKYNGLTPNQIIDMKGLMGD 185  
QY 109 ---PIPPVILABELGS-----DPTKGTVCFYGHLDVQPADRGDWLTDPVVLTEVD 155  
Db 186 TSDNIPGV--AGVEKTAIKLLNQFDTEGV---YEHLD-----EIS 222  
QY 156 GKLYGRGATDNK-----GPVLAWINAVSAFRA-LEQDL-----PVNIKFI 194  
Db 223 GKLLKEKLQNSKEDALMSKELATINVDSPIEVKLEDTLMTHQDEQQEKIEFKLEFKQL 282  
QY 195 IEGMEEAGSVALEELVEK--EKDRFFSGVDYIVIVISDNLWISQRKPAITYGTRGNSYFMVE 252  
Db 283 LADIDQSASV--EDAIEKTFEIETSFNDVDF-----TSLKEAVIHFEIDGGNYLRNN 332  
QY 253 VKCRDQDFHSGTGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA 312  
Db 333 I-----LKFSLFTGEKHIVI-----NADDINNY-- 355  
QY 313 IHLDLLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIG- 371  
Db 356 --AELVSWLENPNTKKVVDK-----KTVVASHRLGI 386  
QY 372 ----KFSIRLV-----PHMNVSAVEKQVTRH---LEDVFSKRNSSNKMVVSMTLGLHP 417  
Db 387 DIQNISFDIMLASYIIDPSRTISDVQSVSLYQSFVKDDVSIYGKKGKVPDDVLIPL 446  
QY 418 WIANIDDTQYLAAKRAIRTVFGTEPDMIRD-----GSTIPIAKMFQEI 460  
Db 447 YVASITDAIYFA-----XPNMDKQLEEYNQVELLADLELPLAKILSEM 489

RESULT 949  
AAW84011  
ID AAW84011 standard; protein; 893 AA.  
XX  
AC AAW84011;  
XX  
DT 08-FEB-1999 (first entry)  
XX  
DE The DNA polymerase mutant D137A, D323A, R722N.  
XX  
KW Tne; O-helix; DNA polymerase; polymorphic; amplicon; thermostable;  
KW mutant; forensic; paternity testing; nucleic acid amplification; cancer;  
KW pathogen; genetic disease; cystic fibrosis; haemophilia; transplanting;  
KW Alzheimer's disease; screening; organ; diagnosis; plant breeding.  
XX  
OS Thermotoga neapolitana.  
OS Synthetic.  
XX

[illegible]





Db 379 LS-----PTFTQQQLRNFGFPDQLAMDRFEVDGKLRDFVVAARELDPNALQQNQDWI 433  
Qy 166 NKGPVLAWINAVSAFRALEQD-----LPV-NIKFIIEGMEEAGSVALEEL-VE 211  
Db 434 NRHTVYTHGNGFIAAQANQVDEAVDVGSTRGGYPVYTVSDLQSNARAAESEDAEELGIK 493  
Qy 212 KEKDRFF-----SGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDPS 262  
Db 494 VDEPRVYGPLIASATDGADYAIVGDT-----GDGPVEYDITDSSY-----TYE 537  
Qy 263 GTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTBEIEINTYKAIHLDLEEYRN 322  
Db 538 GA-GGV-----DIGNMVNRAFAL---RYQEMNMLLSDRVGSSEKI---LFERDP 580  
Qy 323 SSRVEK-----FLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGR----VIGKES 374  
Db 581 RSRVEKVPWLTTDSK-----TYP-----TVIDGRIKWIVDGYTT 615  
Qy 375 IRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNMVMSM--TLGLHP 417  
Db 616 LDSPY-----STRTSLTEATQDAVMPDGTGPQLITDRVGYTRNSVKAADVAYDGTVELYE 671  
Qy 418 WIANIDTQYLAAKRAIRTVFGTEPDMIRDGSTI 451  
Db 672 F-----DTEDPVLK-AWRGVF---PDTVKDGSEI 696

RESULT 952  
ABU14646  
ID ABU14646 standard; protein; 989 AA.  
XX ABU14646;  
XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #173.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Enterococcus faecalis.

OS WO200277183-A2.  
PN 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA18516.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 42570; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 989 AA;

Query Match 3.3%; Score 87; DB 6; Length 989;  
Best Local Similarity 21.5%; Pred. No. 3.2e+02;  
Matches 69; Conservative 38; Mismatches 90; Indels 124; Gaps 17;  
Qy 167 KGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVI 226  
Db 370 KGPA-----KKIALDAEGNWSKAAQGFVRGGVTTEDIVFKE----LNGVEYVY- 414  
Qy 227 SDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILH-----EPMADLV 277  
Db 415 -----VTKFTKGSQSAKEVLTCLNDV-ITSLTFPVTMHWANYDFEYIRPIHWIV 461  
Qy 278 ALLGSLVDSSGHILVPGIYDEVVP-----LTEEINTYKAIHLD 316  
Db 462 ALLD-----DEVIPFKVLDVTTGQTSRGHRFLGDDVTFOHANEYEAKLUKE 506  
Qy 317 -----LEEYRNSSRVEK-FLFDTKEEIL---MHLWRYPSLSIHGIEGAFDEP 359  
Db 507 QFVVVQPNRKQMIVDQANALAAEKNQALALDEELLEVTNLVEYPTAFV---GSFDEK 562  
Qy 360 GFKTVIPGRVI-----GKFSIR-----LVPHMNVSAVEKQVTRHLEDVFSKRNSNK 406  
Db 563 YLS--VPDEVLTSMKEHQRYFDVRNDQGLLMPHF--IAVRNGDNVHLENI-----KGNE 614  
Qy 407 MVVSMTLGLHPWIANIDDTQY 427  
Db 615 KVL-----IARLEDAEF 626

RESULT 953  
ABU43694  
ID ABU43694 standard; protein; 1069 AA.  
XX  
AC ABU43694;  
XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #29221.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Staphylococcus haemolyticus.  
PN WO200277183-A2.



CC coli SANK 70599 (FERM BP-6707) which contains a plasmid encoding mouse  
CC apoptosis- associated protein. The mouse apoptosis-associated protein and  
CC DNA encoding it may be used to screen potential apoptosis inhibitors and  
CC promoters of apoptosis induction. The compounds thus identified can be  
CC used in the treatment of diseases associated with abnormal Fas-mediated  
CC apoptosis. The present sequence represents mouse apoptosis-associated  
CC protein  
XX  
SQ Sequence 1107 AA;

Query Match 3.3%; Score 87; DB 3; Length 1107;  
Best Local Similarity 22.0%; Pred. No. 3.8e+02;  
Matches 93; Conservative 56; Mismatches 146; Indels 128; Gaps 24;

QY 158 LYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGM--EEAGSVALEELVEKEKD 215  
Db 445 LQGSLLDTSGETKA-----EWELKTPEKQLLESLSKCESAPACATEELVSE--- 490

QY 216 RFFSGVDYI--VISDNLW---ISQKPAITYGTR-----GNSYFMVEVKC---RDQ 258  
Db 491 ---GASLCPKVISDDNWSLLSSEKGPSLSSGLSPVHPDVLDCMFEVSSNTALGKDN 546

QY 259 DFHS----GTFGGILHEPMADLVAL-LGSLVDSSGHI--LVPGIYDEVWP----- 301  
Db 547 VYSSEKSKPCISSILLEDLA--VSLTVSPPLKSDGHLFLKPEVLSTSTPEEVISAHFSE 604

QY 302 --LTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGI--EGAFD 357  
Db 605 DALLEEDASEQDIHLALESNDSSSKSSCSW--TSRSVASGFQYHPNLPMAVIMEKSD 663

QY 358 E-----PGTKTVIPGRVIGKFSIRLVPHMNVSA----- 385  
Db 664 HFIVKIRRAPSTSPGLKHGVVAEESLTSPLRTGKEAGVATEKEPNLFQSTVLKPVKDLE 723

QY 386 -----VEKQVTRHLE-----DVFS-KRNSSNM-----VVSMTLGLHP-WIANI- 422  
Db 724 NTDKNIDKSKLTHEEQNSIVQTPVDIYEFCLKDASNKVHVCHDQVVDVDCFKLHQVWEPKVS 783

QY 423 DDTQYLAAKRAI-----RTVFGTEPDMIRDGSTIPIAKMFQEIYVHKS VWLIPLGAVDDGE 477  
Db 784 ENLQELPSMEKIPHSLDNHLDPDTHIDLTKDSAT--ETKSLGELMEVTVL-----NVDHLE 836

QY 478 HSQ 480  
Db 837 CSQ 839

RESULT 955  
ADBE70296  
ID ADB70296 standard; protein; 1114 AA.  
XX  
AC ADB70296;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE C. neoformans amino acid sequence SEQ ID NO:3340.  
XX  
KW fungicide; gene therapy; infection.

OS Cryptococcus neoformans.  
XX  
PN WO2003052076-A2.

XX 26-JUN-2003.  
XX  
XX 17-DEC-2002; 2002WO-US040225.  
PF  
XX 17-DEC-2001; 2001US-0341261P.  
PR

XX (ELIT-) ELITRA PHARM INC.  
XX  
XX Zamudio C, Eroshkin AM;

DR WPI; 2003-533017/50.  
DR N-PSDB; ADB69213.  
XX  
PT New nucleic acid, useful for preparing a composition for treating an  
infection caused by Cryptococcus neoformans.  
XX  
PS Claim 9; SEQ ID NO 3340; 136pp; English.

XX  
CC The invention relates to a novel purified or isolated Cryptococcus  
CC neoformans nucleic acid molecule comprising a sequence encoding a  
CC polypeptide comprising a sequence not given in the specification. A  
CC polynucleotide of the invention has fungicide activity, and may have a  
CC use in gene therapy. The nucleic acid is useful for preparing a  
CC composition for treating an infection caused by Cryptococcus neoformans.  
CC The present sequence represents a C. neoformans sequence of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 1114 AA;

Query Match 3.3%; Score 87; DB 7; Length 1114;  
Best Local Similarity 19.9%; Pred. No. 3.8e+02;  
Matches 93; Conservative 64; Mismatches 125; Indels 186; Gaps 25;

QY 6 GRMAASLLAVLLLLLERGMFSSPPPPALL-----EKVQYIDLHQDEFVQTLKEWVA 58  
Db 154 GQAAVTLIAELIKTSDRNL-----ALLGRSLDAQKFF-----HDVTYDHLRLR---- 196

QY 59 IESDSVQVPVPRFRQELFRMMAVAADT-----LQRLGARVASVDMG----- 98  
Db 197 ---DNPKEVYRFKD---RLAAPFTDTNGNGESPVSSEGLTRNGSGASSTAMGLGGGLKAL 250

QY 99 -----POQLPDGQSLPIPPVILAEELGSDP 122  
Db 251 TAARPADSSSMHTESTPVSMTPSRSSTMPFLDSDSPGLDSEDTLPGVFTLLTDCYSP 310

QY 123 T--KGTVCF-----YGHLDVQPADRGDGLTDPVLTVEVDGKLYGRGATDNKGPV 170  
Db 311 TCSRDSLCSINCPRRLEQMKNLMKP-----EP-----GLNRKLSRESLVDVKETG 357

QY 171 LAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNL 230  
Db 358 TLMWHSVQ-----EILDSVDDKEKKRQEAINEVIYTERD-FVRDLEYLRDS--- 403

QY 231 WISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMADLVALGSLVDSSGHI 290  
Db 404 WV---KPLRTQE-----VIDAKRRD-DFVRQVFWNV-HD-----VLSVNVHV 439

QY 291 L-----VPGIYDEVVPLTEEEINTYKAHIL-----DLEEYRNSRV-EKF 329  
Db 440 LAERLTQRQKEPWSRIGDIFLERVPLFEPFV-TYGAHQLFGKYEFEKEKGANPVQKF 498

QY 330 LFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRL 377  
Db 499 VDDTE-----RKPESRKLELNGYLTKPTTR-----LGRYPPLL 531

RESULT 956  
AAAY71384  
ID AAAY71384 standard; protein; 1163 AA.

XX  
AC AAAY71384;  
XX  
XX 02-NOV-2000 (first entry)

XX Alternative version of rat neurite growth inhibitor Nogo A.

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;



KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
XX structural plasticity; screening.  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT Inhibitory-site 1. .171  
FT /note= "Inhibits NIH 3T3 fibroblast spreading"  
FT Modified-site 30  
FT /note= "Casein kinase II site"  
FT Region 31. .58  
FT /note= "Acidic region"  
FT Region 172. .259  
FT /note= "This region is not essential for inhibitory  
FT activity"  
FT Misc-difference 223  
FT /label= Unknown  
FT /note= "There is Leu at this position in the sequence  
FT shown in AAY71310"  
FT Modified-site 233  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 242. .244  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 291  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 295  
FT /note= "Protein kinase C (PKC) site"  
FT Misc-difference 404  
FT /note= "There is Ile at this position in the sequence  
FT shown in AAY71310"  
FT Modified-site 436  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 468. .470  
FT /note= "Asn is N-glycosylated"  
FT Misc-difference 469  
FT /label= Unknown  
FT /note= "There is Lys at this position in the sequence  
FT shown in AAY71310"  
FT Modified-site 484  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 488  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 502  
FT /note= "Casein kinase II site"  
FT Inhibitory-site 542. .722  
FT Modified-site 576  
FT /note= "Casein kinase II site"  
FT Peptide 623. .640  
FT /note= "used as immunogen to generate antibody AS 472"  
FT Modified-site 626  
FT /note= "Protein kinase C (PKC) site"  
FT Misc-difference 661  
FT /note= "There is Asn at this position in the sequence  
FT shown in AAY71310"  
FT Modified-site 694. .696  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 715  
FT /note= "Casein kinase II site"  
FT Peptide 762. .1163  
FT /note= "used as immunogen to generate antibody AS Bruna"  
FT Modified-site 784  
FT /note= "Protein kinase C (PKC) site"  
FT Misc-difference 820  
FT /note= "There is Leu at this position in the sequence  
FT shown in AAY71310"  
FT Modified-site 821  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 850  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 855  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 863  
FT /note= "Casein kinase II site"

FT Modified-site 868  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 893  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 912. .914  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 925. .927  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 954  
FT /note= "PKC and casein kinase II sites"  
FT Modified-site 956  
FT /note= "PKC and casein kinase II sites"  
FT Region 975. .1162  
FT /note= "This region is not essential for inhibitory  
FT activity"  
FT Region 976. .1163  
FT /note= "C-terminal common region found in Nogo A, B and C  
FT isoforms"  
FT Domain 988. .1023  
FT /label= Transmembrane domain  
FT /note= "C-terminal hydrophobic region"  
FT Modified-site 1024  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 1071. .1073  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 1073  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 1089  
FT /note= "Protein kinase C (PKC) site"  
FT Domain 1090. .1125  
FT /label= Transmembrane domain  
FT /note= "C-terminal hydrophobic region"  
FT Modified-site 1141. .1143  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 1143  
FT /note= "Protein kinase C (PKC) site"  
FT XX  
PN WO200031235-A2.  
XX  
PD 02-JUN-2000.  
XX  
XX  
PF 05-NOV-1999; 99WO-US026160.  
XX  
PR 06-NOV-1998; 98US-0107446P.  
XX  
PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX WPI; 2000-400052/34.  
DR  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Claim 3; Fig 13; 122pp; English.  
XX  
CC The present sequence is an alternative version of rat Nogo A protein  
CC which is a potent neural cell growth inhibitor and is free of all central  
CC nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for

CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. Note: The present  
CC sequence is an alternative version of the Nogo A sequence shown in Fig.  
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ  
CC ID NO: 29 in disclosure of the specification. However the specification  
CC does not include sequences for these SEQ ID numbers

XX  
SQ Sequence 1163 AA;

Query Match	3.3%;	Score 87;	DB 3;	Length 1163;
Best Local Similarity	20.1%;	Pred. No.	4.1e+02;	
Matches 107;	Conservative	61;	Mismatches 146;	Indels 218; Gaps 29;

QY	26	SSPSPPALLEKVFQYI-----DLHQDEFVQTLKEWVAIE-----	60
Db	16	SPRPPPAF---KYQFVTEPEDEDEDEDEDEDEDELEVLERKPAAGLSAAAVPP	72
QY	61	-----SDSVQPVR-----FRQELF-RMMAVAADTLQRLGARVASVDMG	98
Db	73	AAAPLLDFSSDSVPPAPRGLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVL-----	126
QY	99	PQQLPDGQSLPI-----PPV---ILAEIGSDPTKGTVCFCYGHLDVQPADRGDWL-----	145
Db	127	PSKLPEDDEPPARPPPPAGASPLAEPAPPS-----TPAAPKRRGSGSVDETLEF	177
QY	146	-----TDPYV-----LTEVDGKLYGRGATD-----NKGVLAWINAVSAFRA	182
Db	178	ALPAASEPVISSAEKIMDLMEQFCNTVSSGOEDFPSVLLETAASXPSPLSPLSTVS-FK-	235
QY	183	LEQDLPVNIKFI--IEG-MEEAGSVALEELVEKEKDRF-----PSGVYIVISDNLWI	232
Db	236	-EHGYLGNLSAVSSSEGTIEELNEASKELPERATNPFVNRDLAEFSLEY-----	285
QY	233	SQRKPAITYGTRGNSYFMV-----EVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSS	287
Db	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQE-----SPVGKE	338
QY	288	GHLVLP-----GIYDE-----VVPLTEEEINTYKAIHLDLEEYRNSRRVEKFLPDTKEEIL	338
Db	339	DRVVSPEKTMDFNEMQMSVAVPVREE-----YADFKPFEQAWEVK-----DTYE---	383
QY	339	MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRH-LEDV	397
Db	384	-----GSRDVLAA-----ANVESKVDKCKLEDS	407
QY	398	FSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGS	449
Db	408	LEOK-----SLGKDSSEGRNEDAS-----FPSTPEPVKDSS	437

RESULT 957  
ABR52763  
ID ABR52763 standard: protein: 1224 AA.

20-JUN-2003 (first entry)

Protein sequence #SEQ ID 391.

Multi-protein complex: eukaryote: drug target; diagnosis.

*Saccharomyces cerevisiae*.

EP1258494-A1.

20-NOV-2002.

20-DEC-2001;

15-MAY-2001: 2001EP-00111774.

(CELL-) CELLZOME AG.

XX

Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;  
Marzioch M, Schultz JD, Superti-Furga GD;

WPT: 2003-250078/25.

WFI; 2003-230078/  
N-PSDB; ACC60805.

XX New isolated protein complexes useful for diagnosing a disease or  
PT disorder, or as a target for an active agent of a pharmaceutical,  
PT preferably a drug target in the treatment or prevention of diseases  
PT disorder.

Disclosure: SEQ ID NO 391: 17pp + Sequence Listing; English.

The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records of the invention and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM

Sequence 1224 AA;

Query Match 3.3%; Score 87; DB 6; Length 1224;  
Best Local Similarity 20.1%; Pred. No. 4.4e+02;  
Matches 79; Conservative 54; Mismatches 123; Indels 1

QY	147	DPYVLTEVDGKLYGRGATDNKGPVLA---	WINAVSAFRALEQDLPVNIKFIIEGMEEAGS	203
Db	14	DPY-----GFEDESAPITAEDSWA-VISAF	-----FREKG-	42
QY	204	VALEELVEKEKDRFFSGVDY-----	IVISDNLWISQ-----RKPAITYGTRGN	246
Db	43	-----LVSQQLDSFNQFVDYTLQDIICEDSTLILEQLAQHTTESDNISRKYEISFG	-----	93
QY	247	SYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE	306	
Db	94	KIYVTKPMVNESD-----GVTH-ALYPQEARLRNLTYSS-----	GLFVDVKKRTYEA	139
QY	307	INT-----YKAIHLDLEEYRNSRV-----	EKFLFDTKEEILMHLWRYPSSL	348
Db	140	IDVPGRELKYEILABESEDSDSESGKVFIGRLPIMLRSKNCYLSEATEDSLYKLKECP---	196	
QY	349	IHGIEGAFDEPGTKTVI-----	PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRN	402
Db	197	-FDMGGYFIINGSEKVLIAQERSAGNIVQVFK-----	KAAPSPIS-HVAEIRSALE	245
QY	403	SSNMVYSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVH	462	
Db	246	KGRFRTSTLQVKL-----	YGRESARTIKATLPYIKQD---IPIVIIFR---	287
QY	463	KSVVLIPLGAVDDGEHSON--	EKINRWNVIEGTK	494
Db	288	-----ALGLIPDGEILEIHICYDVNDQWMLMLK	315	

RESULT 958

ADK62094

ADK62094 standard; protein; 1224 AA.

ADK62094:

06-MAY-2004 (first entry)

Disease treating protein complex-derived protein #173.  
protein complex; drug target; diagnosis.

protein complex; drug target; diagnosis.

XX OS Unidentified.

XX PN EP1338608-A2.

XX PD 27-AUG-2003.

XX PF 20-DEC-2002; 2002EP-00102902.

XX PR 20-DEC-2001; 2001EP-00130253.

XX PA (CELL-) CELLZOME AG.

PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;

PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;

PI Michon A, Leutwein C, Rick J;

XX WPI; 2003-638460/61.

DR N-PSDB; ADK62095.

XX New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.

XX Disclosure; SEQ ID NO 345; 13pp; English.

XX The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).

XX SQ Sequence 1224 AA;

Query Match 3.3%; Score 87; DB 7; Length 1224;

Best Local Similarity 20.1%; Pred. No. 4.4e+02;

Matches 79; Conservative 54; Mismatches 123; Indels 138; Gaps 21;

QY 147 DPYLTVEVDGKLYGRGATDNKGPVLA---WNAVSAFRALEQDLPVNIKFIIEGMEEAGS 203

Db 14 DPY-----GFEDESAPITAEDSWA-VISAF-----FREKG- 42

QY 204 VALEELVEKEKORFFSGVDY----IVISDNLWISQ-----RKPAITYGTRGN 246

Db 43 -----LVSQQLDSFNQFVDYTLQDIICEDSTLILEQLAHTTESDNISRKVEISFG---- 93

QY 247 SYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306

Db 94 KIYVTKPMVNESD-----GVTH-ALYPQEARLNLTYSS-----GLEVDVKKRTYEA 139

QY 307 INT-----YKAHLDLDEYRNSRV-----EKFLDFTKKEILMHLWRYP SLS 348

Db 140 IDVPGRELKYELIAEESDDSESGKVFIGRLPIMLRSKNCYLSEATESDLYKLKECP--- 196

QY 349 IHGIEGAFDEPGTKTVI-----PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRN 402

Db 197 -FDMGGYFIINGSEKVLIAQERSAGNIVQVFK-----KAAPSPIS-HVAEIRSALE 245

QY 403 SSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI V H 462

Db 246 KGSRFISTLQVKL-----YGRESSARTIKATLPYIKQD---IPIVIIFR----- 287

QY 463 KSVVLIPLGAVDDGEHSQN--EKINRWNYIEGTK 494

Db 288 -----ALGIIPDGEILEHICYDVNDWQWLEMLK 315

RESULT 959

ADS43949

ID ADS43949 standard; protein; 1224 AA.

XX ADS43949;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #22379.

XX Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 22379; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the













Db 407 D-----IVRRQLLTIF-----REG-----KDGQQDVVDVAILQALLKASRSQDHFGHEN 450

QY 484 INR-----WNYIE 491

Db 451 WDHLKLAVANRVD 465

RESULT 966

AAB29694

ID AAB29694 standard; protein; 1962 AA.

XX

AC AAB29694;

XX

DT 23-FEB-2001 (first entry)

XX

DE Mouse FLASH protein, SEQ ID NO:22.

XX

KW FLASH protein; FLICE-associated huge protein;

KW apoptosis-associated protein; mouse; murine; pro-apoptotic;

KW Fas-mediated apoptosis induction; drug screening; inhibitor; inducer;

KW Escherichia coli SANK 70599; FERM BP-6707.

XX

OS Mus musculus.

XX

PN WO200065044-A1.

XX

PD 02-NOV-2000.

XX

PF 21-APR-2000; 2000WO-JP002615.

XX

PR 23-APR-1999; 99JP-00117103.

XX

PA (SANY ) SANKYO CO LTD.

XX

PI Yonehara S, Imai Y;

XX

DR WPI; 2000-687337/67.

DR N-PSDB; AAC81309.

XX

PT DNA and encoded apoptosis-associated proteins, applicable in screening

PT apoptosis inhibitors and apoptosis-induction promoters for treating

PT diseases due to abnormal Fas-mediated apoptosis.

XX

PS Example; Page 90-103; 109pp; Japanese.

XX

CC The invention relates to a novel mouse apoptosis-associated protein

CC (AAB29693) and to nucleic acids encoding it (AAC81290). The mouse

CC apoptosis- associated protein potentiates the induction of Fas-mediated

CC apoptosis. The invention also relates to variants of the protein which

CC retain activity, recombinant vectors and host cells comprising DNA

CC encoding mouse apoptosis-associated protein, recombinant production of

CC the protein, an antibody which specifically binds the protein, and

CC methods of screening compounds for their ability to promote or inhibit

CC apoptosis induction. The invention additionally discloses Escherichia

CC coli SANK 70599 (FERM BP-6707) which contains a plasmid encoding mouse

CC apoptosis- associated protein. The mouse apoptosis-associated protein and

CC DNA encoding it may be used to screen potential apoptosis inhibitors and

CC promoters of apoptosis induction. The compounds thus identified can be

CC used in the treatment of diseases associated with abnormal Fas-mediated

CC apoptosis. The present sequence represents mouse FLASH (FLICE- associated

CC huge) protein which is involved in Fas-mediated activation of caspase-8

CC during apoptosis

XX

SQ Sequence 1962 AA;

Query Match 3.3%; Score 87; DB 3; Length 1962;

Best Local Similarity 22.0%; Pred. No. 9.2e+02;

Matches 93; Conservative 56; Mismatches 146; Indels 128; Gaps 24;

QY 158 LYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGM--BEAGSVALEELVEKEKD 215

Db 1300 LQGSDDLDTSGTEKA-----EWELKTPEKQLLESKCESAPACATEELVSE--- 1345

QY 216 RFFSGVDYI--VISDNLM---ISQKPAITYGTR-----GNSYFMVEVKC---RDQ 258

Db 1346 ----GASLCPKVISDDNWSLLSSEKGPSLSGLSLPVHPDVLDCNCFEVSNTALGKDN 1401

QY 259 DFHS----GTFGGILHEPMADLVAL-LGSLVDSSGHI--LVPGIYDEVVP----- 301

Db 1402 VYSEKSKPCISSILLEDLA--VSLTVPSPLKSDGHLNFLKPEVLSTSTPEEVISAHFSE 1459

QY 302 --LTEEEINTYKAHLDLEEYRNSSRVEKFLDPTKEEILMHLWRYPSPSLIHGI--EGAFD 357

Db 1460 DALLEEEDASEQDIHIALESNDSSSKSSCSW-TSRSVASGFQYHPNLPMAHVI MEKSND 1518

QY 358 E-----PGTKTVIPGRVIGKFSIRLVPHMNVSA----- 385

Db 1519 HFIVKIRRAPSTSPGLKHGVAEESLTSPLRTGKEAGVATEKEPNLFQSTVLKPVKDL E 1578

QY 386 -----VEKQVTRHLE-----DVFS-KRNSSNKM-----VVSMTLGLHP-WIANI- 422

Db 1579 NTDKNIDKSKLTHEEQNSIVQTQVPDIYEFLKASNKVVHCDQVDDCFKLHQVWEPKVS 1638

QY 423 DDTQYLAAKRAI-----RTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDDGE 477

Db 1639 ENLQELPSMEKIPHSLDNHLDPDTHIDLTKDSAT--ETKSLGELMEVTVL-----NVDHLE 1691

QY 478 HSQ 480

Db 1692 CSQ 1694

RESULT 967

ABB59970

ID ABB59970 standard; protein; 2438 AA.

XX

AC ABB59970;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 6702.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US009231.

XX

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE ) PE CORP NY.

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

DR WPI; 2001-656860/75.

DR N-PSDB; ABL04073.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell

PT interactions.

XX

PS Disclosure; SEQ ID NO 6702; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA





XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 40110.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX DT 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL15209.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX PT interactions.

XX PS Disclosure; SEQ ID NO 40110; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 4623 AA;

Query Match 3.3%; Score 87; DB 4; Length 4623;

Best Local Similarity 20.7%; Pred. No. 3.5e+03;

Matches 107; Conservative 72; Mismatches 141; Indels 198; Gaps 31;

QY 22 RGMFSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDVQVPFRFQELFRMMAVA 81

Db 1320 RGVWSE-----LSKVTQTIDETRE-----KPWL-----SVQP-RKLRQQLEAMWA-- 1358

QY 82 ADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTGVCYGHLDVQPADRG 141

Db 1359 --QLKELPARLRMYESYEYVKKLIQSYIKVNMMLIVELKSDALKER--HWKQLTKQ----- 1409

QY 142 DGWLTDPYVLTEVD-GKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEE 200

Db 1410 ---LRNVWVLSDLGSGQWVDVNLQKNEGIV-----WQNYVELDLINY-----QNKCR---- 1475

QY 201 AGSVALEELVEKEKDRFFSGVDYIVISDNLWTSQRKPAITYGTRGNSYFMVEVKCRDQDF 260

Db 1444 QGEMALEEFLKQVRES-----WQNYVELDLINY-----QNKCR---- 1475

QY 261 HSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD----- 316

Db 1476 -----IIRG-WDDLNFKNVKEHINSVAAMKLSPYK 1504

QY 317 -----LEEYRNSRVEKFLFDTKEEILHMLWRYPSLSIHGIEGAFD-EPGTKTVIP- 366

Db 1505 VFEEEAALTWEKLN--RINA-LFDVWIDV-QRRWY-----LEGIFSGSADIKTLTPV 1553

QY 367 -----GRVIGKF-----SIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVVSM 412

Db 1554 ETSRFQSISSSEFLGLMKKVKTKSPKVMVDVLNIPAVQRSLE-LADLLCK-----IQKA 1604

QY 413 LGLHPWIANIDDTQYLAAKRAI--RTVFGTEPDMIR-DGSTIPIA-----KMFQEIIV- 461

Db 1605 LG-----EYLERERTSFRFYFVGDEDLLEIIGNSKNIARLQKHFKKMFAGVAA 1653

QY 462 ----HKSVVLIPLGAVDDGE-HSQN-----EKINRW 487

Db 1654 ILLNEENVILGISREGEVHFHMPNPVSTVEHPKINEW 1691

RESULT 970

ADS26942

ID ADS26942 standard; protein; 240 AA.

XX ADS26942;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #15975.

XX KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 15975; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or



XX NL9301929-A.  
PN  
XX  
PD 17-OCT-1994.  
XX  
PF 05-NOV-1993; 93NL-00001929.  
XX  
PR 29-MAR-1993; 93EP-00200907.  
XX  
PA (REGA-) STICHTING REGA VZW.  
XX  
PI Billiau AJDA, Vandenbroeck K;  
XX  
DR WPI; 1994-322838/40.  
DR N-PSDB; AAQ73473.  
XX  
PT DNA coding for porcine interleukin 1-beta - and new recombinant porcine  
PT interleukin 1-beta useful as growth factor and immunostimulant.  
XX  
PS Claim 1; Fig 3b; 40pp; Dutch.  
XX  
CC The genomic DNA sequence coding for porcine interleukin-1 beta was  
CC determined (AAQ73473). The mature porcine IL-1beta polypeptide is useful  
CC as a metabolic growth factor in healthy pigs, e.g. modifying glucose  
CC turnover, energy consumption and lipid metabolism. It is also useful as  
CC an immunostimulant, esp. as a vaccine adjuvant  
XX  
SQ Sequence 267 AA;  
  
Query Match 3.3%; Score 86.5; DB 2; Length 267;  
Best Local Similarity 22.5%; Pred. No. 46;  
Matches 43; Conservative 26; Mismatches 67; Indels 55; Gaps 7;  
  
QY 82 ADTLQRLGARVASVDMGP-----QQLPDQSLPIPPPVILA-ELGSDPTKGTVC- 128  
Db 26 ADGPKEMKCRQTQNLDSLPLDGSIQLOISHQLCNESRPMVSVIVAKEPMNPSSQVVC 85  
  
QY 129 -----FYGHLDVQP---ADRGDWLTDPVLTVEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 86 DDPKSISSVFEEPIVLEKHANGFLCDATPVQSVDCKLQDK---DEKALVLAGPHELKA 142  
  
QY 180 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAI 239  
Db 143 LHLKLGDLKREVVFMS-----FVQGGD-----SDDKIPV 172  
  
QY 240 TYGTRGNSYFM 250  
Db 173 TLGIKGNLYL 183  
  
RESULT 973  
ABU27643  
ID ABU27643 standard; protein; 323 AA.  
XX  
AC ABU27643;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #13170.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Enterobacter cloacae.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA31513.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 55567; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 323 AA;  
  
Query Match 3.3%; Score 86.5; DB 6; Length 323;  
Best Local Similarity 19.5%; Pred. No. 62;  
Matches 65; Conservative 42; Mismatches 109; Indels 117; Gaps 12;  
  
QY 78 MAVAADTLQRLGARVASVDMGPQQLPDQSLPIPPPVILAEILGSDPTKGTVCFYGHLDVQP 137  
Db 42 LAISTDTL--VCGRHFLPDIDPADLA-YKALAVNVSDLAAMGADP----- 83  
  
QY 138 ADRGDGWLTDPPVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEG 197  
Db 84 -----AWLTALTLPVEDE-----AWLEAFS--DALFEQLSYDDMQLIGG 121  
  
QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPA---ITYGTRGNS---YFMV 251  
Db 122 DTTAGPLSMTLAIH-----GYVPLGRALKRSGAKPGDWIYVVTGTPGDSAAGLAIL 171  
  
QY 252 EVKCRDQDFHSGTF-----GGILHEPMADLVALLGSLVDSSGHIL-VPGIY 296  
Db 172 QNRLTVEEDADDAAYLVKRHLRPTFRILHGQALRRERASSAIDSLDGLHILKASGV- 230  
  
QY 297 DEVVPLTEEEINTYKAIHLDLEBYRNSSRVEKFLFDTKKEIIMHL----- 341











QY 312 AIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD-DAKEMKRKYDE-----LAGRAL- 329  
QY 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVVSMTLGLHPWIANIDDT----- 425  
Db 330 -----SEMKRLRERRLEAYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377  
QY 426 QYLAAKRAIRTVEGTE 441  
Db 378 KFLEFNQMLRLVADAE 393  
RESULT 979  
ABB93002  
ID ABB93002 standard; protein; 468 AA.  
XX AC ABB93002;  
XX DT 31-MAY-2002 (first entry)  
XX DE Herbicidally active polypeptide SEQ ID NO 2213.  
XX DE Herbicidally active polypeptide SEQ ID NO 2213.  
XX KW Herbicidal; plant; agriculture; herbicide.  
XX KW Herbicidal; plant; agriculture; herbicide.  
XX OS Arabidopsis thaliana.  
XX PN WO200210210-A2.  
XX PD 07-FEB-2002.  
XX PF 28-AUG-2001; 2001WO-EP009892.  
XX PF 28-AUG-2001; 2001WO-EP009892.  
XX PR (FARB ) BAYER AG.  
XX PA Tietjen K, Weidler M;  
XX PI WPI; 2002-269010/31.  
XX DR  
XX PS Identifying plant target proteins for herbicidally active compounds,  
XX PT comprising aligning and comparing nucleic acid or amino acid sequences  
XX PT from plant with nucleic acid or amino acid sequences from non-plant  
XX PT organisms.  
XX PS Claim 5; SEQ ID NO 2213; 261pp + Sequence Listing; English.  
XX CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
XX CC for herbicidally active compounds, comprising aligning and comparing  
XX CC nucleic acid or amino acid sequences from plant with nucleic acid or  
XX CC amino acid sequences from non-plant organisms using suitable search  
XX CC parameters, where plant sequences having an E-value greater by a factor  
XX CC of 3 than the E-value of most similar non-plant sequences are selected.  
XX CC The polypeptides or nucleic acids encoding them are useful for  
XX CC identifying modulators. The identified modulators are useful as  
XX CC herbicides  
XX SX Sequence 468 AA;  
Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;  
QY 117 ELGSDPTKGTVCFYGHLDVQPADRGDWLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173  
Db 76 EGEDPNNVFVMF-----QCRGDSYWSKCPICISTAVSG--LRRRCPRNKGAI--WY 124  
QY 174 -----INAVSAFRAL--EQDL-----PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215  
Db 125 DQCLLKISSVASFNKIDYENDFYLSNPNN-----MSDRGLFNKETSALLEKLAYKASD 177

QY 216 R-----FFSGVDYI-----VISDNLWISQKKPAITYGTRGNSYF-----MVEV 253  
Db 178 RNNLDGKQLVLYAAGEKRIGTKKVYAMVQWILRKFPQCCDGKRGGRVFTGSCNFRKSIEV 237  
QY 254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311  
Db 238 -CSPSGFDSNFFFE-LH-----SLDTLFVQAIAEWDRLTYLYERCVRSL 280  
QY 312 AIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD-DAKEMKRKYDE-----LAGRAL- 329  
QY 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVVSMTLGLHPWIANIDDT----- 425  
Db 330 -----SEMKRLRERRLEAYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377  
QY 426 QYLAAKRAIRTVEGTE 441  
Db 378 KFLEFNQMLRLVADAE 393  
RESULT 980  
ABB93011  
ID ABB93011 standard; protein; 468 AA.  
XX AC ABB93011;  
XX DT 31-MAY-2002 (first entry)  
XX DE Herbicidally active polypeptide SEQ ID NO 2222.  
XX DE Herbicidally active polypeptide SEQ ID NO 2222.  
XX KW Herbicidal; plant; agriculture; herbicide.  
XX KW Herbicidal; plant; agriculture; herbicide.  
XX OS Arabidopsis thaliana.  
XX PN WO200210210-A2.  
XX PD 07-FEB-2002.  
XX PF 28-AUG-2001; 2001WO-EP009892.  
XX PF 28-AUG-2001; 2001WO-EP009892.  
XX PR (FARB ) BAYER AG.  
XX PA Tietjen K, Weidler M;  
XX PI WPI; 2002-269010/31.  
XX DR  
XX PS Identifying plant target proteins for herbicidally active compounds,  
XX PT comprising aligning and comparing nucleic acid or amino acid sequences  
XX PT from plant with nucleic acid or amino acid sequences from non-plant  
XX PT organisms.  
XX PS Claim 5; SEQ ID NO 2222; 261pp + Sequence Listing; English.  
XX CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
XX CC for herbicidally active compounds, comprising aligning and comparing  
XX CC nucleic acid or amino acid sequences from plant with nucleic acid or  
XX CC amino acid sequences from non-plant organisms using suitable search  
XX CC parameters, where plant sequences having an E-value greater by a factor  
XX CC of 3 than the E-value of most similar non-plant sequences are selected.  
XX CC The polypeptides or nucleic acids encoding them are useful for  
XX CC identifying modulators. The identified modulators are useful as  
XX CC herbicides  
XX SX Sequence 468 AA;  
Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;  
QY 117 ELGSDPTKGTVCFYGHLDVQPADRGDWLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173

Db 76 EGEDPNNVFMF-----QCRGDSYWSKCPPCISTAVSG--LRRRCPRNKGAI--WY 124

Qy 174 -----INAVSAFRAL--EQDL-----PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215

Db 125 DQCLLKISSVASFNKIDYENDFYLSNPN-----MSDRGLFNKETSALLEKLAYKASD 177

Qy 216 R-----FFSGVDYI-----VISDNLWISQRPKPAITYGTRGNSYF-----MVEV 253

Db 178 RNNLDGQLVLYAAGEKRIGTKKYVAMVQWILRKFPQCCDGKRGGRVFGTSCNFRKSIEV 237

Qy 254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311

Db 238 -CSPSGFDSNFFFE-LH-----SLDTLFFVQAIAEWDRLTYLYERCVSLS 280

Qy 312 AIHLDLLEEYRNSSRVEKFLFDTKKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIG 371

Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD-DAKEMKRKYDE-----LAGRAL- 329

Qy 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVVSMTLGLHPWIANIDDT----- 425

Db 330 -----SEMKRLRERRLEAYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377

Qy 426 QYLAAKRAIRTVFGTE 441

Db 378 KFLEFNQMLRLVADAE 393

RESULT 981

ABB93005

ID ABB93005 standard; protein; 468 AA.

XX AC ABB93005;

DT 31-MAY-2002 (first entry)

XX Herbicidally active polypeptide SEQ ID NO 2216.

DE Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP009892.

XX PR 28-AUG-2001; 2001WO-EP009892.

XX PA (FARB ) BAYER AG.

XX PI Tietjen K, Weidler M;

XX DR WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.

PS Claim 5; SEQ ID NO 2216; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides

SQ Sequence 468 AA;

Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;

Qy 117 ELGSDPTKGTVCFYGHLDVQPADRGDGLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173

Db 76 EGEDPNNVFMF-----QCRGDSYWSKCPPCISTAVSG--LRRRCPRNKGAI--WY 124

Qy 174 -----INAVSAFRAL--EQDL-----PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215

Db 125 DQCLLKISSVASFNKIDYENDFYLSNPN-----MSDRGLFNKETSALLEKLAYKASD 177

Qy 216 R-----FFSGVDYI-----VISDNLWISQRPKPAITYGTRGNSYF-----MVEV 253

Db 178 RNNLDGQLVLYAAGEKRIGTKKYVAMVQWILRKFPQCCDGKRGGRVFGTSCNFRKSIEV 237

Qy 254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311

Db 238 -CSPSGFDSNFFFE-LH-----SLDTLFFVQAIAEWDRLTYLYERCVSLS 280

Qy 312 AIHLDLLEEYRNSSRVEKFLFDTKKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIG 371

Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD-DAKEMKRKYDE-----LAGRAL- 329

Qy 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVVSMTLGLHPWIANIDDT----- 425

Db 330 -----SEMKRLRERRLEAYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377

Qy 426 QYLAAKRAIRTVFGTE 441

Db 378 KFLEFNQMLRLVADAE 393

RESULT 982

ABB93004

ID ABB93004 standard; protein; 468 AA.

XX AC ABB93004;

XX 31-MAY-2002 (first entry)

XX Herbicidally active polypeptide SEQ ID NO 2215.

DE Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

XX PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP009892.

XX PR 28-AUG-2001; 2001WO-EP009892.

XX PA (FARB ) BAYER AG.

XX PI Tietjen K, Weidler M;

XX DR WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.

PS Claim 5; SEQ ID NO 2215; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant

CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 468 AA;  
  
Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;  
  
QY 117 ELGSDPTKGTVCYGHLDVQPADRGDWLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173  
Db 76 EGEDPNNVFMF-----QCRGDSYWSKPCPCISTAVSG--LRRRCPRNKGAII-WY 124  
  
QY 174 -----INAVSAFRAL--EQDL----PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215  
Db 125 DQCLLKISSVASFNKIDYENDFYLSNPN-----MSDRGLFNKETSALLEKLAYKASD 177  
  
QY 216 R-----FFSGVDYI----VISDNLWISQRKPAITYGTRGNSYF-----MVEV 253  
Db 178 RNNLDGKQLVLYAAGEKRIGTKKVYAMVQWILRKFPQCCDGKRGGRVFGTSCNFRKSIEV 237  
  
QY 254 KCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311  
Db 238 -CSPSGFDSNFFFE-LH-----SLDTLFVQAIAEWDRLTYLYERCVRSL 280  
  
QY 312 AIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYP SLSIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD-DAKEMKRKYDE-----LAGRAL- 329  
  
QY 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVVSMTLGLHPWIANIDDT----- 425  
Db 330 -----SEMKRLRERRLEAYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377  
  
QY 426 QYLAAKRAIRTVFGTE 441  
Db 378 KFLEFNQMLRLVADAE 393  
  
RESULT 983  
ABB93006  
ID ABB93006 standard; protein; 468 AA.  
XX  
AC ABB93006;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 2217.  
XX  
KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX  
PR 28-AUG-2001; 2001WO-EP009892.  
PA (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;  
XX  
DR WPI; 2002-269010/31.  
XX  
PT Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms.  
XX Claim 5; SEQ ID NO 2217; 261pp + Sequence Listing; English.  
PS  
XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 468 AA;  
  
Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;  
  
QY 117 ELGSDPTKGTVCYGHLDVQPADRGDWLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173  
Db 76 EGEDPNNVFMF-----QCRGDSYWSKPCPCISTAVSG--LRRRCPRNKGAII-WY 124  
  
QY 174 -----INAVSAFRAL--EQDL----PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215  
Db 125 DQCLLKISSVASFNKIDYENDFYLSNPN-----MSDRGLFNKETSALLEKLAYKASD 177  
  
QY 216 R-----FFSGVDYI----VISDNLWISQRKPAITYGTRGNSYF-----MVEV 253  
Db 178 RNNLDGKQLVLYAAGEKRIGTKKVYAMVQWILRKFPQCCDGKRGGRVFGTSCNFRKSIEV 237  
  
QY 254 KCRDQDFHSGTGGILHEPMDLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311  
Db 238 -CSPSGFDSNFFFE-LH-----SLDTLFVQAIAEWDRLTYLYERCVRSL 280  
  
QY 312 AIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYP SLSIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD-DAKEMKRKYDE-----LAGRAL- 329  
  
QY 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVVSMTLGLHPWIANIDDT----- 425  
Db 330 -----SEMKRLRERRLEAYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377  
  
QY 426 QYLAAKRAIRTVFGTE 441  
Db 378 KFLEFNQMLRLVADAE 393  
  
RESULT 984  
ABB93010  
ID ABB93010 standard; protein; 468 AA.  
XX  
AC ABB93010;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 2221.  
XX  
KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX  
PR 28-AUG-2001; 2001WO-EP009892.  
PA (FARB ) BAYER AG.  
XX





KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX  
PR 28-AUG-2001; 2001WO-EP009892.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;  
XX  
DR WPI; 2002-269010/31.  
XX  
PS Identifying plant target proteins for herbicidally active compounds,  
XX comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
PS Claim 5; SEQ ID NO 2218; 261pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 468 AA;  
  
Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;  
  
QY 117 ELGSDPTKGTVCYGHLDVQPADRGDWLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173  
Db 76 EGEDPNNVFMF-----QCRGDSYWSKCPPCISTAVSG--LRRRCPRNKGAII-WY 124  
  
QY 174 -----INAVSAFRAL--EQDL---PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215  
Db 125 DQCLLKISSVASFNKIDYENDFYLSNPN-----MSDRGLFNKETSALLEKLAYKASD 177  
  
QY 216 R-----FFSGVDYI-----VISDNLMISQKPKAITYGTRGNSYF-----MVEV 253  
Db 178 RNNLDGKQLVLYAAGEKRIGTKKVYAMVQWILRKFPQCCDKRGRGVFGTSCNFRKSIEV 237  
  
QY 254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311  
Db 238 -CSPSGFDSNFFEB-LH-----SLDTLFVQALAEWDRLTYLYERCVRSL 280  
  
QY 312 AIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD--DAKEMKRYDE-----LAGRAL- 329  
  
QY 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVSMVMTLGLHPWIANIDDT----- 425  
Db 330 -----SEMKRLRRLRLEYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377  
  
QY 426 QYLAAKRAIRTVFGE 441  
Db 378 KFEFNQMLRLVADAE 393  
  
RESULT 987  
ABB93012  
ID ABB93012 standard; protein; 468 AA.

XX ABB93012;  
AC  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 2223.  
XX  
KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX  
PR 28-AUG-2001; 2001WO-EP009892.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;  
XX  
DR WPI; 2002-269010/31.  
XX  
PT Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
PS Claim 5; SEQ ID NO 2223; 261pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 468 AA;  
  
Query Match 3.3%; Score 86.5; DB 5; Length 468;  
Best Local Similarity 22.9%; Pred. No. 1.1e+02;  
Matches 86; Conservative 47; Mismatches 134; Indels 109; Gaps 22;  
  
QY 117 ELGSDPTKGTVCYGHLDVQPADRGDWLT--DPYVLTEVDGKLYGRGATDNKGPVLAW- 173  
Db 76 EGEDPNNVFMF-----QCRGDSYWSKCPPCISTAVSG--LRRRCPRNKGAII-WY 124  
  
QY 174 -----INAVSAFRAL--EQDL---PVNIKFIIEGMEEAG-----SVALEELVEKEKD 215  
Db 125 DQCLLKISSVASFNKIDYENDFYLSNPN-----MSDRGLFNKETSALLEKLAYKASD 177  
  
QY 216 R-----FFSGVDYI-----VISDNLMISQKPKAITYGTRGNSYF-----MVEV 253  
Db 178 RNNLDGKQLVLYAAGEKRIGTKKVYAMVQWILRKFPQCCDKRGRGVFGTSCNFRKSIEV 237  
  
QY 254 KCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGI--YDEVVPLTEEEINTYK 311  
Db 238 -CSPSGFDSNFFEB-LH-----SLDTLFVQALAEWDRLTYLYERCVRSL 280  
  
QY 312 AIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 281 VEATNAKDAHEALAVEK---EKVAQALADLARSQD--DAKEMKRYDE-----LAGRAL- 329  
  
QY 372 KFSIRLVPHMNVSAVEKQVTRHLEDV-FSKRNSNKMVSMVMTLGLHPWIANIDDT----- 425  
Db 330 -----SEMKRLRRLRLEYAEFVRRSALDKMAELVQKRLDRIKAHIDDTKAAEP 377  
  
QY 426 QYLAAKRAIRTVFGE 441







WPI; 2003-799836/75.  
N-PSDB; ADC91348.

New isolated nucleic acid derived from *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection.

Example 1; SEQ ID NO 4629; 243pp; English.

The invention relates to an isolated nucleic acid derived from *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from *E. faecium* bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of *Candida albicans* - derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating *Enterococcus faecium* infections. The present sequence represents one if the disclosed *E. faecium* proteins.

Sequence 471 AA;

Query Match	3.3%	Score 86.5;	DB 7;	Length 471;
Best Local Similarity	20.4%	Pred. No. 1.1e+02;		
Matches 91;	Conservative	59;	Mismatches 160;	
			Indels 135;	Gaps 21;

QY	45	HQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMMAVAADTLQRLGARVASVDMGPPQQLPD	104
Db	36	HTNKIDQTYVDYVT-DID-----PNLSNNIGFTRTTGINLLRDVNGKQVPVSFNQN-PD	88
QY	105	QOSLPPIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGAT	164
Db	89	TESLSLSSTMSAMTG---VGVSSPFTQLDTSK---ENFLKDNYSLL---AGSYPASAT	137
QY	165	DNKGPVLAWINAVSAFRALEQDLFPVNIKFIEGMEEAGSVALEEL---VEKEKDRF--F	218
Db	138	D-----VVLIVDGNNTNINAKNLGDFDKEDKLDFFDDI	172
QY	219	SGVDYIVISDNLWISQRKPAITYGTR--GNSYFMVEVKCRDQDFHSGTFGGILHEPMAD	275
Db	173	VGTTFKLVNN-----TYTTLPTGN-----FIPNTDYDAMYQNASD	209
QY	276	LVALLGSL-VDSSG--HILVPGI-----YDEVVP-----LTEEEI-	307
Db	210	ELKISGILRVKSSSTWNLSPGIAYSQDLTTOIVNENKESEIVKAQRDSGVNVLTTTEKVD	269
QY	308	-NTYKAI--HLDLEEYRNSSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGAFDE-----	358
Db	270	ENAKQTLLSYLGDSFPSSIMIYPNNFEDKEKILDYLLDDYN-----KGKSDEDIITYT	322
QY	359	--PGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLH	416
Db	323	DLAGTMTLGTGLMDAITVYVLIAPAGISLVTSMIMISIIITYTSVIERTKEIGVLKALG--	380
QY	417	PWIANIDDTQYLAAKRAIRTVFGTE	441
Db	381	-----ARKKIDITRVFDAE	393

RESULT 992  
AAU75169  
ID AAU75169 standard; protein; 516 AA.  
XX  
AC AAU75169;

XX	08-MAY-2002 (first entry)	
DT		
XX		
DE	Mouse RORgamma polypeptide.	
XX		
KW	Mouse; transgenic; disruption of target gene; disease model;	
KW	modulation of gene expression; behavioural phenotype; spleen; kidney;	
KW	liver; thymus; lymph node; lymphocyte; bone marrow; RORgamma.	
XX		
OS	Mus musculus.	
XX		
PN	WO200201950-A2.	
XX		
PD	10-JAN-2002.	
XX		
PF	29-JUN-2001; 2001WO-US020795.	
XX		
PR	29-JUN-2000; 2000US-0215178P.	
PR	29-JUN-2000; 2000US-0215179P.	
PR	29-JUN-2000; 2000US-0215366P.	
PR	29-JUN-2000; 2000US-0215402P.	
PR	29-JUN-2000; 2000US-0215404P.	
PR	29-JUN-2000; 2000US-0215466P.	
PR	29-JUN-2000; 2000US-0215467P.	
PR	27-JUL-2000; 2000US-0221667P.	
PR	26-OCT-2000; 2000US-0244083P.	
XX		
PA	(DELT-) DELTAGEN INC.	
XX		
PI	Leviten MW, Brennan TJ, Guenther C, Klein R, Matthews W, Moore M;	
XX		
DR	WPI; 2002-164479/21.	
DR	N-PSDB; ABK13754.	
XX		
PT	Novel transgenic mouse comprising disruption in target gene e.g., an	
PT	anaphylatoxin C3a receptor gene, chordin gene, useful for identifying	
PT	agents that modulate expression or function of target gene.	
XX		
PS	Disclosure; Fig 8; 90pp; English.	
XX		
CC	The present invention relates to a method of creating transgenic animals,	
CC	particularly transgenic mice, comprising a disruption in a target gene.	
CC	Examples of target genes given in the specification include the mouse	
CC	anaphylatoxin C3a receptor gene, 5-HT5A gene, chordin gene, RORgamma	
CC	gene, BMP gene, airway trypsin-like protease gene and the aquaporin gene.	
CC	The transgenic mice are useful as models for disease and for identifying	
CC	an agent that modulates the expression or function of a gene. The	
CC	transgenic mice models are useful for identifying drugs and	
CC	pharmaceutical therapies. They are also useful for testing and developing	
CC	new treatments relating to behavioural phenotypes. They are useful for	
CC	potential treatments for various diseases. For example, a transgenic	
CC	mouse comprising a disruption in the RORgamma gene is useful for	
CC	identifying an agent that ameliorates an abnormality in the spleen,	
CC	kidney, liver, thymus, lymph nodes, lymphocytes, bone marrow or bones.	
CC	The present sequence represents mouse RORgamma polypeptide. The encoding	
CC	gene is disrupted to produce transgenic mice in the methods of the	
CC	present invention	
XX		
SQ	Sequence 516 AA;	

```

Query Match      3.3%; Score 86.5; DB 5; Length 516;
Best Local Similarity 22.4%; Pred. No. 1.3e+02;
Matches 88; Conservative 47; Mismatches 138; Indels 119; Gaps 23;

QY      82 ADTLQRLGARVASVDMGPPQLPDGQS--LP-----IPPVILAEGLSDP-----TKG 125
      |||||  :: : ||||| ||| ||| ||| ||| ||| : |||
Db      142 ADTL-----TYTGLSDGQLPLGASPDLPASACPPGLLRASGGPPYSNTLAKTEVQG 195
      |||||  :: : ||||| ||| ||| ||| ||| ||| : |||

QY      126 TVCFYGHLDVQPADRGDGLWLTDPYVLTVDGKL-YGRG-----ATDNKGP--- 169
      |      ||| : ||| ||| ||| ||| ||| ||| : |||
Db      196 ASC---HLEYSP-ERGKAEGRDSIYST--DGQLTLGRCLGRFEETRHPELGEPEQGPDSh 249
      |||||  :: : ||||| ||| ||| ||| ||| ||| : |||

QY      170 -VLAWINAVSAFRALEODLPVNIKFIEGMEEGASVAAEELVEKEKDRFFS----- 219
      |||||  :: : ||||| ||| ||| ||| ||| ||| : |||

```

Db 250 CIPSFCSAPEVPYASLTIDIEYLVQNVCKSFRETQCLRLEDLL-RQRTNLFSSREEVTSYQR 308  
QY 220 -----GVDYIV-----ISDNLWISQKPAITYGTRGNSYFMVEVKCRDQ 258  
Db 309 KSMWEMWERC AHLTEA IQYVVEFAKRLSGFMELCQNDQIILL-TAGAMEVVLVRMCRA Y 367  
QY 259 D-----FHSGTFGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEBEEINTYKA 312  
Db 368 NANNHTVFFEGKYGGVELFRALGCSELISIFDFS-HFL-----SALCFSEDEIALYTA 420  
QY 313 IHL-----DLEEYRNSSRVEKFLFDTKBEILMHLWRYPYSLSIHGIEGAFDEPGTKTVIP 366  
Db 421 LVLINANRPGLOEKR---RVE-----HLQYNLELAFHHHLCKTHRQGLLAKLP 465  
QY 367 GRVIGKFSIRLVPHMNVSAVEK-QVTRHLEDV 397  
Db 466 PK--GKLRSLCSQH-----VEKLQIFQHLHPI 490  
RESULT 993  
ADP05679  
ID ADP05679 standard; protein; 516 AA.  
XX AC ADP05679;  
XX DT 26-AUG-2004 (first entry)  
XX DE Mouse nuclear receptor protein SeqID53.  
XX KW disease risk; disorder risk; mutation; polymorphism;  
KW nuclear receptor protein; antibacterial; antithyroid; cardiovascular-Gen;  
KW cytostatic; dermatological; eating-Disorders-Gen; gastrointestinal-Gen;  
KW gynaecological; hepatotropic; immunosuppressive; muscular-Gen;  
KW nephrotropic; osteopathic; virucide; adrenal gland; colon;  
KW cardiovascular; intestine; kidney; liver; lung; muscular; ovary; blood;  
KW prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus;  
KW pancreas; bone; joint; breast; immune system; metabolic;  
KW nutritive disease; mouse; murine.  
XX Mus sp.  
XX WO2004045369-A2.  
XX PN 03-JUN-2004.  
XX PF 12-NOV-2003; 2003WO-US036229.  
XX PR 14-NOV-2002; 2002US-0426305P.  
XX (NURA-) NURA INC.  
XX PI Gaitanaris GA, Bergmann JE, Gracarov A, Hohmann J, Li F;  
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX WPI; 2004-449627/42.  
DR N-PSDB; ADP05680.  
XX Determining an increased risk for e.g. colon, brain or breast disease or  
PT disorder, by detecting a mutation or polymorphism in the nuclear receptor  
PT gene, or measuring expression or biological activity level of the nuclear  
PT receptor.  
XX Claim 1; SEQ ID NO 53; 508pp; English.  
XX This invention relates to a novel method of determining whether a patient  
CC has an increased risk for developing a disease or disorder which  
CC comprises determining the presence of a mutation or polymorphism in the  
CC patient's gene encoding a nuclear receptor protein or measuring the  
CC expression or level of biological activity of a nuclear receptor  
CC polypeptide in the patient or in a cell of the patient. The invention may  
CC be useful for the development of compounds with an antibacterial,  
CC antithyroid, cardiovascular-Gen, cytostatic, dermatological, eating-

CC Disorders-Gen, gastrointestinal-Gen, gynaecological, hepatotropic,  
CC immunosuppressive, muscular-Gen, nephrotropic, osteopathic or virucide  
CC activity. The method is useful for determining whether a patient has an  
CC increased risk for developing a disease or disorder. The nucleic acid  
CC encoding a nuclear receptor polypeptide, an expression vector comprising  
CC the nucleic acid operably linked to a promoter, or a compound that  
CC modulates the biological activity of a nuclear receptor polypeptide, is  
CC useful for treating or preventing a disease or disorder of the adrenal  
CC gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular,  
CC ovary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid,  
CC uterus, pancreas, bone and joints, breast, or immune system, or metabolic  
CC or nutritive disease or disorder. The present sequence is that of a  
CC nuclear receptor protein which may be used in the method of the  
CC invention.  
XX  
SQ Sequence 516 AA;  
Query Match 3.3%; Score 86.5; DB 8; Length 516;  
Best Local Similarity 22.4%; Pred. No. 1.3e+02;  
Matches 88; Conservative 47; Mismatches 138; Indels 119; Gaps 23;  
QY 82 ADTLQRLGARVASVDMGPPQLPDGQS--LP----IPPVILAE L GSDP-----TKG 125  
Db 142 ADTL-----TYTLGLSDGQLPLGASPDLP EASACPPGLLRASGSGPPYSNTLAKTEVQG 195  
QY 126 TVCFYGHLDVQPADRGDGNLTDPYVLTEVDGKL-YGRG-----ATDNKGP--- 169  
Db 196 ASC---HLEYSP-ERGKAERDSIYST--DGQLTLGRGCLRFEETRHP ELGEPEQGPD SH 249  
QY 170 -VLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFS----- 219  
Db 250 CIPSFCSAPEVPYASLTIDIEYLVQNVCKSFRETQCLRLEDLL-RQRTNLFSSREEVTSYQR 308  
QY 220 -----GVDYIV-----ISDNLWISQKPAITYGTRGNSYFMVEVKCRDQ 258  
Db 309 KSMWEMWERC AHLTEA IQYVVEFAKRLSGFMELCQNDQIILL-TAGAMEVVLVRMCRA Y 367  
QY 259 D-----FHSGTFGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEBEEINTYKA 312  
Db 368 NANNHTVFFEGKYGGVELFRALGCSELISIFDFS-HFL-----SALCFSEDEIALYTA 420  
QY 313 IHL-----DLEEYRNSSRVEKFLFDTKBEILMHLWRYPYSLSIHGIEGAFDEPGTKTVIP 366  
Db 421 LVLINANRPGLOEKR---RVE-----HLQYNLELAFHHHLCKTHRQGLLAKLP 465  
QY 367 GRVIGKFSIRLVPHMNVSAVEK-QVTRHLEDV 397  
Db 466 PK--GKLRSLCSQH-----VEKLQIFQHLHPI 490  
RESULT 994  
ABG15443  
ID ABG15443 standard; protein; 527 AA.  
XX AC ABG15443;  
XX DT 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #15434.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX WO200175067-A2.  
PN 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.







QY 200 EAGSVALEELV-----EKEKDRFFSGVDYIVISDNLWISQRKPAITYG 242  
Db 261 EDGSRVTALIPLWDMCNHTNGLITTYGNLEDDR-----CECVALQD--FRAGEQIYIFYG 314  
QY 243 TRGNSYFMVEVKCRDQDFHSGTF-----GGILHEPMADLVALLGSLVD 285  
Db 315 TRSNAEFVI-----HSGFFFDNNSHDRVKIKLGVSksDRLYAMKAEVLARAGIPTS 365  
QY 286 S---SGHILVPGI-----YDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFL-----F 331  
Db 366 SVFALHFTPEPPISAQLLAFLRVFCMTEELK-----EHLGDSRIDRIFTLGNSEF 416  
QY 332 DTKEEILMHLWRY-----PSLSIHGIEGAFDEPGTKTVIPGR---VIGKFSIR----- 376  
Db 417 PVSWDNEVKLWTFLEDRASLLKTYKTTEE--DKSVLKNHDLVSRAKMAIKRLGEKEI 474  
QY 377 LVPHMNVSAVEKQVTR-HLED--VFSKRNSSNMVVSMTLG--LHPWIANIDD---TQ 426  
Db 475 LEKAVKSAAVNREYRQOMEKAPLPKYEESNLGLLESSVGDsrLPLVLRNLEEEAGVQD 534  
QY 427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPLGAVDDGHSQNEKINR 486  
Db 535 ALNIREAISKAKATENGLVNGENSIP-----NGTRSENESLNQ 572

RESULT 997  
ADK71013  
ID ADK71013 standard; protein; 594 AA.  
XX AC ADK71013;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human methyltransferase sequence.

XX KW Methyltransferase; human; chromosome 14q32; cardiant;  
KW antiarteriosclerotic; cytostatic; dermatological; antipsoriatic;  
KW antiseborrheic; antiulcer; hepatotropic; gastrointestinal;  
KW antiinflammatory; virucide; osteopathic; neuroprotective; nootropic;  
KW antiparkinsonian; vasotropic; antiinfertility; gynaecological;  
KW antiasthmatic; respiratory; uropathic; enzyme.

XX OS Homo sapiens.  
XX PN WO2004013320-A1.  
XX PD 12-FEB-2004.  
XX PF 29-JUL-2003; 2003WO-EP008340.  
XX PR 30-JUL-2002; 2002US-0399155P.  
PR 04-DEC-2002; 2002US-0430666P.  
PR 08-APR-2003; 2003US-0460959P.  
XX PA (FARB ) BAYER HEALTHCARE AG.  
XX PI Smith TJ;  
XX DR WPI; 2004-157130/15.  
DR N-PSDB; ADK71012, ADK71014.

XX PT New methyltransferase polynucleotide and its encoded protein, useful for  
PT identifying modulators of methyltransferase activity and in gene therapy  
PT for preventing or treating e.g. atherosclerosis, cancer or Alzheimer's  
PT disease.

XX PS Claim 1; SEQ ID NO 2; 134pp; English.  
XX CC The invention relates to an isolated polynucleotide encoding a  
CC methyltransferase. The polypeptide can be expressed by standard  
CC recombinant methodology. The polynucleotide and polypeptide are useful in  
CC identifying test compounds which may act as agonists or antagonists at  
CC the receptor site and which can be regulated to provide therapeutic

CC effects. The expression vector or reagent comprising the  
CC methyltransferase polypeptide are useful in the preparation of a  
CC medicament for modulating the activity of a methyltransferase in a  
CC disease e.g. a cardiovascular disorder, a dermatological disorder, a  
CC gastrointestinal disorder and a liver disorder, cancer, a musculoskeletal  
CC disorder, a neurological disorder, a respiratory disorder, a reproductive  
CC disorder or a genitourinary disorder. These diseases may include  
CC myocardial infarction, atherosclerosis, leukaemia, psoriasis, dermatitis,  
CC acne, gastric ulcer, cirrhosis, hepatitis, osteoporosis, Alzheimer's  
CC disease, Parkinson's disease, impotence, infertility, vaginitis, benign  
CC prostatic hyperplasia and asthma. These are also useful for diagnosing,  
CC preventing or ameliorating the diseases cited above. The present sequence  
CC represents a human methyltransferase sequence.  
XX XX  
SQ Sequence 594 AA;

Query Match 3.3%; Score 86.5; DB 8; Length 594;  
Best Local Similarity 19.0%; Pred. No. 1.6e+02;  
Matches 114; Conservative 81; Mismatches 202; Indels 203; Gaps 30;

QY 26 SSPSPPP-----ALLEKVQ-----YIDLHQDEFVQTLKEWVAIESDSVQ-- 65  
Db 37 SSPAPGPGKEWEYVQIRTLVEKIRKKQGLSVTFDGKREDYFPDLMKWASENGASVEGF 96  
QY 66 PVPRFRQELFRMMA---VAADTL-----QRLGARVASVD---MGPPQLPDGQSLPIPPVI 114  
Db 97 EMVNFKEEGFGLRATRDIAEELFLWVPRKLLMTVESAKNSVLGPLYSQDR-----I 148  
QY 115 LAELGSDPTKGTVCYGHLDVQPADRGDGLTDPYVLT--EVDGKLYGR----- 161  
Db 149 LQAMGN-----IALAFHLLCERASPNF--QPYIQTLPSEYDTPLYFEEDEVRYLQST 200  
QY 162 -----GATDNKGPVLAWINAVSAFRALEQDLVPNIKFIEGME----- 199  
Db 201 QAIHDFVSQYKNTARQAYFYKVIQTHPHANKLPLKDSFTYEDYRWAVSSVMTNRQNIPT 260  
QY 200 EAGSVALEELV-----EKEKDRFFSGVDYIVISDNLWISQRKPAITYG 242  
Db 261 EDGSRVTALIPLWDMCNHTNGLITTYGNLEDDR---CECVALQD--FRAGEQIYIFYG 314  
QY 243 TRGNSYFMVEVKCRDQDFHSGTF-----GGILHEPMADLVALLGSLVD 285  
Db 315 TRSNAEFVI-----HSGFFFDNNSHDRVKIKLGVSksDRLYAMKAEVLARAGIPTS 365  
QY 286 S---SGHILVPGI-----YDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFL-----F 331  
Db 366 SVFALHFTPEPPISAQLLAFLRVFCMTEELK-----EHLGDSRIDRIFTLGNSEF 416  
QY 332 DTKEEILMHLWRY-----PSLSIHGIEGAFDEPGTKTVIPGR---VIGKFSIR----- 376  
Db 417 PVSWDNEVKLWTFLEDRASLLKTYKTTEE--DKSVLKNHDLVSRAKMAIKRLGEKEI 474  
QY 377 LVPHMNVSAVEKQVTR-HLED--VFSKRNSSNMVVSMTLG--LHPWIANIDD---TQ 426  
Db 475 LEKAVKSAAVNREYRQOMEKAPLPKYEESNLGLLESSVGDsrLPLVLRNLEEEAGVQD 534  
QY 427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPLGAVDDGHSQNEKINR 486  
Db 535 ALNIREAISKAKATENGLVNGENSIP-----NGTRSENESLNQ 572

RESULT 998  
ABB64289  
ID ABB64289 standard; protein; 625 AA.  
XX AC ABB64289;  
XX DT 26-MAR-2002 (first entry)  
XX DE Drosophila melanogaster polypeptide SEQ ID NO 19659.  
XX KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.





Db 442 GIPQRRQNIKQPYANIVSPIRTYTKSG---TAPLMSTFRPTSSDMLST-----LAISE 493  
QY 320 YRNSSRV--EKFLDFTKEEILMHLWRYP-----SLSIHGIEGAFDEPGTKTVIPGRVIG 371  
Db 494 LEQESRLCHPKALFATKDET-----PKSSEAESLJINGIDSAADLLPKKAYISSEIKH 546  
QY 372 KFSIRL-----VPHMNV---SAVEKQVTRH 393  
Db 547 VVDERTPLPMKVPQIQKYLNSAVEPTVMRH 577

RESULT 1000  
ABU47175  
ID ABU47175 standard; protein; 635 AA.  
XX  
AC ABU47175;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #32702.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmomella typhimurium.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA51045.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 75099; 1766pp; English.  
XX

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 635 AA;

Query Match 3.3%; Score 86.5; DB 6; Length 635;  
Best Local Similarity 18.4%; Pred. No. 1.8e+02;  
Matches 115; Conservative 90; Mismatches 194; Indels 225; Gaps 28;  
QY 30 PPPALLEKVFQYIDLHQDEFVQTLKEWVAI-----ESDSVQVPVPRQE-----LFR 76  
Db 75 PPRNIAGSVYDFVAEGIEEQAAYLKRYHEISRLVMTDPSEKNLNMARVQEQLDHHNLWQ 134  
QY 77 MMAVAADTLQRLG---ARVASVDMG-PQQLPDGQSLPIPPVILAEGLSDPTKGTVCIFYG 131  
Db 135 LENRINEVLAQLGLDPNAALSSLSGGWLRKAALGRALVSNPRVL--LLDEPT-----N 185  
QY 132 HLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 186 HLDIETID---WL-----EGFLKTFNGT-----IIFISHDRSFIRNMATRI 223  
QY 192 KFIIEG-----MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ----- 234  
Db 224 VLDLRGKLVTPGNYDQYLLEKEEARLVEELQNAEFDRKLA-----QEEVWIRQGIKA 276  
QY 235 -----RKPAITYGTRG-----NSYFVVEVKCRDQ 258  
Db 277 RRTNRNEGRVRAKAMRRERSERREVMGTAKMQVEEATRSGKIVFEMENVDYQVEGKQLVK 336  
QY 259 DFHSGTFGGILHEPMADLVAL-----LGSLVDSSGHILVPGIYDEVVPLT 303  
Db 337 DFSAQVQRG-----DKIALIGPNGCGKGTLLKMLGLQADSGRIHV-GTKLEVAYFD 388  
QY 304 EE--EINTYKAIHLDLEEYRNSRV-----EKFLDFTKEEILMHLWRYPVSLSIH 350  
Db 389 QHRAELDPEKTVMNDNLAEKGQEVVMVNGKPRHVLGYLQDFLFHPKRAMT-----PVRALS 442  
QY 351 GIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRN-----SS 404  
Db 443 GGE-----RNRLLLARLFKPSNLLILDDEPTNDLDVETLELLEELIDGYQGTVLLVSH 495  
QY 405 NKMVVSMTLGLHPWI-----ANIDDTQYLAACKRAI-----RTVFGTEPDM 444  
Db 496 DRQFVDNTV-TECWIFEGGGKIGRYIGGYHDARAQQEQHLATKQPMAKKNEEVIAPKAEI 554  
QY 445 IRDGSTIPIAKMFOEIVHKSVVLIPLGAVDDE-----HSQNEKI- 484  
Db 555 VKRGSSKLSYKLQRELEQ-----LP-GQLEDLEAKLEALQAVADAAPFSQPHEQTQKVL 608  
QY 485 -----NRWNYIEGTK 494  
Db 609 ADLSQAEQLEQAFAFERWEYLEGLK 632

RESULT 1001  
ABU49632  
ID ABU49632 standard; protein; 705 AA.  
XX  
AC ABU49632;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #35159.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX

















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PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US0009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA43759.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 67813; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation; (7) identifying a gene in an operon required for
CC proliferation; (8) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1357 AA;
```

```
Query Match          3.3%; Score 86.5; DB 6; Length 1357;
Best Local Similarity 19.2%; Pred. No. 5.8e+02;
Matches 108; Conservative 78; Mismatches 203; Indels 173; Gaps 27;
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```
QY 34 LLEKVFQYIDLHQDEFVQT-LKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV 92
Db 823 LSERVVQ-----EDRFTTHIQELTCVARDTKLGPEEITADIPNVGEAALNKLDEAGIVY 877
QY 93 ASVDMGPQQL-----PDGQSLPIPP-----VILAEFGSD-----PTKGTVCFYG 131
Db 878 VGEVAGAGDILVGKVPKGETQLTPEEKLRLAIFGEKASDVKDTSLRVTGKTGTV---- 933
QY 132 HLDVQPADRGDGLTDPYVL-----TEVDGKLYGR 161
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Db 934 -IDVQVTR-DGVERDSRALAIEKMQLMDEIRKDLNEEFRIVEGATFERLPSALNGQVVDG 991
QY 162 GATDNKGPVLA-----WINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELV 210
Db 992 GAGLKKGTIVITDEVLDGLEHGQWFKLRMAEDALNEQLEKAQQYIVDRRR-----LLDDKF 1046
QY 211 EKEKDRFFSGVDYI-----VISDNLWISQR-----KPAITYGTRGNSYFMVEVKCRDQDF 260
Db 1047 EDKRRKLQQGDDDLAPGVLVKIVKYLAIARRRIQPGDKMAGRHGKGVSVIMPVEDMPHD- 1105
QY 261 HSGTFFGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVPLTJEEIINTYKAHLDL-- 317
Db 1106 ANGTPVDVVLNPLGVPSRMNVGQILETHLGLAAKGLGEKIDRMLEEQ---RKAALRVFL 1162
QY 318 -BEYRN-SSRVEKFLPDTKEEILM--HLMRYPSLSIHGIEGA-----FDEP 359
Db 1163 TEVYNEIGGRQENLDEFTDEEILALANNLKKGVPMATPVFDGAKEREIKAMLKLADLPES 1222
QY 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVT-----RHLED--VFESKRNSSNKMV 408
Db 1223 GQMVLFDRGTGNKF-----ERPVTGVMYMLKLNHLVDDKMHARSTGYSYLV 1269
QY 409 VSMTLG-----LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRGSGTIPIAKM 456
Db 1270 TQQPLGGKAQFGGQRFEGEMEVWALEAYGAAY-----TLQEMLTVKSDDV-NGRT----KM 1319
QY 457 FQEIVHKSVVLIPLGAVDDGEH 478
Db 1320 YKNIV-----DGDH 1328
RESULT 1011
ABU38544
ID ABU38544 standard; protein; 1448 AA.
XX AC ABU38544;
XX 19-JUN-2003 (first entry)
DT Protein encoded by Prokaryotic essential gene #24071.
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX KW Pseudomonas aeruginosa.
XX OS WO200277183-A2.
XX PN 03-OCT-2002.
XX PD 21-MAR-2002; 2002WO-US0009107.
XX PF 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA42414.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 66468; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
```



CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1448 AA;

Query Match 3.3%; Score 86.5; DB 6; Length 1448;  
Best Local Similarity 20.1%; Pred. No. 6.4e+02;  
Matches 108; Conservative 59; Mismatches 196; Indels 173; Gaps 25;

QY 6 GRMAASLLAVLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIESDSVQ 65  
Db 499 GRRGRLTA---LTSGGTIPDTGDYSVLEP-----QGLLVGTNEDFAVES---- 542  
QY 66 PVPFRQELFRMMAVAADTLQ--RLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPT 123  
Db 543 -----LAGDVFLQNGTYSRIIRIEFGRVRVEDAQGQ--PPNIPFWLGEAP- 585  
QY 124 KGTVCYPYGHLDVQPADRGDGLWLTDPYVLTVDVKLYGRGATDNKG----PVLAWINAV-- 177  
Db 586 -----GRSDELSASVARLRTLDELLGEGQALPEGRRLPEPAIWLATGLG 630  
QY 178 ---SAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFF---SGVDYIVISDNLW 231  
Db 631 LDDGAARQIVEYL-ARARQALGGLPGSRRLVLE-----RFFDESQGMQLIHS---- 677  
QY 232 ISQRKPAITYGTRGNSYFMVEVK---CRDQDFH---SGTFFGIL-----HE-PMADLVA 278  
Db 678 -----PHGSRNLNRAWGLALRKFRCSFNFELQAAATEDAILLSLSTSHSFPDLDEVWR 729  
QY 279 LLGSLVDSSGHILVPGIYDEVVPLTEEEINITYKAIHLDL EEYRNSRVEKFLFDTKEEIL 338  
Db 730 YLHSA--SAEHLVQAVLD--APLFGVRWRWNLTSLGLPRYAGGRKVPFPQLLRMKSEDL 785  
QY 339 MHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVF 398  
Db 786 L-----ASVFPDQV-----ACLENIV 801  
QY 399 SKRNSNMVMSMTLG--LHP-----WIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST 450  
Db 802 GEREVPDHPVLAQTLDCLHEAMDCEGWLALLRDMESGAV-----DLIARDLP 849  
QY 451 IPIAKMFQEI VHKSVVLIPLGAVDDG----EHSQNEKINRWNYIEGTLKFAAFFLE 502  
Db 850 APSA-----LAAEILTARPYAYLDDAPLEERTQAVQNRNRWSDPESADDLGALDLE 900

RESULT 1012

ABO80117  
ID ABO80117 standard; protein; 1627 AA.  
XX  
AC ABO80117;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #12292.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
PF 18-FEB-1999; 99US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
DR WPI; 2003-615309/58.  
DR N-PSDB; ABD13688.  
XX  
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 28863; 455pp; English.  
XX  
CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 1627 AA;

Query Match 3.3%; Score 86.5; DB 7; Length 1627;  
Best Local Similarity 18.8%; Pred. No. 7.6e+02;  
Matches 121; Conservative 89; Mismatches 231; Indels 203; Gaps 30;

QY 10 ASLLAVLLLLLERGMFS-----SPSPPPALLEKFQYIDLHQDEFVQTLKEWVAIESDSV 64  
Db 884 ALVLAVAGLVVEVGPQGRLDQVEVAPQDAVLVHLDLDFVEGTEDRLQLLLLVFQV----- 938  
QY 65 QVPRFRQELFRMM-----AVAADT---LQRLGARVASV-----D 96  
Db 939 -----FRGEFARQVEAGLEQPHQLAGDVGVGIQRTG-DVAEVEAQAADLLQVTRVGTQQGD 992  
QY 97 MGPOQLPDGQSLPIPPVILAEELGSDPTKGTVCYFYGHL---DVQPADRGDGLWLTDPYVLTE 153  
Db 993 VAPROV-GGQHQAQVEGVVLGVAADDVDEGVLEDLVELLDVHVQPFVGEGEVDVPVFAAV 1051  
QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEBAGSVAL----- 206

Db	1052	LVAQAVGEFAEHAQAEVL-----QDR-----QDVGGQRGVGVVQLAVQQLLA	1094
QY	207	--EELVEKEKDRFFSG-----VDY-IVISDNLWISQRKP-----	237
Db	1095	LRQRLVEAHHQALLGEAEQVLQVDHREVRGEALAVAGREAFREVGQDVGALGLAEVFHH	1154
QY	238	---AITYGTRGNSYFMVEVKCRDQD-----FHSG-----TFGGI--LH	270
Db	1155	QAAVVVLPGTAGLDHFFLQARRVDVDARLVRDAEDLHAGQHRLGEEGPPELAVALQALH	1214
QY	271	EPMADLVALLGSLVDSSGHI---LVPGIYDEVVPLTEEEINTYKAIHLDLEEVNRRVE	327
Db	1215	QDLLDLQARLGGI-----HVARHVGQVAEATVGVLAQEHADLVAL-LDADDRQCGA--E	1266
QY	328	KFLFDTKKEIL-----MHLWRYPSLSIHGIE-GAPDEPGTKTVIPGRVIGKFSIR----	376
Db	1267	QLVHRGLEQVVARQYFQHLGQFLAEVGLGVETGPHHFGDLAADEGDVVDALVVHRGGEQ	1326
QY	377	----LVPH--MNVSAVEKQVTRHLEDVFSKRNS-----NKMVVSM	411
Db	1327	AHEAALADHPALAVQLADRHVVVRVGRAVHTARMGSLGEGQDRFAQVGDGVLVDQVILA	1386
QY	412	TLGLH-----PWIANIDTQYLAAKRAIRTVFTEPDMIRDCGSTIPIAKM	456
Db	1387	QAGTQQTGOAEEGFLVVDHAPAVGLVGDAEFLVABEG--EVVVQQP-----FEIAAY	1436
QY	457	FQEIYHKSUVLIPLGAVDGDSQNEKINRWNYIEGTXLFAAFF	500
Db	1437	FLOFLRRH---LOGLAKPGQOOFAGLGLHRFEVGDGHAYFTEHF	1477

RESULT 1013  
ABG66725  
ID ABG66725 standard; protein: 1651 AA.

Claim 10; Page 629-632; 672pp; English.

The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention

XX	Sequence 1651 AA;	
PS	Query Match	3.3%; Score 86.5; DB 5; Length 1651;
XX	Best Local Similarity	19.6%; Pred. No. 7.8e+02;
CC	Matches	83; Conservative 73; Mismatches 160; Indels 107; Gaps 19;
CC	QY	32 PALLEKVFQYIDLH-QDEFVQTLKENWVAIESDSVQVPRFRQELFRMMAVAADTLQLRGA 90
CC	Db	217 PADLTRKMHLETPHPQVTHVSSQSGCSIASDSGS-----SSLSDIYQATES 263
CC	QY	91 RVASVDMGPQQLPDGQSLPIPPVILAEFG-----SDPTKGTVCFYGHLDVQPADRGDWL 145
CC	Db	264 EVGDVDL--TRLPEG---PVDSEDEEEDRIDTDPLOGRDLVRECLEKEPADKTD--- 315
CC	QY	146 TDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI--KFIIEGMEEAGS 203
CC	Db	316 -----DDIEQLLEEMHQLPAFANMTMSVRRLECSVMFEVVEQAGA 356
CC	QY	204 VALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVVEVKCRDQDFHSG 263
CC	Db	357 IILED--QBELDSW-----YVILNGTVEISHPDGKVENLFMGNSFGITPT--LDKQYMHG 407
CC	QY	264 TFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA-----IHL 315
CC	Db	408 -----IVRTKVDDCCQFVCI-AQQDYWRILNHVEKNTHKVEEIGEIVMVHE 451
CC	QY	316 DLEEYRNSRVEKFLFD-TKEEILMHLWRYPSLSIHGEGAFDEP---GTFKVIPIGRVIG 371
CC	Db	452 HRELDRSGRKGHIVIKATPERLIMHLIEHSI----VDPTYIEDFLTYRTFLESPL-- 505
CC	QY	372 KFSIRLVPHMNVSAVEKQVTR-----HLEDVFSKRNSNKMVSMILGLHPWIANID 423
CC	Db	506 DVGIKLLEWFKIDSLRDKVTRIVLLWVNNHFNDFEGD-----PAMTRFEEFEKNLE 557
CC	QY	424 DTQ 426
CC	Db	558 DTK 560
CC	RESULT 1014	
CC	ADE47740	
CC	ID ADE47740	standard; protein; 1664 AA.
CC	XX ADE47740;	
CC	AC ADE47740;	
CC	XX ADE47740;	
CC	DT 29-JAN-2004	(first entry)









PR	17-AUG-2001; 2001US-0313280P.	XX	WO200214368-A2.
PR	29-AUG-2001; 2001US-0315614P.	PN	
PR	17-SEP-2001; 2001US-0322818P.	XX	
PR	25-FEB-2002; 2002US-00322818.	PD	21-FEB-2002.
XX		XX	
PA	(CURA-) CURAGEN CORP.	PF	16-AUG-2001; 2001WO-US025624.
XX		XX	
PI	Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;	PR	16-AUG-2000; 2000US-0225692P.
PI	Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;	PR	16-AUG-2000; 2000US-0225693P.
PI	Gorman L, Guo X, Gusev VY, Kekuda R, Li L, Liu X, Malyankar UM;	PR	16-AUG-2000; 2000US-0225837P.
PI	Miller CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Peyman JA;	PR	18-AUG-2000; 2000US-0226236P.
PI	Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DJ;	PR	18-AUG-2000; 2000US-0226353P.
PI	Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;	PR	22-AUG-2000; 2000US-0227085P.
XX		PR	23-AUG-2000; 2000US-0227395P.
DR	WPI; 2002-698672/75.	PR	24-AUG-2000; 2000US-0227492P.
DR	N-PSDB; ADH48723.	PR	24-AUG-2000; 2000US-0227600P.
XX		PR	14-MAR-2001; 2001US-0275952P.
PT	New NOVX polypeptides or polynucleotides, useful for preventing or	PR	15-AUG-2001; 2001US-00930512.
PT	treating disorders or syndromes e.g., atherosclerosis, hypertension,	XX	
PT	obesity or cancer.	PA	(CURA-) CURAGEN CORP.
XX		XX	
PS	Claim 1; Page 29-30; 923pp; English.	PI	Zerhusen BD, Padigaru M, Spytek KA, Spaderna SK, Gangolli EA;
XX		PI	Rastelli L, Burgess CE, Majumder K, Shinkets R, Mishra V;
CC	The present invention relates to novel human NOVX proteins, where X is	PI	Vernet CAM, Szekeres ES, Grosse WM, Alsobrook JP, Liu X, Gerlach VL;
CC	any number from 1 to 91 and their coding sequences. The proteins and	PI	Ellerman K, Smithson G, Peyman J, Stone D, Macdougall J;
CC	coding sequences are useful for preventing or treating disorders or	XX	
CC	syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV4 is	DR	WPI; 2002-329571/36.
CC	a transient receptor potential-related protein-like protein and its	DR	N-PSDB; ABK48386.
CC	coding sequence maps to chromosome 15.	XX	
XX		PT	Novel cytoplasmic, nuclear membrane bound and secreted NOVX polypeptides,
SQ	Sequence 1856 AA;	PT	useful for treating cancers and tumors, bone disorders, Paget's disease,
		PT	hematopoietic disorders, spinal diseases and immune disorders.
		XX	
		PS	Claim 1; Page 28-29; 234pp; English.
		XX	
		CC	The present invention relates to new isolated NOVX polypeptides named
QY	303 TEEE-INTYKAHLDLEEYRNSRVEKFLFDTKKEILMHL----WR--YPSL--SIHGIE 353	CC	NOV1-NOV9. The invention can be used for identifying an agent (a cellular
Db	84 TEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEVILQLLKEWQMELPKLVISVHGGM 143	CC	receptor or downstream effector) that binds to the polypeptide. The
QY	354 GAFD-EPGKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMT 412	CC	molecules of the invention are useful for treating or preventing NOVX-
Db	144 QKFELHPRIKQLL-GKGLIKAAVTTGAWILTGGVNTGVAKHVGDAL-KEHASRSSRKICT 201	CC	associated disorders in humans. The antibody of the invention is useful
QY	413 LGLHPW--IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTI--PIAKM-FQEIVHKSVVL 467	CC	for determining the presence or amount of NOVX in a sample, and for
Db	202 IGIAPGWGVENRND---LVGR-----DVAAPYQTLNPLSKLVNLLNLSHFIL 247	CC	treating a pathological state in a mammal. The method of the invention is
QY	468 IPLGAVDDGEHSQNEKINR 486	CC	useful for determining the presence of an amount of NOVX in a sample
Db	248 VDDGTV--GKYGAEVRLRR 264	CC	which is used as a marker for cancerous cell or tissue type. The
		CC	molecules of the invention are useful in the manufacture of a medicament
		CC	for treating or preventing cancer, tumour, bone disorders, avascular
		CC	necrosis, allergy, haematopoietic disorders, immune disorders,
		CC	endometriosis, renal diseases, infections, inflammatory diseases, lung
		CC	diseases, scleroderma, ataxia, bowel diseases, appendicitis, blood
		CC	disorders, cardiovascular disorders, ocular disorders, hepatitis C virus
		CC	lymphoedema, brain disorders, cardiac disorders and autosomal dominant deafness (DFNA-2).
		CC	The present amino acid sequence represents the human melastatin-like
		CC	protein NOV3 that is one of the NOVX proteins described in the invention.
		CC	This sequence is encoded by the human melastatin-like protein NOV3 gene
		CC	located on chromosome 15
		XX	
		SQ	Sequence 1864 AA;
			Query Match 3.3%; Score 86.5; DB 5; Length 1864;
			Best Local Similarity 22.1%; Pred. No. 9.4e+02;
			Matches 44; Conservative 42; Mismatches 80; Indels 33; Gaps 13;
		QY	303 TEEE-INTYKAHLDLEEYRNSRVEKFLFDTKKEILMHL----WR--YPSL--SIHGIE 353
		Db	84 TEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEVILQLLKEWQMELPKLVISVHGGM 143
		QY	354 GAFD-EPGKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMT 412
		Db	144 QKFELHPRIKQLL-GKGLIKAAVTTGAWILTGGVNTGVAKHVGDAL-KEHASRSSRKICT 201
		QY	413 LGLHPW--IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTI--PIAKM-FQEIVHKSVVL 467
		OS	Homo sapiens.



Db 202 IGIAPWGVIENRND---LVGR-----DVVAPYQTLNPLSKLNLNLHSHFIL 247

QY 468 IPLGAVDDGEHSQNEKINR 486

Db 248 VDDGTV--GKYGAEVRLRR 264

RESULT 1019

AAE211179

ID AAE211179 standard; protein; 1864 AA.

XX

AC AAE211179;

DT 01-JUL-2002 (first entry)

XX

DE Human TRICH-23 protein.

XX

KW Human; transporter and ion channel; TRICH-23; transport disorder; angina;

KW amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;

KW cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;

KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;

KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;

KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;

KW acquired immune deficiency syndrome; immunological disorder; scleroderma;

KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;

KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;

KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;

KW muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 858..878

FT /note= "Transmembrane domain"

FT Domain 999..1022

FT /note= "Transmembrane domain"

FT Domain 1079..1102

FT /note= "Transmembrane domain"

XX

PN WO200212340-A2.

XX

PD 14-FEB-2002.

XX

PF 01-AUG-2001; 2001WO-US024217.

XX

PR 03-AUG-2000; 2000US-0223269P.

PR 10-AUG-2000; 2000US-0224456P.

PR 18-AUG-2000; 2000US-0226410P.

PR 25-AUG-2000; 2000US-0228140P.

PR 31-AUG-2000; 2000US-0230067P.

PR 08-SEP-2000; 2000US-0231434P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn MR;

PI Yang J, Yao MG, Lal P, Walia NK, Gandhi AR, Hafalia AJA, Nguyen DB;

PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;

PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;

PI Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;

PI Das D, Kallick DA, Khan FA, Seilhamer JJ;

XX

DR WPI; 2002-206330/26.

DR N-PSDB; AAD33668.

XX

PT New human transporters and ion channels polypeptides and polynucleotides

PT for diagnosing, preventing or treating transport, neurological, muscle,

PT immunological and cell proliferative disorders.

XX

PS Claim 67; Page 182-186; 230pp; English.

XX

CC The invention relates to human transporter and ion channel polypeptides

CC designated TRICH and nucleic acid molecules encoding such polypeptides.

CC TRICH sequences are useful for diagnosis, treatment and prevention of

CC transport, muscle, neurological, immunological and cell proliferative

CC disorders. Transport disorders include akinesia, amyotrophic lateral

CC sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular

CC dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,

CC myocarditis, prostate cancer, cardiac disorders associated with transport

CC e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological

CC disorders associated with transport e.g. amnesia, bipolar disorder,

CC depression, Tourette's disorder, schizophrenia, other disorders

CC associated with transport e.g. neurofibromatosis, sickle cell anaemia,

CC Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,

CC goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell

CC proliferated disorders include cancer, actinic keratosis, cirrhosis,

CC arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.

CC Neurological disorders include Alzheimer's, pick's and Parkinson's

CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's

CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,

CC motor neuron disorder, prion disease, metabolic disease of the nervous

CC system and other developmental disorders of the central nervous system,

CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,

CC periodic paralysis, mental disorders including mood, anxiety; and

CC immunological disorders include acquired immune deficiency syndrome

CC (AIDS), adult respiratory distress syndrome, Addison's disease,

CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic

CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,

CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,

CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,

CC haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal,

CC helminthic infections and trauma; and muscle disorders include cardiac

CC myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The

CC TRICH polynucleotides are used in gene therapy. The present sequence is

CC human TRICH-23 protein

XX

SQ Sequence 1864 AA;

Query Match 3.3%; Score 86.5; DB 5; Length 1864;

Best Local Similarity 22.1%; Pred. No. 9.4e+02;

Matches 44; Conservative 42; Mismatches 80; Indels 33; Gaps 13;

QY 303 TEE-INTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHL----WP--YPSL--SINGIE 353

Db 84 TEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEVILQLLKEWQMEPLKLVISVHGGM 143

QY 354 GAFD-EPGKTVIPGRVIGKFSIRLVPHNMVSAVEKQVTRHLEDVFSKRNSSNKQVVSMT 412

Db 144 QKFELHPRIKQLL-GKGLIKAAVTTGAWILTGGVNTGVAKHVGDAL-KEHASRSSRKICT 201

QY 413 LGLHPW--IANIDDTQYLAAKRAIRTVFTEPDMDRGSTI--PIAKM-FQEIVHKSVVL 467

Db 202 IGIAPWGVIENRND---LVGR-----DVVAPYQTLNPLSKLNLNLHSHFIL 247

QY 468 IPLGAVDDGEHSQNEKINR 486

Db 248 VDDGTV--GKYGAEVRLRR 264

RESULT 1020

ABU62065

ID ABU62065 standard; protein; 1864 AA.

XX

AC ABU62065;

XX

DT 04-SEP-2003 (first entry)

XX

DE Human melanoma alpha-kinase (MK).

XX

KW Human; mammalian kinase; melanoma alpha-kinase; MK; HK; KK; SK; LK;

KW heart alpha-kinase; kidney alpha-kinase; skeletal muscle alpha-kinase;

KW lymphocyte alpha-kinase; alpha-kinase catalytic domain;

KW ion channel domain; enzyme.

XX

OS Homo sapiens.

XX







its fragment with a candidate agent, and determining the binding of the candidate agent to the LTRPC7 protein or its fragment. The method of the invention is useful for detecting modulators of LTRPC7 ion channel. LTRPC7 polypeptides are useful as hybridisation probes, in chromosome and gene mapping, and in generating anti-sense RNA and DNA. LTRPC7 nucleic acids may be used in diagnostic applications to detect naturally occurring LTRPC7 nucleic acids

Query Match	3.3%;	Score 86.5;	DB 5;	Length 1865;
Best Local Similarity	22.1%;	Pred. No. 9.4e+02;		
Matches 44;	Conservative 42;	Mismatches 80;	Indels 33;	Gaps 13;

QY	303	TEEE--INTYKAIHLDEEYRNSSRVEKF <del>F</del> LFDTKKEILMHL-----WR--YPSL--SIHGIE	353
Dd	84	TEQSPTDAYGVINFGGSSHSYRAKVYRLSYDTKPEVILQLLLKEWQMELPKLVISVHGM	143
QY	354	GAFD-EPGKTVIPGRVIGKFSIRLVPHMNVS <del>A</del> VEKQVTRHLEDVFSEKRNSSNKVVSMT	412
Dd	144	KFELHPRIKOLL-GKGLIKAAVTTGAWILTGGVNTGVAKHVGDAL-XEHASRSRKICT	201
QY	413	LGLHPW--IANIDDTQYLAakrairtvfgtEpdmiRGSTI--PIAKM-FQEIVHKSVVL	467
Dd	202	IGIAPWGVIENRND---LVGR-----DWAPYOTLLNPLSKLNVLNNLSHFIL	247

Domain	884. .1096	/note= "Transport protein domain"
Domain	923. .941	/note= "Transmembrane (TM) domain 3"
Domain	957. .974	/note= "Transmembrane (TM) domain 4"
Domain	1000. .1016	/note= "Transmembrane (TM) domain 5"
Domain	1036. .1055	/note= "Pore domain"
Domain	1071. .1096	/note= "Transmembrane (TM) domain 6"
Domain	1079. .1137	/note= "Transient receptor domain"
Domain	1127. .1146	/note= "Transmembrane (TM) domain"

WO200210391-A2.

07-FEB-2002.

31-JUL-2001: 2001WO-US024190.

31-JUL-2000: 2000US-0221925P.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ;

WPI; 2002-206190/26.  
N-PSDB: AAD30341.

New human transient receptor polypeptide for diagnosing and treating central nervous system disorders such as cognitive and neurodegenerative disorders, pain and cardiovascular disorders.

Claim 13a; Fig 1; 133pp; English.

The invention relates to human transient receptor (TR-1) polypeptides, designated as 18610 and nucleic acid molecules encoding such polypeptides. Sequence of the invention are useful as modulating agents in regulating various cellular processes, e.g. membrane excitability, neurite outgrowth and synaptogenesis, signal transduction, cell proliferation, growth, differentiation, migration and nociception. They are useful for treating disorders associated with aberrant or unwanted TR-1 expression or activity e.g. an ion channel-associated disorders such as calcium channel associated disorders which include central nervous system (CNS) disorders such as cognitive and neurodegenerative disorders including Alzheimer's disease, dementias, Parkinson's, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis, and epilepsy; autonomic function disorders such as hypertension, sleep disorders and neuropsychiatric disorders such as depression, schizophrenia, mania and anxiety disorders; learning or memory disorders e.g. amnesia, attention deficit disorder, phobias, panic disorder, bipolar affective disorder e.g. severe bipolar affective and bipolar affective neurological disorders e.g. migraine and obesity; pain disorder, cellular proliferation, growth, differentiation or migration disorder, cancer, hepatic disorders, cardiovascular and haematopoietic and/or myeloproliferative disorders. TR-1 polypeptides are also useful as an immunogen. TR-1 polynucleotides are used in gene therapy. The present sequence is human TR-1 protein

Sequence 1885 AA;

Query Match 3.3%; Score 86.5; DB 5; Length 1885;  
Best Local Similarity 22.1%; Pred. No. 9.6e+02;  
Matches 44; Conservative 42; Mismatches 80; Indels 33; Gaps 13;

QY	303	TEEE--INTYKAIHLDEEYRNSRVEKFLDFTKEEILMHL----	WR--YPSL--SIHGIE	353
		: :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :		
D6	84	TEQSPD DAYGVINFGGSHSYRAKYVRLSYDTKPEVILQ LLLKEWQMLPKLVISVHGGM	143	

QV 354 GAFD-EPGKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSM 412

Db 144 QKFELHPRIKQLL-GKGLIKAAVTTGAWILTTGGVNTGVAKHVGDAL-KEHASRSSRKICT 201  
QY 413 LGLHPW--IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTI--PIAKM-FQEIIVHKSVVVL 467  
Db 202 IGIAPWGVIENRND---LVGR-----DVAAPYQTLNPLSKLNVLNLDHSHFIL 247  
QY 468 IPLGAVDGGEHSQNEKINR 486  
Db 248 VDDGTV--GKYGAEVRLRR 264

RESULT 1025  
ADE31711  
ID ADE31711 standard; protein; 1885 AA.

KW Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;  
KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;  
KW cardiovascular; disorder; ischaemia; aortic bending;  
KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;  
KW angina; cardiomyopathy; cardiac death.

OS Homo sapiens.

PN WO2003065984-A2.

PD 14-AUG-2003.

PF 29-JAN-2003: 2003WO-US002571.

PR 01-FEB-2002; 2002US-0353224P.

PR 15-MAR-2002; 2002US-0364529P.

PR 19-APR-2002; 2002US-0373861P.

PR 29-APR-2002; 2002US-0376287P.

PR 12-JUN-2002; 2002US-0388080P.  
 24 JUN 2002; 2002US-0388080P.  
 24 JUN 2002; 2002US-0388080P.

FR 24-JUN-2002; 2002US-03909/IF.  
PB 03-JUL-2002; 2002US-0394130P

PR 10-JUL-2002: 2002US-0394797P

PR 21-AUG-2002: 2002US-0404904P.

PR 23-AUG-2002; 2002US-0405450P.

PR 04-SEP-2002; 2002US-0408070P.

PR 06-NOV-2002; 2002US-0424300P.

PR 05-DEC-2002; 2002US-0431042P.

PR 05-DEC-2002; 2002US-0431079P.  
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PA (MILL.) MILL. ENTITUM PHARM INC

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PI Loqan TJ, Chun M, Galvin KM

DR WPI: 2003-731468/69.

DR N-PSDB; ADE31710.

PT Identifying a compound capable of treating a cardiovascular disorder  
PT (e.g. atherosclerosis) comprises assaying the ability of the compound to  
PT modulate the expression or activity of e.g. 1682, 6169 or 6193  
PT polypeptide or nucleic acid.

PS Disclosure; SEQ ID NO 68; 328pp; English.

The invention relates to a method for identifying a compound capable of treating a cardiovascular disorder. The present invention identifies the differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216, 43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,









CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytotstatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 304 AA;

Query Match 3.3%; Score 86; DB 7; Length 304;  
Best Local Similarity 22.1%; Pred. No. 63;  
Matches 81; Conservative 37; Mismatches 107; Indels 142; Gaps 20;

QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MAPRRVRSFLRGLPALLLLL---LFLGPWPAAS-----HGGKYSR-----E 38

QY 61 SDSVQVPV-RFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIG 119  
Db 39 KNQPKPSPKRESGEEFRM-----EKLNLWEK-----AQRLLHLPVRLAEIH 80

QY 120 SDPTKGTVCFYGHLDVQPAD-----RGDGWLT-----PYVLTE--VDGKLY 159  
Db 81 AD-----LKIQRDELAWKLLKLDGLDEGEKEARLIRNLNVLAKYGLDGKKD 129

QY 160 GRGATDNKGPVLAWINAVSAFRALEQDLFPVNIKFIEGMEEG--SVALEELVEKEK-DR 216  
Db 130 ARQVTSNS-----LSGTQEDGLDDPRLEKLMWHKAKTSG 162

QY 217 FFSGVYIVISDNLWISQKPAITYGTRGNSY-FMVEVKCRDQDFHSGTF-----G 266  
Db 163 KFSGEEL---DKLW----REFLHKKEKVHEYNVLETLSTRTEIHNENIVSPDLSDIKG 214

QY 267 GILHEPMADLVALIGSL-----VDSSGHILVPGIYDEVVPLTEETINYYKAIHL-D 316  
Db 215 SVLHSRHTELKEKLSINQGLDRLRRVSHQY-----STEAETEEPRVIDLWD 262

QY 317 LEEYRNS 323  
Db 263 LAQSANS 269

RESULT 1031  
ABP27121  
ID ABP27121 standard; protein; 330 AA.  
XX  
AC ABP27121;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 3418.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB004789.  
XX  
PR 27-OCT-2000; 2000GB-00026333.  
PR 24-NOV-2000; 2000GB-00028727.  
PR 07-MAR-2001; 2001GB-00005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;  
PI Tettelin H;  
XX

DR WPI; 2002-352536/38.  
DR N-PSDB; ABN67752.  
XX  
PT New Streptococcus protein for the treatment or prevention of infection or  
PT disease caused by Streptococcus bacteria, such as meningitis, and for  
PT detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 3495; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins  
XX  
SQ Sequence 330 AA;

Query Match 3.3%; Score 86; DB 5; Length 330;  
Best Local Similarity 22.2%; Pred. No. 72;  
Matches 60; Conservative 46; Mismatches 82; Indels 82; Gaps 15;

QY 80 VAADTLQ--RLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPTKGTVCFYGHLDVQP 137  
Db 118 VAANIIKESKDGIKALPEDLNVE---ETAATEKVVNALQGAIPA-CTVIGDGKLIKIN- 171

QY 138 ADRGDGWLTDPPVLTETVDGK-LYGRGATDNKGPVLAWINAVSAFRALE---EQDLPV 189  
Db 172 -----LARVDTRLHGGVAT-----AWTPASKADRIIVASDEVAQDDLK 211

QY 190 N-IKFIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSY 248  
Db 212 QLIKQAAFGVKANVVPISKLEASKDPRF-----GNTH 245

QY 249 FMVEVKCRDQDFHSGTFGGI-LHEPMADLVALIGSLVDSSGHILVPGIYDEVVPLTEEEI 307  
Db 246 ALILFQ-TPQDALRAVEGGVEINE-----LNVGSMASHSTGKTMV---NNVLSMDKEDV 294

QY 308 NTYK-----AIHLDLEEYRNSRVEKFLFD 332  
Db 295 ATFEKRLDLGVTFDVRKVPNDK--KNLFE 322

RESULT 1032  
ABU46776  
ID ABU46776 standard; protein; 330 AA.  
XX  
AC ABU46776;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #32303.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
PF 21-MAR-2002; 2002WO-US009107.





Query Match 3.3%; Score 86; DB 5; Length 334;  
Best Local Similarity 23.3%; Pred. No. 73;  
Matches 60; Conservative 29; Mismatches 95; Indels 74; Gaps 14;  
QY 133 LDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNK---GPVLAWINAVSAFRALEQDLP 188  
Db 91 LSARPFKYATEWSPEEY--HTADSIILATGASARRLHLPGECKYWQNGISACAVCDGAVP 148  
QY 189 V--NIKFIIEGMEEGSVALEE-----LVEKEKDRFFSGVDYIVISDNLWIS 233  
Db 149 IFRNKHLVVIG---GGDSAEEAMYLTKYGSHTVTLVRKDKLRASS-----IMAHRLLN 199  
QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHS-----GTFGGILHEPMAD 275  
Db 200 HEKVTVRFTNVG-----VEVKGDDKGLMSHLVVKDVTGKETEANGLEFYAIGHDPATA 254  
QY 276 LVALLGSL-VDSSGHILV-PGIYDEVVPLTEEEINTYKAHLDLEEYRNSR----- 325  
Db 255 LVK--GOLETDADGYVVTKPG-----TTLTSVE-GVFAAGDVQDKRYRQAITSAGTGCMA 306  
QY 326 ---VEKFLFDTKEEILMH 340  
Db 307 ALDAEKFLSEHEETPAEH 324

RESULT 1034  
AAO20620  
ID AAO20620 standard; protein; 334 AA.  
XX AAO20620;  
XX  
DT 10-APR-2003. (first entry)  
XX  
DE  
XX  
KW Thioredoxin reductase variant protein sequence #19.

XX Ophthalmological; virucide; vulnery; vasotropic; antiallergic;  
KW cofactor specificity; thioredoxin reductase; TR; non-allergenic food;  
KW computational mutagenesis; scaffold protein; oil body; animal feed;  
KW digestibility; gluten; protein disulfide isomerase; PDI; enzyme;  
KW scleroprotein; gelled; food; nitrosative stress response; eye disease;  
KW cataract; oxidative stress; ischemic-reperfusion; acute lung injury.  
XX Neurospora crassa.  
XX  
PN WO200290300-A2.  
XX  
PD 14-NOV-2002.  
XX  
PF 06-MAY-2002; 2002WO-US014358.  
XX  
PR 04-MAY-2001; 2001US-0289029P.  
PR 05-APR-2002; 2002US-0370609P.  
PR 29-APR-2002; 2002US-00370609.

XX (XENC-) XENCOR.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;  
PI Luginbuhl P, Muchhal U;  
XX  
XX WPI; 2003-111951/10.  
XX

PT Altering cofactor specificity of target protein, e.g. thioredoxin  
PT reductase, useful for reducing antigenicity of glutens in wheat, barley,  
PT or treating disulfide linkages present in proteins, by computational  
PT mutagenesis.  
XX  
PS Disclosure; Fig 21D; 212pp; English.  
XX  
CC The invention relates to a novel method for altering the cofactor  
CC specificity of a target protein (e.g. thioredoxin reductase (TR)) by  
CC computational mutagenesis. This method involves inputting a set of

CC coordinates for a scaffold protein comprising amino acid positions,  
CC applying at least one protein design cycle; and generating a set of  
CC candidate variant proteins with altered cofactor specificity. The novel  
CC method is useful for altering the cofactor specificity of TR scaffold  
CC proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium  
CC leprae, Saccharomyces, Neurospora crassa, Arabidopsis, and human. Another  
CC method of the invention is useful for making oil bodies which are useful  
CC in the preparation of non-allergenic foods, or in the preparation of  
CC animal feeds to improve the digestibility of the feeds. The variant TR  
CC protein is useful for reducing the antigenicity of glutens in wheat, rye  
CC or barley, to reduce alternative substrates for thioredoxin reductases,  
CC including a number of plant and mammalian proteins found to contain  
CC thioredoxin domains e.g. protein disulfide isomerase (PDI). The variant  
CC TR protein is useful as a redox partner in compositions used for treating  
CC disulfide linkages present in proteins such as enzymes, e.g., proteases,  
CC amylases, etc; and structural proteins such as scleroproteins.  
CC Compositions comprising variant TR proteins and PDI are useful for  
CC generating protein disulfide crosslinks yielding high molecular weight or  
CC gelled compositions, and thus is useful in food processing. A further  
CC method of the invention is useful for producing plants expressing variant  
CC TR protein, e.g., corn and soybean provides grains with altered storage  
CC protein quality as well as grains that perform qualitatively different  
CC from normal grain during industrial processing or animal digestion of  
CC variant TR proteins in combination with thioredoxin, which can be used to  
CC manipulate nitrosative stress, to upregulate nitrosative stress  
CC responses, and thus is useful for treating eye diseases, such as  
CC cataracts, where it inhibits or reverse formation of cataract in eye. The  
CC variant TR protein in combination with thioredoxin is also useful for  
CC minimizing oxidative stress and ischemic-reperfusion induced in acute  
CC lung injury. This sequence represents a thioredoxin reductase variant  
CC protein of the invention  
XX  
SQ Sequence 334 AA;

Query Match 3.3%; Score 86; DB 6; Length 334;  
Best Local Similarity 23.3%; Pred. No. 73;  
Matches 60; Conservative 29; Mismatches 95; Indels 74; Gaps 14;  
QY 133 LDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNK---GPVLAWINAVSAFRALEQDLP 188  
Db 91 LSARPFKYATEWSPEEY--HTADSIILATGASARRLHLPGECKYWQNGISACAVCDGAVP 148  
QY 189 V--NIKFIIEGMEEGSVALEE-----LVEKEKDRFFSGVDYIVISDNLWIS 233  
Db 149 IFRNKHLVVIG---GGDSAEEAMYLTKYGSHTVTLVRKDKLRASS-----IMAHRLLN 199  
QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHS-----GTFGGILHEPMAD 275  
Db 200 HEKVTVRFTNVG-----VEVKGDDKGLMSHLVVKDVTGKETEANGLEFYAIGHDPATA 254  
QY 276 LVALLGSL-VDSSGHILV-PGIYDEVVPLTEEEINTYKAHLDLEEYRNSR----- 325  
Db 255 LVK--GOLETDADGYVVTKPG-----TTLTSVE-GVFAAGDVQDKRYRQAITSAGTGCMA 306  
QY 326 ---VEKFLFDTKEEILMH 340  
Db 307 ALDAEKFLSEHEETPAEH 324

RESULT 1035  
AAO20629  
ID AAO20629 standard; protein; 334 AA.  
XX  
AC AAO20629;  
XX  
DT 10-APR-2003 (first entry)  
XX  
DE Thioredoxin reductase variant protein sequence #28.  
XX  
KW Ophthalmological; virucide; vulnery; vasotropic; antiallergic;  
KW cofactor specificity; thioredoxin reductase; TR; non-allergenic food;  
KW computational mutagenesis; scaffold protein; oil body; animal feed;  
KW digestibility; gluten; protein disulfide isomerase; PDI; enzyme;







CC to a second protein (that is either a wild-type TRR protein, thioredoxin,  
CC or a variant TRR protein), producing a plant with a modified TRR protein,  
CC a transformed plant prepared by the method and a transformed seed of the  
CC transformed plant. The cofactor specificity of the variant TRR is altered  
CC such that the variant preferentially binds NADPH compared to NADH, or  
CC vice versa. The protein design cycle comprises protein design automation  
CC (PDA (RTM)). This design cycle comprises the sequence design algorithm,  
CC or a force field calculation. The variant TRR protein is fused to the  
CC second protein through a linker. The variant TRR protein has 1-3 amino  
CC acid substitutions as compared to the wild-type Arabidopsis TR protein.  
CC The amino acid substitutions are selected from positions A4, A5 and A6,  
CC preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5V, RA5Y, RA6T, RA68,  
CC RA6Q, RA6g, and RA6N. The method is useful for reducing the toxicity of  
CC toxic proteins, reducing allergenicity of food and increasing the  
CC digestibility of food. The invention provides an efficient and low cost  
CC method as compared to prior art. The present sequence is a wild-type TRR  
CC protein.

XX  
SQ Sequence 334 AA;

Query Match 3.3%; Score 86; DB 7; Length 334;

Best Local Similarity 23.3%; Pred. No. 73;

Matches 60; Conservative 29; Mismatches 95; Indels 74; Gaps 14;

QY 133 LDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNK---GPVLAWINAVSAFRALEQDLP 188  
Db 91 LSARPFKYATEWSPEEY--HTADSIILATGASARRLHLPGEKEYWQNGISACAVCDGAVP 148  
QY 189 V--NIKFIIEGMEEGAGSVALEE-----LVEKEKDRFFSGVDYIVISDNLWIS 233  
Db 149 IFRNKHLLVVG---GGDSAAEEAMYLTKYGSHTVTLVRKDKLRASS-----IMAHRLLN 199  
QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHS-----GTFGGILHEPMAD 275  
Db 200 HEKVTVRFTVG-----VEVKGDDKGLMSHLVVKDVTTGKEETLEANGLFYAIGHDPATA 254  
QY 276 LVALLGSL-VDSSGHILV-PGIYDEVVPLTEEEINTYKAHLDLEEYRNSR----- 325  
Db 255 LVK--GQLETDADGYVVTKPG-----TTLTSVE-GVFAAGDVQDKRYRQAITSAGTGCMA 306  
QY 326 ---VEKFLFDTKEEILMH 340  
Db 307 ALDAEKFLSEHEETPAEH 324

RESULT 1037

ID ADM30945 standard; protein; 334 AA.

XX ADM30945;

XX 20-MAY-2004 (first entry)

DT N. crassa TK protein.

DE thioredoxin; thioredoxin reductase; oil body; non-allergenic food;

XX non-allergenic animal feed; feed digestibility; radical scavenger;

XX stress; injury; oxidative stress; eye disease; cataract.

OS Neurospora crassa.

XX US2003211511-A1.

PN 13-NOV-2003.

PD 06-NOV-2002; 2002US-00290072.

XX 04-MAY-2001; 2001US-0289029P.

PR 05-APR-2002; 2002US-0370609P.

PR 29-APR-2002; 2002US-0376682P.

PR 06-MAY-2002; 2002US-00141531.

XX (BRIG/) BRIGGS S P.

PA (DALM/) DALMIA B K.  
PA (DVAL/) DEL VAL G.  
PA (DESJ/) DESJARLAIS J R.  
PA (HEIF/) HEIFETZ P.  
PA (LUGI/) LUGINBUHL P.  
PA (MUCH/) MUCHHAL U.

PI Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;  
PI Luginbuhl P, Muchhal U;  
XX WPI; 2004-010666/01.

PT New thioredoxin protein and thioredoxin reductase protein fusion  
PT polypeptide, useful as a radical scavenger, for making oil bodies in  
PT preparing non-allergenic food, and in preventing or treating diseases  
PT caused by oxidative stress.

PS Disclosure; SEQ ID NO 68; 140pp; English.

XX

CC The invention relates to a fusion polypeptide comprising a thioredoxin  
CC protein and a thioredoxin reductase protein. The thioredoxin protein and  
CC thioredoxin reductase protein are selected from the group of Escherichia  
CC coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces, Neurospora  
CC crassa, Arabidopsis or human. The thioredoxin reductase is a wild type  
CC protein or a variant thioredoxin reductase protein, where the cofactor  
CC specificity of the variant thioredoxin reductase protein is NADPH or  
CC NADH. The fusion polypeptide is useful for making oil bodies, which are  
CC used in the preparation of non-allergenic food and animal feeds to  
CC improve the digestibility of the feeds (claimed). The fusion polypeptide  
CC is also useful as a radical scavenger, in protection against stress and  
CC injury, and in prevention or treatment of diseases caused by oxidative  
CC stress or eye diseases such as cataracts. The present sequence is used in  
CC the exemplification of the present invention.

XX Sequence 334 AA;

Query Match 3.3%; Score 86; DB 8; Length 334;

Best Local Similarity 23.3%; Pred. No. 73;

Matches 60; Conservative 29; Mismatches 95; Indels 74; Gaps 14;

QY 133 LDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNK---GPVLAWINAVSAFRALEQDLP 188  
Db 91 LSARPFKYATEWSPEEY--HTADSIILATGASARRLHLPGEKEYWQNGISACAVCDGAVP 148  
QY 189 V--NIKFIIEGMEEGAGSVALEE-----LVEKEKDRFFSGVDYIVISDNLWIS 233  
Db 149 IFRNKHLLVVG---GGDSAAEEAMYLTKYGSHTVTLVRKDKLRASS-----IMAHRLLN 199  
QY 234 QRKPAITYGTRGNSYFMVEVKCRDQDFHS-----GTFGGILHEPMAD 275  
Db 200 HEKVTVRFTVG-----VEVKGDDKGLMSHLVVKDVTTGKEETLEANGLFYAIGHDPATA 254  
QY 276 LVALLGSL-VDSSGHILV-PGIYDEVVPLTEEEINTYKAHLDLEEYRNSR----- 325  
Db 255 LVK--GQLETDADGYVVTKPG-----TTLTSVE-GVFAAGDVQDKRYRQAITSAGTGCMA 306  
QY 326 ---VEKFLFDTKEEILMH 340  
Db 307 ALDAEKFLSEHEETPAEH 324

RESULT 1038

AAM52357

ID AAM52357 standard; protein; 363 AA.

XX AAM52357;

XX 25-JAN-2002 (first entry)

DT NDP-hexose pyrophosphorylase homolog.

XX Geminivirus; plant; viral infection; transgenic plant;

DE tomato yellow leaf curl virus.

XX

KW

XX OS Schizosaccharomyces pombe.  
XX PN FR2806095-A1.  
XX PD 14-SEP-2001.  
XX PF 10-MAR-2000; 2000FR-00003140.  
XX PR 10-MAR-2000; 2000FR-00003140.  
XX PA (GENT-) GENTECH SARL.  
XX PI Bejarano ER, Castillo GA, Colinet D, Donoso CI, Iniesta JR;  
PI Grevesse C, Hericourt F;  
XX WPI; 2001-628275/73.  
DR N-PSDB; ABA01227.  
XX New polynucleotides for producing transgenic plants resistant to  
PT geminivirus infection comprising polynucleotides encoding proteins which  
PT interact with at least one of the products of the geminivirus genome.  
XX Claim 4; Page 38-39; 106pp; French.  
XX The present invention relates to coding sequences encoding proteins which  
CC interact with at least one of the six products of the geminivirus genome  
CC necessary for infection of a plant by the virus. The present sequence is  
CC one such protein. The coding sequences are useful for producing  
CC transgenic plants resistant to geminivirus infection, particularly tomato  
CC yellow leaf curl virus  
XX Sequence 363 AA;  
SQ  
Query Match 3.3%; Score 86; DB 4; Length 363;  
Best Local Similarity 20.4%; Pred. No. 83;  
Matches 76; Conservative 62; Mismatches 128; Indels 106; Gaps 22;  
QY 148 PYVLTEVDGKLYGRGATDNKGPVLAWIN-----AVSAFRALEQDLPVNIKFIIEG--MEE 200  
Db 32 PMILHQVEA-LAAAGVTD----IVLAVNYRPEIMVEALKKYEKYNVITFSVENEPLGT 86  
QY 201 AGSVAL-EELVEKEKDRFFSGVDYIVISDNLWISQRK-----AITYGTRGNSYFMVEVKC 255  
Db 87 AGPLALARDILAKDHSPPF-----VLNSD---VICEYPFADLAAFHKAHGAEGTIVVTKV 138  
QY 256 RDQDFHSGTFFGILHEPMADL-----VALLGSLVDSSGHILVPGIYDEVVP---LT 303  
Db 139 EE-----PSKYGVVVHYPNSESLIERFVEKPFVFSNRINGGIYILNPSVLDRIEPRPTSI 194  
QY 304 EEE-----INTYKAHLDLEEY-RNSSRVEKFLFDT-----KKEILMHLWRYPSL 347  
Db 195 EKEVFPAMVNDKQLHSFDLEGYWMVGQPKDYLTGTCLYLSSLRKHKPEIL-----245  
QY 348 SIHGIEGAFDEPGTKTVI-----PGRVIGKFSIRLVPHM-----NVSAVEKQVTRHLEDV 397  
Db 246 -----APASSNIIGNVLIDPSATIGK-NCKIGPNVVIGPNVTIGDGVRLQRCAIL 294  
QY 398 FSKRNSNKMVVSMTLG---LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 295 KSSRVRDHAWKSSIVGWNSTLGSW-SRLENVSVLG-----DDVVVNDEIYVNGGSILP- 347  
QY 454 AKMFQEIYVHKSV 465  
Db 348 -----HKSI 351  
RESULT 1039  
ABG91574  
ID ABG91574 standard; protein; 363 AA.  
XX  
AC ABG91574;  
XX

DT 18-NOV-2002 (first entry)  
XX Purine/pyrimidine triphosphate type nucleotidyltransferase #159.  
DE  
XX Nucleotidyltransferase; enzyme; active site engineering;  
KW alpha-D-glucopyranosyl phosphate thymidyltransferase; Ep;  
KW substrate specificity; nucleotide sugar;  
KW glycosylated bioactive natural product.  
XX Vibrio cholerae.  
OS  
XX WO200248331-A2.  
PN  
XX 20-JUN-2002.  
PD  
XX 13-DEC-2001; 2001WO-US047953.  
PF  
XX 13-DEC-2000; 2000US-0254927P.  
PR  
XX (SLOK ) SLOAN KETTERING INST CANCER RES.  
PA  
XX Thorson JS, Nikilov DB;  
PI  
XX WPI; 2002-608282/65.  
DR  
XX Nucleotidyltransferase mutated at one or more amino acids, useful in  
PT the synthesis of nucleotide sugars.  
PT  
XX Claim 3; Page; 182pp; English.  
PS  
XX The invention relates to a Nucleotidyltransferase mutated at one or  
CC more amino acids selected from V173, G147, W224, N112, G175, D111, E162,  
CC T201, I200, E199, R195, L89, L89T, L109, Y146 or Y177 (with reference to  
CC the Salmonella enterica rmlA-encoded alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase, Ep, enzyme appearing as ABG91798). The mutations  
CC alter the substrate specificity of the enzymes. The mutants and methods  
CC involving them are used in the synthesis of nucleotide sugars for  
CC altering nucleotidyltransferase substrate specificity. The  
CC nucleotidyltransferase exhibits different substrate specificity for  
CC GTP, CTP, TTP, UTP and ATP than a non-mutated nucleotidyltransferase.  
CC The mutant may also exhibit a high degree of sequence identity to  
CC Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase (Ep) and can convert a wide variety of phosphates.  
CC The mutants can be exploited in the biosynthesis of glycosylated  
CC bioactive natural products of pharmacological use. The present sequence  
CC is a nucleotidyltransferase exhibiting a high degree of sequence  
CC identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase (Ep). Note: The present sequence is not displayed  
CC in the specification but was obtained from Genbank  
XX  
SQ Sequence 363 AA;  
Query Match 3.3%; Score 86; DB 5; Length 363;  
Best Local Similarity 20.4%; Pred. No. 83;  
Matches 76; Conservative 62; Mismatches 128; Indels 106; Gaps 22;  
QY 148 PYVLTEVDGKLYGRGATDNKGPVLAWIN-----AVSAFRALEQDLPVNIKFIIEG--MEE 200  
Db 32 PMILHQVEA-LAAAGVTD----IVLAVNYRPEIMVEALKKYEKYNVITFSVENEPLGT 86  
QY 201 AGSVAL-EELVEKEKDRFFSGVDYIVISDNLWISQRK-----AITYGTRGNSYFMVEVKC 255  
Db 87 AGPLALARDILAKDHSPPF-----VLNSD---VICEYPFADLAAFHKAHGAEGTIVVTKV 138  
QY 256 RDQDFHSGTFFGILHEPMADL-----VALLGSLVDSSGHILVPGIYDEVVP---LT 303  
Db 139 EE-----PSKYGVVVHYPNSESLIERFVEKPFVFSNRINGGIYILNPSVLDRIEPRPTSI 194  
QY 304 EEE-----INTYKAHLDLEEY-RNSSRVEKFLFDT-----KKEILMHLWRYPSL 347  
Db 195 EKEVFPAMVNDKQLHSFDLEGYWMVGQPKDYLTGTCLYLSSLRKHKPEIL-----245  
QY 348 SIHGIEGAFDEPGTKTVI-----PGRVIGKFSIRLVPHM-----NVSAVEKQVTRHLEDV 397

Db 246 -----APASSNIIGNVLIDPSATIGK-NCKIGPNVVIGPNVTIGDGVRLQRCAIL 294  
QY 398 FSKRNSSNKMVVSMTLG----LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 295 KSSRVRDHAWVKSSIVGWNSTLGSW-SRLENVSVLG-----DDVVVNDEIYVNGGSILP- 347  
QY 454 AKMFQEIIVHKSIV 465  
Db 348 -----HKSI 351  
  
RESULT 1040  
ABG91573  
ID ABG91573 standard; protein; 363 AA.  
XX  
AC ABG91573;  
XX  
DT 18-NOV-2002 (first entry)  
XX  
DE Purine/pyrimidine triphosphate type nucleotidyltransferase #158.  
XX  
KW Nucleotidyltransferase; enzyme; active site engineering;  
KW alpha-D-glucopyranosyl phosphate thymidyltransferase; Ep;  
KW substrate specificity; nucleotide sugar;  
KW glycosylated bioactive natural product.  
XX  
OS Schizosaccharomyces pombe.  
XX  
PN WO200248331-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 13-DEC-2001; 2001WO-US047953.  
XX  
PR 13-DEC-2000; 2000US-0254927P.  
XX  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX  
PI Thorson JS, Nikilov DB;  
XX  
WPI; 2002-608282/65.  
DR  
XX  
PT Nucleotidyltransferase mutated at one or more amino acids, useful in  
PT the synthesis of nucleotide sugars.  
XX  
PS Claim 3; Page; 182pp; English.  
XX  
CC The invention relates to a Nucleotidyltransferase mutated at one or  
CC more amino acids selected from V173, G147, W224, N112, G175, D111, E162,  
CC T201, I200, E199, R195, L89, L89T, L109, Y146 or Y177 (with reference to  
CC the Salmonella enterica rmlA-encoded alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase, Ep, enzyme appearing as ABG91798). The mutations  
CC altering the substrate specificity of the enzymes. The mutants and methods  
CC involving them are used in the synthesis of nucleotide sugars for  
CC altering nucleotidyltransferase substrate specificity. The  
CC nucleotidyltransferase exhibits different substrate specificity for  
CC GTP, CTP, TTP, UTP and ATP than a non-mutated nucleotidyltransferase.  
CC The mutant may also exhibit a high degree of sequence identity to  
CC Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase (Ep) and can convert a wide variety of phosphates.  
CC The mutants can be exploited in the biosynthesis of glycosylated  
CC bioactive natural products of pharmacological use. The present sequence  
CC is a nucleotidyltransferase exhibiting a high degree of sequence  
CC identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase (Ep). Note: The present sequence is not displayed  
CC in the specification but was obtained from Genbank  
XX  
SQ Sequence 363 AA;  
  
Query Match 3.3%; Score 86; DB 5; Length 363;  
Best Local Similarity 20.4%; Pred. No. 83;  
Matches 76; Conservative .62; Mismatches 128; Indels 106; Gaps 22;

QY 148 PYVLTEVDGKLYGRGATDNKGPVLAWIN-----AVSAFRALEQDLPVNIKFIIEG--MEE 200  
Db 32 PMILHQVEA-LAAAGVTD---IVLAVNYRPEIMVEALKKYEKNVNITFSVENEPLGT 86  
QY 201 AGSVAL-EELVEKEKDRFFSGVDYIVISDNLWISQRKP---AITYGTRGNSYFMVEVKC 255  
Db 87 AGPLALARDILAKDHSPPF-----VLNSD---VICEYPFADLAAAFKHAHGAEGTIVVTKV 138  
QY 256 RDQDFHSGTFGGILHEPMADL-----VALLGSLVDSSGHILVPGIYDEVVP---LT 303  
Db 139 EE---PSKYGVVVVHYPNSES LIERFVEKPVFEVFSNRINGGIYILNPSVLDRIEPRPTSI 194  
QY 304 EEE-----INTYKAIHLDLLEY-RNSSRVEKFLFDT-----KEEILMHLWRYPSL 347  
Db 195 EKEVFPAMVNDKQLHSFDLEGYWMDVGQPKDYLTGTCLYLSLRKHKPEIL----- 245  
QY 348 SIHGIEGAFDEPGTKTVI-----PGRVIGKFSIRLVPHM-----NVSAREKQVTRHLEDV 397  
Db 246 -----APASSNIIGNVLIDPSATIGK-NCKIGPNVVIGPNVTIGDGVRLQRCAIL 294  
QY 398 FSKRNSSNKMVVSMTLG---LHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 295 KSSRVRDHAWVKSSIVGWNSTLGSW-SRLENVSVLG-----DDVVVNDEIYVNGGSILP- 347  
QY 454 AKMFQEIIVHKSIV 465  
Db 348 -----HKSI 351  
  
RESULT 1041  
AAB14144  
ID AAB14144 standard; protein; 381 AA.  
XX  
AC AAB14144;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Bordetella pertussis class II gene protein Orf13.  
KW Orf13; bacterial infection; anti-bacterial; vaccine; whooping cough;  
KW type III secretion system; virulence factor; pathogenicity island.  
XX  
OS Bordetella pertussis.  
XX  
PN WO200037493-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 21-DEC-1999; 99WO-EP010297.  
XX  
PR 21-DEC-1998; 98GB-00028217.  
XX (ULBR ) UNIV LIBRE BRUXELLES.  
XX  
PI Bollen A, Fauconnier A, Godfroid E;  
XX  
DR WPI; 2000-452178/39.  
DR N-PSDB; AAA64882, AAA64890.  
XX  
PT Novel polypeptides derived from Bordetella pertussis, useful for treating  
PT and diagnosing Bordetella infection.  
XX  
PS Claim 1; Page 145-146; 165pp; English.  
XX  
CC Bordetella pertussis possesses a type III secretion system. Type III  
CC secretion systems allow bacteria to target virulence factors directly at  
CC host cells. The present sequence is the Orf13 protein of B. pertussis.  
CC The present protein is encoded by a Class II type gene and is an effector  
CC protein involved in the type III secretion system of B. pertussis i.e. a  
CC Bordetella pathogenicity protein. The gene of the present protein is  
CC located within a pathogenicity island (see AAA64890). A pathogenicity  
CC island is a compact, distinct genetic unit carrying virulence genes. The







XX PN EP1188826-A2.  
XX PD 20-MAR-2002.  
XX PF 09-AUG-2001; 2001EP-00119275.  
XX PR 13-SEP-2000; 2000JP-00278571.  
XX PR 08-MAR-2001; 2001JP-00065815.  
XX PA (AJIN ) AJINOMOTO CO INC.  
XX PI Suzuki S, Onishi N, Yokozeki K;  
XX DR WPI; 2002-510588/55.  
XX DR N-PSDB; ABN86381, ABN86383.  
XX PT New 5-substituted hydantoin racemase, useful in production of optically  
PT active amino acids, comprises high working temperature, from  
PT Microbacterium species.  
XX PS Disclosure; Page 23-25; 40pp; English.  
XX CC The invention relates to a 5-substituted hydantoin racemase (Hrase) that  
CC is derived from a Microbacterium by culture, disruption or lysis, and  
CC purification. Hrase has a high working temperature of 5-60 plusOC and is  
CC used to racemize optically active 5-substituted hydantoins for subsequent  
CC enzymatic conversion to N-carbamoyl-amino acids and then optically active  
CC amino acids (useful in pharmaceuticals, the chemical industry and as food  
CC additives). The present sequence represents the M. liquefaciens  
CC hydantoinase (Hhase) enzyme  
XX SQ Sequence 459 AA;  
Query Match 3.3%; Score 86; DB 5; Length 459;  
Best Local Similarity 20.6%; Pred. No. 1.2e+02;  
Matches 76; Conservative 55; Mismatches 112; Indels 126; Gaps 21;  
QY 8 MAASLLAVLLLLLLERGMFSSPPPPALLEKVFQ-----YIDLHQDEFVQTL----- 53  
Db 150 MAASV-----PGMFEAVD--DQQLFEIFQEIAACGSVIVVHAENEMLIQTLQKQLK 198  
QY 54 ----KEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASV----- 95  
Db 199 AAGRKDLAAVEAS--QPVFQENEAIQRALLLQKEA----GCLIVVHVSNPGGVELIHKA 252  
QY 96 -----DMGPQQL-----IPPVILAEKSDPTKGTVCF-----YGH 133  
Db 253 QSEGQDVHCEGSPQYLNLTMDDAEKVGPYMKIAPPVRSaelna-----VLWEQLEKGYI 306  
QY 134 DVQPADRGDGLWTDYPVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKF 193  
Db 307 DTLGSDHGG-----HPVENK-----EGGWDD-----IW-TASNGALGLETSLPM---M 345  
QY 194 IIEGMEEAGSVALEELVEKEKORFFSGVDYIVISDN----LWISQRKPAITYGTRGNSYF 249  
Db 346 LTNGVNK-GRVSLERLVE-----VMCENPAKLFGIYPQKGTQLQVGSAD-LL 390  
QY 250 MVEVKCRDQDFHSGTGGILHEPMAD-----LVALLGSLVDSSGHILVPGIYDEVV 300  
Db 391 ILDLIEIEDRKVDASQFRSLHYSPFDGRPPVTGAPVLTMRGTVVQADGEILVDQGFQFV 450  
QY 301 PLTEEEINT 309  
Db 451 TRRDSEVSS 459  
RESULT 1046  
ADG33838  
ID ADG33838 standard; protein; 467 AA.  
XX  
AC ADG33838;  
XX

DT 26-FEB-2004 (first entry)  
XX Actinomycetes dual condensation/epimerisation NRPS domain protein ID 97.  
DE non-ribosomal peptide synthetase; NRPS; dual condensation; epimerisation;  
XX ramoplanin; complestatin; actinomycetes taxon.  
KW Streptomyces griseofuscus.  
XX WO2003089641-A2.  
XX 30-OCT-2003.  
XX 17-APR-2003; 2003WO-CA000575.  
XX 17-APR-2002; 2002US-0372790P.  
XX (ECOP-) ECOPIA BIOSCIENCES INC.  
XX Farnet CM, Staffa A;  
XX WPI; 2003-854123/79.  
XX N-PSDB; ADG33839.  
XX New dual condensation/epimerization non-ribosomal peptide synthetase  
PT domain and encoding polynucleotide, useful for modifying the  
PT stereochemistry of synthesized peptides (e.g. ramoplanin or complestatin)  
PT in vitro or in vivo.  
XX Claim 9; SEQ ID NO 97; 245pp; English.  
XX This invention relates to novel domains of non-ribosomal peptide  
CC synthetases (NRPSs) that exhibit dual condensation and epimerisation  
CC activities. Specifically, these domains allow incorporation of non-  
CC proteinogenic substrates (e.g. D-amino acids) into peptide products.  
CC Furthermore, they can be used in vivo to modify the stereochemistry of  
CC synthesized peptides (e.g. ramoplanin or complestatin) at selected amino  
CC acid sites by the addition of non-chiral residues. The present invention  
CC describes the identification of isolated polynucleotide NRPS domains in  
CC various organisms from the actinomycetes taxon, and the encoded  
CC polypeptides thereof, as well as suitable expression vectors. This  
CC polypeptide sequence is a dual condensation/ epimerisation NRPS domain  
CC protein of the invention.  
XX SQ Sequence 467 AA;  
Query Match 3.3%; Score 86; DB 7; Length 467;  
Best Local Similarity 19.2%; Pred. No. 1.2e+02;  
Matches 97; Conservative 77; Mismatches 173; Indels 158; Gaps 27;  
QY 34 LLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVA 93  
Db 48 VLQKV---VDRH--DILRTAVLWEGLR-EPVQVVCRRHAILFR----- 84  
QY 94 SVDMPQQLPDGQSLPIPPVILAEKLS--DPTKGTVCFCYGHLDVQPADRGDGLWTDYPVL 151  
Db 85 EVELG--QIPDGDVQGVADGGLLAVRGSLMDITTAPLV---HVTVAEVPGTTRWV----AL 135  
QY 152 TEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELVE 211  
Db 136 VQVHHLIQDHTAVD---VLFAEVQAFLTGRAAEPLTPLPFRNFVAQARLGIPVA----- 186  
QY 212 KEKDRFFSG-----VDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD 257  
Db 187 -EHEAFFTDLLGDVTEPTAPFGIVD--VRGDGTAVAESRAAVSEATAA---AVREAARR 239  
QY 258 QDFHSGTGGILHEPMADLVA-----LLGSLVDSSGHILVPGIYDEVVPLTE 304  
Db 240 LGVSAAT---VLHVMFAWVVAAGREDVVFGLTFCRMOAGAGADRIPGLFINLTPVRL 296  
QY 305 EE-----INTYKAHLDLEEYNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEP 359  
Db 297 DTGRGGVLDVAVRSMQGD L-----AELLVH-----EHA----- 323



Qy 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTL-GL--- 415  
Db 324 -----PLAQAQRMGSVAAEAPLFTAL---FNYRHSAGATDAGMEVEGIEVL 366  
Qy 416 -----HPWIANIDDT--QYLAAKRAIRTVFGTEPDMI--RDGSTIPIAKMFQEIIVHK 463  
Db 367 FAQERTNYPLTVSVDDTGDGFVFTVCVDPI---DPDLVLSLMDTATGRLVQALDDAPGT 423  
Qy 464 SVVLIPLGAVDDGEGHSQNEKINRW 488  
Db 424 PLHTLP---VLDDTH-LNQVLTRWN 444

RESULT 1047  
ADS28136  
ID ADS28136 standard; protein; 468 AA.  
XX  
AC ADS28136;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #17169.  
XX

KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX

OS Bacteria.  
XX  
XX US2003233675-A1.  
PN  
XX

PD 18-DEC-2003.  
XX  
XX 20-FEB-2003; 2003US-00369493.  
PF  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
XX WPI; 2004-061375/06.  
DR

XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX

PS Claim 1; SEQ ID NO 17169; 122pp; English.  
XX

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transforming plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX

SQ Sequence 468 AA;

Query Match 3.3%; Score 86; DB 8; Length 468;  
Best Local Similarity 19.5%; Pred. No. 1.2e+02;  
Matches 75; Conservative 51; Mismatches 120; Indels 138; Gaps 18;

Qy 35 LEKVFOYIDLHQDE-----FVQTLKEWVAIESDSV----- 64  
Db 64 LMRWFQLIDEQQDEIGEIMTKEQGKPLREAIGEVQYANSFIQWYAEAKRIYGDTIPASA 123

Qy 65 -----QPVRFRQELFRMMAVAADTLQRLGARVASVDMGPQ-----LPDGGQSL 108  
Db 124 INKRILVQKQPVG-----VIAAITPWNEPAAMITRKVAPALAAAGCTAIVKPAEQT 173

Qy 109 PIPPVILAEIGSD---PTKGTVCFYGHLDV---QPADRGDGLTDPYV-----LTEVD 155  
Db 174 PLTALKLAQLAEAGIPA-----GVLNVITGNAQDIGEAWLEDSRVRKITFTGSTEV- 225

Qy 156 GKLYGRGATDNKGPFVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALLELVEKE-K 214  
Db 226 GKLLMRG-----AAQTVKKISLELGCHAPFII--MDDAN---LSEAVDQVIA 267

Qy 215 DRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMA 274  
Db 268 SKFRNAGQTCVCANRIYVA-REIAEAFTEK-----FAKVNELKVGNGLEEGVTIGPLI 320

Qy 275 DLVAL-----LGSLVDSGGH-----ILVPGIYDEVVPLTEEEINTYKAIH 314  
Db 321 DKAAVEKVEAHIDALKKGGQVTVGGRWTHHFFETIITGATDEMLCMNEETFGPLAPV- 379

Qy 315 LDLEEYRNSSRVEKFLFDTKEEIL 338  
Db 380 -----ATFDTEEEVI 389

RESULT 1048

ADS28317

ID ADS28317 standard; protein; 470 AA.

XX ADS28317;

AC ADS28317;  
XX

DT 02-DEC-2004 (first entry)  
XX

DE Bacterial polypeptide #17350.  
XX

KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX

OS Bacteria.  
XX

XX US2003233675-A1.  
PN

XX 18-DEC-2003.  
PD

XX 20-FEB-2003; 2003US-00369493.  
PF

XX 21-FEB-2002; 2002US-0360039P.  
PR

XX



CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 6678; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

	Query Match	3.3%;	Score 86;	DB 8;	Length 520;	
	Best Local Similarity	21.0%;	Pred. No. 1.5e+02;			
	Matches 80;	Conservative	53;	Mismatches 130;	Indels 118;	Gaps 22;
QY	168	GPVLAWINAVSAFRALEQDLPVNIKFIIEGMBEAGSVALEELVEKEKDRFFSGVDYIVIS	227			
Db	59	GPIFTFWANKPFIIVIIASYEKMKETFVKDG---DTYVDKQLTHTEKERL--GENYGVLD	112			
QY	228	DN--LWISQRKPAITYGTRGNSYFMWEVKCRDQDFHSGTFFGGILHEPMA DLVALLGSLVD	285			
Db	113	TNGHMKWKEHRRFTLT-----QLRDLG----LGKOLMQEKADL-----	145			
QY	286	SSG-----HILVPGIYDEVVPLTEE-----EINTYKAIHLDL EY--RNSSRV---	326			
Db	146	--GRNRLKAKKLHVLTVSYSENILMEVEBELFKELDAHGEEIDL PKLIDRSVGNVINL	203			
QY	327	---EKFLPDTKEEILMHLWRYP SLSIHGIEGAFDE-----PGTKTVIPGRVIGK-	372			
Db	204	TLFNKRFDMDKRDE-FAHL---KSL-IDGMRNVT SQFRYLIOYLVPWTSTVLPGPTLSEK	258			
QY	373	-----FSIRLVPHMN-----VSAVEKQVTRHLEDFVFSKRNSNNKMVV	409			
Db	259	VRAKREELDDFFYSQIDEHRNEIDFNTENLD FVEAYLKEQKKREEDGDFX-TFCNKQLC	317			
QY	410	SMTGLGHPWIANIDDT-----QYL---AAKRAIR-----TVFGTEPDM-IRDGSTIP	452			
Db	318	AMLFDL--WIAGLMTTMTMTWGLSYLYLNPEVQKIREELDKVIGNDRLLISTADKNDLP	375			
QY	453	IAKMFQEI VHKSVVLIPLGAV	473			
Db	376	YLQAFVTETQRTANIPLNLI	396			



RESULT 1051  
AAR77859  
ID AAR77859 standard; protein; 573 AA.  
XX  
AC AAR77859;  
XX  
DT 13-NOV-1995 (first entry)  
XX  
DE S. clavuligerus ORF2 product.  
XX  
KW Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;  
KW acetohydroxyacid synthase.  
XX  
OS Streptomyces clavuligerus.  
XX  
PN CA2108113-A.  
XX  
PD 09-APR-1995.  
XX  
PF 08-OCT-1993; 93CA-02108113.  
XX  
PR 08-OCT-1993; 93CA-02108113.  
XX  
PA (UYAL-) UNIV ALBERTA.  
XX  
PI Jensen SE, Aidoo KA, Paradkar AS;  
XX  
XX WPI; 1995-207301/28.  
DR N-PSDB; AAQ91580.  
XX  
PT Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for  
PT biosynthesis of the antibiotic in Streptomyces hosts which do not  
PT naturally produce clavulanate.  
XX  
PS Claim 24; Fig 11; 41pp; English.  
XX  
CC A 15 kb fragment S. clavuligerus NRRL 5741 genomic DNA (AAQ91580),  
CC extending downstream from pbcC, included 10 ORFs encoding the enzymes  
CC required for clavulinate biosynthesis. The ORF2 product (AAR77859) showed  
CC a high degree of similarity to acetohydroxyacid synthases from various  
CC sources  
XX  
SQ Sequence 573 AA;  
  
Query Match 3.3%; Score 86; DB 2; Length 573;  
Best Local Similarity 20.3%; Pred. No. 1.7e+02;  
Matches 60; Conservative 47; Mismatches 124; Indels 64; Gaps 13;  
  
QY 29 SPPPALLEKVFQYI-DLHQDEFVQTLKEWVAIESDSVQVPVPRFRQ-----EL 74  
DB 286 APVDLVLTGVGYDYAEDLRPSMWQKGIKKTVRISPTVNPVPRVYRPDVTVDVLA FVEH 345  
  
QY 75 FRMMAVAADTLQR-----LGARVASVDMGPQQLPDGQSLPIPPVI-----LAEIGSDPTK 124  
DB 346 FETATASFGAKQRHDIEPLRAIAEFLADPETYEDG--MRVHQVIDSMNTVMEEAAEPGE 403  
  
QY 125 GTVC-----FYGHLDV--QPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLA----- 172  
DB 404 GTIVSDIGFFRHYGVLFARADQPFGF-----LTSAGCSFGYIGIPAAIGAQMARPDPQT 457  
  
QY 173 -WINAVSAFRALEQDLP-----VNIKFIIEGMEEAGSVALEELVEKEKDR----FFSGV 221  
DB 458 FLIAGDGGFHSNSSDLETIARLNLPITVTVVVNDTNGLTIELYQNIHRSHRDPVAVKFGGV 517  
  
QY 222 DYIVISDNLWISQRK-----PAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268  
DB 518 DFVALAEANGVDATRATNREELLALRLKGAELGRPFLEVPV-NYDFQPGGFGAL 571  
  
RESULT 1052  
AAE14856  
ID AAE14856 standard; protein; 573 AA.  
XX

AC AAE14856;  
XX  
DT 27-AUG-2003 (first entry)  
XX  
DE S. clavuligerus clavulanic acid biosynthesis ORF2 polypeptide.  
XX  
KW Clavulanic acid; clavam compound; beta-lactamase inhibitor;  
KW pharmaceutical agent; ORF2; open reading frame.  
XX  
OS Streptomyces clavuligerus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 47 /note= "Encoded by GAG"  
FT Misc-difference 48 /note= "Encoded by GGG"  
FT Misc-difference 57 /note= "Encoded by GAG"  
FT Misc-difference 98 /note= "Encoded by GAC"  
FT Misc-difference 99 /note= "Encoded by GAC"  
FT Misc-difference 134 /note= "Encoded by CGC"  
FT Misc-difference 241 /note= "Encoded by AAG"  
FT Misc-difference 241 /note= "Encoded by GAG"  
XX  
XX WO2003040372-A2.  
PN  
XX 15-MAY-2003.  
PD  
XX 06-NOV-2002; 2002WO-GB004989.  
PF  
XX 07-NOV-2001; 2001GB-00026756.  
PR 30-NOV-2001; 2001GB-00028776.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
PA  
XX  
PI Anders C, Barton B, Griffin AM, Jensen S;  
XX  
XX WPI; 2003-430668/40.  
DR N-PSDB; AAD36874.  
XX  
PT New polynucleotide for improving or regulating the biosynthesis of clavam  
PT compounds, specifically clavulanic acid, by Streptomyces clavuligerus  
PT host cell.  
XX  
PS Claim 1; Page 52-53; 67pp; English.  
XX  
CC The invention relates to polynucleotides involved in the biosynthesis of  
CC clavulanic acid. The polynucleotides of the invention are useful in  
CC improving or regulating the biosynthesis of clavam compounds,  
CC specifically clavulanic acid, by Streptomyces clavuligerus host cell.  
CC Clavulanic acid is known to be potent inhibitor of beta-lactamase enzymes  
CC and has been successfully used in combination with beta-lactam  
CC antibiotics in drugs such as Augmentin. Clavam compounds including  
CC clavulanic acid are important pharmaceutical agents and hence improved  
CC production of such compounds are desirable. The present sequence is  
CC Streptomyces clavuligerus polypeptide involved in clavulanic acid  
CC biosynthesis. The polypeptide is encoded by open reading frame (ORF)2 of  
CC gene cluster encoding clavulanic acid biosynthesis enzymes  
XX  
SQ Sequence 573 AA;  
  
Query Match 3.3%; Score 86; DB 6; Length 573;  
Best Local Similarity 20.3%; Pred. No. 1.7e+02;  
Matches 60; Conservative 47; Mismatches 124; Indels 64; Gaps 13;  
  
QY 29 SPPPALLEKVFQYI-DLHQDEFVQTLKEWVAIESDSVQVPVPRFRQ-----EL 74  
DB 286 APVDLVLTGVGYDYAEDLRPSMWQKGIKKTVRISPTVNPVPRVYRPDVTVDVLA FVEH 345

QY 75 FRMVAADTLQR-----LGARVASVDMGPQQLPDGQSLPIPPVI-----LAELGSDPTK 124  
Db 346 FETATASFGAKQRHDIPLRARIAEFLADPETYEDG--MRVHQVIDSMNTVMEEAAEPGE 403  
QY 125 GTVC---FYGHLDV--QPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLA----- 172  
Db 404 GTIVSDIGFFRHYGVLFARADQPPFGF-----LTSAGCSSFGYGIPAAIGAQMARPDOPT 457  
QY 173 -WINAVSAFRALEQDLP-----VNIKFIEGMEEAGSVALEELVEKEKDR-----FFSGV 221  
Db 458 FLIAGDGGFHNSDLETTIARLNLPIVTVVVNNDTNGLIELYQNIGHRSHDPAVKFGV 517  
RESULT 1053  
ID AAE07907 standard; protein; 574 AA.  
XX AAE07907;  
AC AAE07907;  
XX 01-NOV-2001 (first entry)  
DT  
DE S. clavuligerus clavulanic acid biosynthesis enzyme #1.  
XX  
KW Clavulanic acid biosynthesis enzyme; antibiotic; infectious disease;  
KW broad spectrum beta-lactamase inhibitor; open reading frame; ORF;  
KW pcbC gene.  
XX  
OS Streptomyces clavuligerus.  
XX  
PH Key Location/Qualifiers  
FT Misc-difference 239 /note= "Amino acid Ile is present in the sequence shown  
FT as SEQ ID NO: 4 in the sequence listing"  
FT Misc-difference 573. .574  
FT /note= "Encoded by ATC"  
XX  
PN US6232106-B1.  
XX  
PD 15-MAY-2001.  
XX  
PF 30-AUG-1999; 99US-00385028.  
XX  
PR 08-OCT-1993; 93US-00134018.  
PR 06-DEC-1995; 95US-00567801.  
PR 29-JAN-1997; 97US-00790462.  
XX  
PA (UYAL-) UNIV ALBERTA.  
XX  
PI Jensen SE, Aidoo KA, Paradkar AS;  
XX  
DR WPI; 2001-342772/36.  
DR N-PSDB; AAD14499, AAD14503.  
XX  
PT Novel enzyme required for clavulanic acid biosynthesis which is useful as  
PT broad spectrum beta-lactamase inhibitor.  
XX  
PS Claim 1; Fig 10; 75pp; English.  
XX  
CC The invention relates to DNA sequences encoding enzymes required for  
CC clavulanic acid biosynthesis. Clavulanic acid is a broad spectrum beta-  
CC lactamase inhibitor and is an important antibiotic for the treatment of  
CC infectious diseases. Also provided in the patent is a 15 Kb genomic DNA  
CC fragment downstream to pcbC gene from Streptomyces clavuligerus. The  
CC genomic DNA comprises 10 open reading frames (ORFs), eight of which are  
CC involved in clavulanic acid biosynthesis. The present sequence is S.  
CC clavuligerus clavulanic acid biosynthesis enzyme encoded by ORF2  
XX  
SQ Sequence 574 AA;

Query Match 3.3%; Score 86; DB 4; Length 574;  
Best Local Similarity 20.3%; Pred. No. 1.7e+02;  
Matches 60; Conservative 47; Mismatches 124; Indels 64; Gaps 13;  
QY 29 SPPPALLEKVFOYI-DLHQDEFVQTLKEWVAIESDSVQVPFRFRQ-----EL 74  
Db 286 APVDLVLTVGYDAEDLRPSMWQKGIKKTVRISPTVNPPIRVPRPDVDVTVLAFVEH 345  
QY 75 FRMVAADTLQR-----LGARVASVDMGPQQLPDGQSLPIPPVI-----LAELGSDPTK 124  
Db 346 FETATASFGAKQRHDIPLRARIAEFLADPETYEDG--MRVHQVIDSMNTVMEEAAEPGE 403  
QY 125 GTVC---FYGHLDV--QPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLA----- 172  
Db 404 GTIVSDIGFFRHYGVLFARADQPPFGF-----LTSAGCSSFGYGIPAAIGAQMARPDOPT 457  
QY 173 -WINAVSAFRALEQDLP-----VNIKFIEGMEEAGSVALEELVEKEKDR-----FFSGV 221  
Db 458 FLIAGDGGFHNSDLETTIARLNLPIVTVVVNNDTNGLIELYQNIGHRSHDPAVKFGV 517  
QY 222 DYIVISDNLWISQRK-----PAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGI 268  
Db 518 DFVALAEANGVDATRATNRRELLAALRKGAELGRPFLEIEVPV-NYDFQPGGFGAL 571  
RESULT 1054  
ABU62215  
ID ABU62215 standard; protein; 574 AA.  
XX  
AC ABU62215;  
XX 26-AUG-2003 (first entry)  
DT  
DE Clavulanic acid synthesis associated protein #2.  
XX  
KW Clavulanic acid synthesis; broad-spectrum beta-lactamase inhibitor;  
KW antibiotic; infectious disease; antibiotic yield; antimicrobial;  
KW beta-lactamase inhibitor; enzyme.  
XX  
OS Streptomyces clavuligerus.  
XX  
PN US6514735-B1.  
XX  
PD 04-FEB-2003.  
XX  
PF 01-DEC-2000; 2000US-00726614.  
XX  
PR 08-OCT-1993; 93US-00134018.  
PR 06-DEC-1995; 95US-00567801.  
PR 29-JAN-1997; 97US-00790462.  
PR 30-AUG-1999; 99US-00385028.  
XX  
PA (UYAL-) UNIV ALBERTA.  
XX  
PI Jensen SE, Aidoo KA, Paradkar AS;  
XX  
DR WPI; 2003-491699/46.  
DR N-PSDB; ACA62922, ABU62926.  
XX  
PT New protein/enzyme encoded by a DNA from Streptomyces clavuligerus,  
PT useful in the synthesis of clavulanic acid, which is a broad spectrum  
PT beta-lactamase inhibitor for treating infections, or for increasing  
PT antibiotic yield.  
XX  
PS Disclosure; Fig 10; 76pp; English.  
XX  
CC The invention describes an isolated protein, which comprises a sequence  
CC having 409 amino acids fully defined in the specification. The protein is  
CC useful in the synthesis of clavulanic acid, which is a broad-spectrum  
CC beta-lactamase inhibitor and an important antibiotic for treating  
CC infectious diseases. The protein is particularly useful for increasing  
CC antibiotic yield. This is the amino acid sequence of a clavulanic acid  
CC synthesis associated protein encoded by a 15kb segment of the

CC	Streptomyces clavuligerus genome	
XX	Sequence 574 AA;	
SQ	Sequence 574 AA;	
	Query Match 3.3%; Score 86; DB 6; Length 574;	
	Best Local Similarity 20.3%; Pred. No. 1.7e+02;	
	Matches 60; Conservative 47; Mismatches 124; Indels 64; Gaps 13;	
QY	29 SPPALLEKVFQYI-DLHQDEFVQTLKEWVAIESDSVQVPFRFQ-----EL 74	
Db	286 APVDLVLTGVGYAEDLRPSMWQKIEKKTVRISPTVNPIRVYRPD VVDVLA FVEH 345	
QY	75 FRMMAVAADTLQR-----LGARVASVDMGPPQQLPDGQSLPIPPVI-----LAELGSDPTK 124	
Db	346 FETATASFGAKQRHDIEPLRARIAEFLADPETYEDG--MRVHQVIDSMNTVMEEAAEPGE 403	
QY	125 GTVC-----FYGHLDV--QPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLA----- 172	
Db	404 GTIVSDIGFFRHYGVLFARADQPFGE-----LTSAGCSSFGYGIPAAIGAQMARPDPQT 457	
QY	173 -WINAVSAFRALEQDLP-----VNIKFIIIEGMEEAGSVALEELVEKEKDR----FFSGV 221	
Db	458 FLIAGDGGFHSNSSDLETIARLNLPITVTVVNNNTNGLIELYQNIHHRSHDPAVKFGGV 517	
QY	222 DYIVISDNLWISQRK-----PAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268	
Db	518 DFVALAEANGVDATRATNREELLAALRKGAELGRPFLEIEVPV-NYDFQPGGFGAL 571	
	RESULT 1055	
	ADD26433	
ID	ADD26433 standard; protein; 574 AA.	
XX		
AC	ADD26433;	
DT	15-JAN-2004 (first entry)	
XX		
DE	Streptomyces clavuligerus ORF2.	
XX		
KW	clavulanic acid synthesis; beta-lactamase inhibitor; clavulanic acid.	
XX		
OS	Streptomyces clavuligerus.	
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 574	
FT	/note= "Encoded by TGA"	
XX		
PN	US6589775-B1.	
XX		
PD	08-JUL-2003.	
XX		
PF	30-AUG-1999; 99US-00385040.	
XX		
PR	08-OCT-1993; 93US-00134018.	
PR	06-DEC-1995; 95US-00567801.	
PR	29-JAN-1997; 97US-00790462.	
XX		
PA	(UYAL-) UNIV ALBERTA.	
XX		
PI	Jensen SE, Aidoo KA, Paradkar AS;	
XX		
DR	WPI; 2003-810383/76.	
DR	N-PSDB; ADD26444.	
XX		
PT	New isolated DNA molecule encoding enzymes of clavulanic acid	
PT	biosynthesis, useful for producing and enhancing production of clavulanic	
PT	acid in a transformant host.	
XX		
PS	Claim 8; SEQ ID NO 4; 67pp; English.	
XX		
CC	The invention relates to an isolated DNA molecule. The methods and	
CC	compositions of the present invention are useful for producing and	
CC	enhancing production of clavulanic acid (beta-lactamase inhibitor) in a	
CC		
CC	clavulanic acid producing host. The present sequence represents the amino	
CC	acid sequence of an ORF involved in clavulanic acid synthesis in	
CC	Streptomyces clavuligerus.	
XX		
SQ	Sequence 574 AA;	
	Query Match 3.3%; Score 86; DB 7; Length 574;	
	Best Local Similarity 20.3%; Pred. No. 1.7e+02;	
	Matches 60; Conservative 47; Mismatches 124; Indels 64; Gaps 13;	
QY	29 SPPALLEKVFQYI-DLHQDEFVQTLKEWVAIESDSVQVPFRFQ-----EL 74	
Db	286 APVDLVLTGVGYAEDLRPSMWQKIEKKTVRISPTVNPIRVYRPD VVDVLA FVEH 345	
QY	75 FRMMAVAADTLQR-----LGARVASVDMGPPQQLPDGQSLPIPPVI-----LAELGSDPTK 124	
Db	346 FETATASFGAKQRHDIEPLRARIAEFLADPETYEDG--MRVHQVIDSMNTVMEEAAEPGE 403	
QY	125 GTVC-----FYGHLDV--QPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLA----- 172	
Db	404 GTIVSDIGFFRHYGVLFARADQPFGE-----LTSAGCSSFGYGIPAAIGAQMARPDPQT 457	
QY	173 -WINAVSAFRALEQDLP-----VNIKFIIIEGMEEAGSVALEELVEKEKDR----FFSGV 221	
Db	458 FLIAGDGGFHSNSSDLETIARLNLPITVTVVNNNTNGLIELYQNIHHRSHDPAVKFGGV 517	
QY	222 DYIVISDNLWISQRK-----PAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI 268	
Db	518 DFVALAEANGVDATRATNREELLAALRKGAELGRPFLEIEVPV-NYDFQPGGFGAL 571	
	RESULT 1056	
	ADG47778	
ID	ADG47778 standard; protein; 574 AA.	
XX		
AC	ADG47778;	
XX		
DT	11-MAR-2004 (first entry)	
XX		
DE	Streptomyces clavuligerus 15 kb gene ORF2 protein.	
XX		
KW	Clavulanic acid; bacterial infection; gene therapy; open reading frame;	
XX		
OS	Streptomyces clavuligerus.	
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 573. .574	
FT	/note= "Encoded by ATC"	
XX		
PN	US2003207411-A1.	
XX		
PD	06-NOV-2003.	
XX		
PF	11-JUN-2003; 2003US-00458201.	
XX		
PR	08-OCT-1993; 93US-00134018.	
PR	06-DEC-1995; 95US-00567801.	
PR	29-JAN-1997; 97US-00790462.	
PR	30-AUG-1999; 99US-00385040.	
XX		
PA	(UYAL-) UNIV ALBERTA.	
XX		
PI	Jensen SE, Aidoo KA, Paradkar AS;	
XX		
DR	WPI; 2003-875866/81.	
DR	N-PSDB; ADG47789, ADG47775.	
XX		
PT	New DNA molecule, useful in producing clavulanic acid in a non-	
PT	clavulanate-producing host or in enhancing clavulanic acid production in	
PT	a clavulanate-producing host for preparing a composition for treating	
PT	bacterial infections.	
XX		







CC carotenoid pigments of various carbon lengths. The present sequence  
CC represents a Methylobionas 6-phosphogluconate dehydratase from the present  
CC invention  
XX  
SQ Sequence 618 AA;

Query Match 3.3%; Score 86; DB 5; Length 618;  
Best Local Similarity 20.3%; Pred. No. 1.9e+02;  
Matches 88; Conservative 60; Mismatches 128; Indels 158; Gaps 23;

QY 72 QELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCIFYG 131  
Db 23 QVIARSRETRAAYLKRIEAAIAE---GPQR-----NKLP-----C--- 54  
QY 132 HLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 55 -----ANLAHGFA---VCSAIEKEELSHGPKPNVGIISAYNDMLSAHEPY-KDYPALI 103  
QY 192 KFIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYG-TRGNSYFM 250  
Db 104 K---QAVREAGGVA-----QFAGGV-----PAMCDGVTQGMPGME 135  
QY 251 VEVKCRDQDFHS-----GTFGGILHEPMDLVA---LLGSLVDSSGHILVPGIYDEVV 300  
Db 136 LSLFSRDVIAMSTAIGLAHNMFDAALYLGVC DKIVPGLLIGAL--SFGHL--PAVFLPAG 191  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 192 PMTSGLSNKEKS--RARQKYAEGKIGEKELLESEAK-----SYHSPG 231  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLH--- 416  
Db 232 TCT-----FYGTANSNQMMVEI-MGLHLP GS 256  
QY 417 ----PWIANIDDTQYLAAKRAIR-TVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPLG 471  
Db 257 SFINPYTPLRDELTKAAARQV LKFTALGND-----FRPIAHVIDE---KAIINAIIG 305  
QY 472 AVDDGEHSQNEKIN 485  
Db 306 LLATG-GSTNHTIH 318

RESULT 1060  
ABG61554  
ID ABG61554 standard; protein; 618 AA.  
XX  
AC ABG61554;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE High growth methanotrophic bacterial strain polypeptide #4.  
XX  
KW High growth methanotrophic bacterial strain; C1 carbon substrate; enzyme;  
KW methane; methanol; Embden-Meyerhof carbon flux pathway; 16s RNA;  
KW pyrophosphate dependent phosphofructokinase; nitrogen-containing compound;  
KW ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill;  
KW methane-containing environment; waste water treatment system; isoprenoid;  
KW nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.  
XX  
OS Methylobionas sp.  
XX  
PN W0200220728-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 28-AUG-2001; 2001WO-US026827.  
XX  
PR 01-SEP-2000; 2000US-0229858P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Koffas M, Odom JM, Schenzle A;

XX  
DR WPI; 2002-454358/48.  
DR N-PSDB; ABK83233.  
XX  
PT New high growth methanotrophic bacterial strain, useful for producing  
PT single cell proteins, grows on a C1 carbon substrate, and comprises a  
PT functional gene encoding in Embden-Meyerhof carbon pathway.  
XX  
PS Claim 7; Page 87-89; 157pp; English.  
XX  
CC The invention relates to a high growth methanotrophic bacterial strain,  
CC which grows on a C1 carbon substrate e.g. methane and methanol, and  
CC comprises a functional Embden-Meyerhof carbon flux pathway comprising a  
CC gene coding a pyrophosphate dependent phosphofructokinase enzyme or a 16s  
CC RNA. The bacterial strain is useful for the production of single cell  
CC protein and for the biotransformation of a nitrogen-containing compound,  
CC e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the  
CC production of a feed product comprising a protein, carbohydrates and a  
CC pigment and for reducing oxygen demand, for removing nitrates and  
CC nitrates in methane-containing environments such as landfills, waste  
CC water treatment systems or anywhere that methane, oxygen and nitrates are  
CC present. The bacterial strain of the invention can be used as a  
CC denitrifying agent for the conversion of nitrate or nitrite to nitrous  
CC oxide with methane or methanol as a carbon source. It is also used in the  
CC production of biomass including proteins, carbohydrates and a wide  
CC variety of pigments (particularly for isoprenoid pigments for the purpose  
CC of generating animal feeds), in production of terpenoid and carotenoid  
CC compounds, useful as pigments and as monomers in polymeric materials and  
CC in production of exopolysaccharides at high levels. Sequences ABG61551-  
CC ABG61590 represent high growth methanotrophic bacterial strain proteins  
CC of the invention  
XX  
SQ Sequence 618 AA;

Query Match 3.3%; Score 86; DB 5; Length 618;  
Best Local Similarity 20.3%; Pred. No. 1.9e+02;  
Matches 88; Conservative 60; Mismatches 128; Indels 158; Gaps 23;

QY 72 QELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCIFYG 131  
Db 23 QVIARSRETRAAYLKRIEAAIAE---GPQR-----NKLP-----C--- 54  
QY 132 HLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI 191  
Db 55 -----ANLAHGFA---VCSAIEKEELSHGPKPNVGIISAYNDMLSAHEPY-KDYPALI 103  
QY 192 KFIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYG-TRGNSYFM 250  
Db 104 K---QAVREAGGVA-----QFAGGV-----PAMCDGVTQGMPGME 135  
QY 251 VEVKCRDQDFHS-----GTFGGILHEPMDLVA---LLGSLVDSSGHILVPGIYDEVV 300  
Db 136 LSLFSRDVIAMSTAIGLAHNMFDAALYLGVC DKIVPGLLIGAL--SFGHL--PAVFLPAG 191  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 192 PMTSGLSNKEKS--RARQKYAEGKIGEKELLESEAK-----SYHSPG 231  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLH--- 416  
Db 232 TCT-----FYGTANSNQMMVEI-MGLHLP GS 256  
QY 417 ----PWIANIDDTQYLAAKRAIR-TVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPLG 471  
Db 257 SFINPYTPLRDELTKAAARQV LKFTALGND-----FRPIAHVIDE---KAIINAIIG 305  
QY 472 AVDDGEHSQNEKIN 485  
Db 306 LLATG-GSTNHTIH 318

RESULT 1061  
ABU41920







Db 167 HAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLTPGVRD---NLVSVTEGHKVSFPYF 222

Qy 221 VDIYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALL 280

Db 223 IAFTSLNNNELI--KQVYLHATEGSRDMI---TKDQILLAAQTMSQITPLEIDILFHL 277

Qy 281 GSLVDSGHILVPGIYDEVVPLTEEINTYKAIHL-DLEEVRNSSRVEKFLFDTKEEILM 339

Db 278 AGAVHQAGRI----DYSDSLNIAPHEHYTKHMTLRLAEIKAVESPADRSAFI-----QVLE 328

Qy 340 HLWRYPSLSIHGIEGA---FDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLED 396

Db 329 SSYRFTLGSFAGAVGATVVYPIDLVKTRMQNRAGSY-IGEVAYRNSWDCFKKVVVRH--- 384

Qy 397 VFSKRNSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST-----I 451

Db 385 -----EGFMGLYRGLLPQLMGV-----APEKAIKL---TVNDLVRDKLTDKKGN 426

Qy 452 P-----IAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAF 499

Db 427 PTWAEVLAGGCAGASQVFTNPLEIVKIRLQVAGEIASGSKIRAWSVVRELGLFLGLY 483

RESULT 1064

AAU33237

ID AAU33237 standard; protein; 695 AA.

XX

AC AAU33237;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #3728.

XX

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

XX WO200179449-A2.

PN

XX

PD 25-OCT-2001.

XX

XX 16-APR-2001; 2001WO-US008656.

PF

XX

XX 18-APR-2000; 2000US-00552929.

PR

XX 26-JAN-2001; 2001US-00770160.

XX

PA (HYSE-) HYSEQ INC.

XX

XX Tang YT, Liu C, Drmanac RT;

PI

XX

XX WPI; 2001-611725/70.

DR

XX

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy.

XX

XX

PS Claim 20; Page 740; 765pp; English.

XX

XX The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising the

CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins

CC are useful in genetic vaccination, testing and therapy, and can be used

CC as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon

CC and/or nerve tissue growth or regeneration; immune suppression and/or

CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

CC AAU29510-AAU33304 represent the amino acid sequences of novel human

CC secreted proteins of the invention

XX

SQ Sequence 695 AA;

Query Match 3.3%; Score 86; DB 4; Length 695;

Best Local Similarity 20.6%; Pred. No. 2.3e+02;

Matches 77; Conservative 30; Mismatches 91; Indels 176; Gaps 18;

Qy 6 GRMAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEW--VAIESDS 63

Db 343 GSLSQSTLKFLLL-----NPAV-----HFAQVVKECRAVVLAGGT 377

Qy 64 VQPVPRFRQELFRMMVAADTLQRLGARVASVDMGPQQLPDGQSLP----IPPVILAELG 119

Db 378 MQPVSDFRQQLLACAGVEAEERVVEF-----SCVFGPSLALTGHVIPPDPNLPVICSGIS 432

Qy 120 SDPTK-----GTVCFY-----GH 132

Db 433 NQPLEFTFKRELPMQMMDEVGRILCNLCGVVPGVGVCFPPSYEYLRQVHAHWEKGGLLGR 492

Qy 133 LD-----VQPADRGDGMLTDPYVLTVEVDGKL-YGRGATDN 166

Db 493 LAARKKIFQEPKSAHQVEQVLLAYSRCIQACGQERGQVTGALLSVVGGKMGSEGINFSDN 552

Qy 167 KGPVLAWI-----NAVSA-----FRALEQDLPVNIKFIIEGMEEAGSVALEEL----- 209

Db 553 LGRCVVMVGMPPFNIRSAELQEKMAYLDQTLF-----RAPGQAPPGKALVENLCMAVNQ 607

Qy 210 -----VEKEKDRFFSGVDYIVISDN-----LWISQKPAITYGTRGNSYFMVE 252

Db 608 SIGRAIRHQKD-FAS----IVLLDQRYARPPVLAKLPWIRAR-----VE 647

Qy 253 VKCRDQDFHSGTFG 266

Db 648 VK-----ATFG 653

RESULT 1065

AAG98343

ID AAG98343 standard; protein; 702 AA.

XX

AC AAG98343;

XX

DT 21-SEP-2001 (first entry)

XX

XX Escherichia coli protein sequence SEQ ID NO:391.

DE

XX Escherichia coli; identification; proliferation; microorganism;

KW antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis;

KW bacterial growth inhibition.

XX

OS Escherichia coli.

XX

PN WO200148209-A2.

XX

PD 05-JUL-2001.

XX

XX 19-DEC-2000; 2000WO-US034419.

PF

XX 23-DEC-1999; 99US-0173005P.

PR

XX (ELIT-) ELITRA PHARM INC.

PA

XX Forsyth RA, Ohlsen KL, Zyskind JW;

PI

XX WPI; 2001-457376/49.

DR N-PSDB; AAH81399.

XX

XX Novel nucleic acids encoding proteins required for Escherichia coli

PT proliferation, useful for screening for antimicrobial agents.

XX





Db 179 -----KTELEELGFEALYPN--RYRVIKEVVKAAGNRKEMIQKI-----LSE 219

Qy 352 IEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVS- 410

Db 220 IEGRLQEAG----IPCRVSGR-----EKHLYSIYCKMWLKEQRFHSI 257

Qy 411 MTLGLHPWIANIDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIV 466

Db 258 MDIYAFRIVNDSCTCYRVLGQ-MHSLYKRPGRVKDYIAIPKANGVQSL-HTSMI 311

RESULT 1067

ABU23243

ID ABU23243 standard; protein; 760 AA.

XX

AC ABU23243;

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #8770.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Bordetella pertussis.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR N-PSDB; ACA27113.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 51167; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 760 AA;

Query Match 3.3%; Score 86; DB 6; Length 760;

Best Local Similarity 19.1%; Pred. No. 2.6e+02;

Matches 66; Conservative 51; Mismatches 101; Indels 128; Gaps 18;

Qy 88 LGARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLTLD 147

Db 261 LGCSTAGV-LTPEMV---KTMAAQPLILALANPEP-----EIRP-ELAKAARPD 304

Qy 148 PYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSV--- 204

Db 305 CIVAT-----GRSDYPNQ-----VNNVLCF-----PFIFRGALDAGATRIT 340

Qy 205 -----ALEELVEKEKD----RFFS-----GVDYIVIS--DNLWISQRKPAITYGT 243

Db 341 EEMKLACVKAIAELAQAEOQNDVARAYAGQELSFGPDYIIPKFPDPRLLIVQIAPAVA--- 397

Qy 244 RGN SYFMVEVKCRDQDFHSGTFGGILHEPMADLVA---LLGSLVDSSGHILVPGIYDEV 299

Db 398 -----QAAADSGVATRPIDIEAYRQKLMG-FVYHSGQLMRP-LFQQA 438

Qy 300 VPLTEEEINTYKAIHLDLEEVRNSSRVEKFLFDTKEEILMHLWRYPSSLIHGIEGAFDEP 359

Db 439 KQAPK-----RVVYADGEDR-----VLRAVQTVIDEK 466

Qy 360 GTKTVIPGRV-----IGKFSIRLVPHMNVSAVEKQVTRHLEDVFS 399

Db 467 LAEPILVGRPSVIEMRIKKFGLRMVPGQNVEIVDPEDDSRFNDTWN 512

RESULT 1068

ADP84542

ID ADP84542 standard; protein; 764 AA.

XX

AC ADP84542;

XX

DT 09-SEP-2004 (first entry)

XX

DE Human breast-specific protein #46.

XX

KW human; breast-specific protein; breast cancer.

OS Homo sapiens.

XX

PN WO2004053077-A2.

XX

PD 24-JUN-2004.

XX

PF 05-DEC-2003; 2003WO-US038815.

XX

PR 05-DEC-2002; 2002US-0431123P.

XX

PA (DIAD-) DIADEXUS INC.

XX

PI Macina RA, Turner LR, Sun Y, Chen H, Rodriguez M;

XX

DR WPI; 2004-468848/44.

DR N-PSDB; ADP84431.

XX

PT New breast specific nucleic acid molecules and polypeptides useful for

PT diagnosing, preventing or treating breast cancer, for producing

PT transgenic animals or cells, or for research purposes.





PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Cahoon RE, Falco SC, Rafalski JA, Sakai H;  
XX  
DR WPI; 2001-647288/74.  
DR N-PSDB; AAD20951.  
XX  
PT New polynucleotide encodes a polypeptide useful for producing transgenic  
PT plants with altered levels of protein degradation and increasing the rate  
PT of growth, comprises the arginyl-trNA-protein transferase.  
XX  
PS Example 4; Col 35-40; 30pp; English.  
XX  
CC The invention relates to an isolated polynucleotide encoding an arginyl-  
CC tRNA-protein transferase or isopeptidase T. The DNA of the invention may  
CC be used to produce transgenic plants that contain arginyl-trNA-protein  
CC transferase at a higher or lower levels than normal or in cell types or  
CC developmental stages in which they are not normally found. This would  
CC have the effect of altering the level of protein degradation in those  
CC cells. Prolonging the half-life of short-lived proteins may lead to cell  
CC proliferation which could then increase the rate of growth of the plants.  
CC All or a substantial portion of the nucleic acid fragments may also be  
CC used as probes for genetically and physically mapping the genes that they  
CC are a part of, and as markers for traits linked to those genes. Such  
CC information may be useful in plant breeding in order to develop lines  
CC with desired phenotypes. In addition, the nucleic acid fragments of the  
CC instant invention may be used to probe Southern blots containing  
CC restriction endonuclease-treated genomic DNAs of a set of individuals  
CC representing parent and progeny of a defined genetic cross. The present  
CC sequence is corn isopeptidase T protein  
XX  
SQ Sequence 795 AA;

Query Match 3.3%; Score 86; DB 4; Length 795;  
Best Local Similarity 20.5%; Pred. No. 2.8e+02;  
Matches 94; Conservative 57; Mismatches 168; Indels 140; Gaps 25;

QY 84 TLQRLGARVASVDMGPQQ-----LPDQGSLLPIPPVILAE---LGSDPT----- 123  
Db 87 TLLAIGVEGGFGDQPEYDETFEIVILPDPFICLPFPSPVDLPEKVRLAVDKVLAEADRK 146  
QY 124 -----KGTVCFYGHLDVQPADRG-----DGW-----LTPDVPVTEVDGK-LYGRG 162  
Db 147 EQLAAWVADKKNISAYA-MDLQQLDNGVIVPPTGWKCKDKTENLWNLTDGMILCGRK 205  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEE-----LVEKEKD 215  
Db 206 LWDGSG--GNNHAIEHYEQTKYPLAVKLGTITADLEAADVFSYPEDSDSVEDPLLAQHLS 262  
QY 216 RFFSGVDYIVIS-----DNLWISQRKPAITYG-----TRGNSYF 249  
Db 263 HF--GIDFSSLQKTEMTTAERELDANTYDWNRIQESGKDAELLFGPGYTGLANLGNCSY 320  
QY 250 MVEV-----KCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYD 297  
Db 321 MASIMQVMFISHPFISRYFEKQSLKAAAFATAPADPTVDLNMQLTKL-----AHGLLSGKYS 376  
QY 298 EVVPLTEEEINT--YKAI-----HLDLEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHG 351  
Db 377 APAKEGQEGIRSRMPKSVITANHPEFSSMRQQDVLEFFL-----HL-----IDR 420  
QY 352 IEGAFDEPGTKTIPGRVIGKFS-IRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVS 410  
Db 421 VEKA--NPGDRELNP-----FSGFKFVVEERVQCPSGKVS-----YNKRSDN---VLS 463  
QY 411 MTLGLHPWIANIDDTQYLAAKRAIRTVFGE---PDMIR 446  
Db 464 LSIPLHE-ATNKEQLEAFNEKKAAMNLDGKEVSNEDIVR 501

RESULT 1071  
ABB78226  
ID ABB78226 standard; protein; 795 AA.

XX ABB78226;  
AC  
XX 25-NOV-2002 (first entry)  
DT  
XX Amino acid sequence of corn isopeptidase T.  
DE  
XX Arginyl tRNA protein transferase; isopeptidase T; plant; enzyme;  
KW N-end rule pathway; protein degradation; transgenic plant.  
KW  
XX Zea mays.  
OS  
XX US2002086388-A1.  
PN  
XX 04-JUL-2002.  
PD  
XX 02-AUG-2001; 2001US-00921259.  
PF  
XX 12-AUG-1998; 98US-0096225P.  
PR 09-AUG-1999; 99US-00370807.  
PR  
XX (CAHO/) CAHOON R E.  
PA (FALC/) FALCO S C.  
PA (RAFA/) RAFALSKI J A.  
PA (SAKA/) SAKAI H.  
XX  
PI Cahoon RE, Falco SC, Rafalski JA, Sakai H;  
XX  
DR WPI; 2002-642243/69.  
DR N-PSDB; ABQ78637.  
XX  
PT Novel isolated nucleic acid fragment which encodes an enzyme involved in  
PT N-end rule pathway of protein degradation, such as arginyl-trNA-protein  
PT transferase or an isopeptidase T, useful as primers and probes.  
XX  
PS Claim 6; Page 19-21; 31pp; English.  
XX  
CC The present sequence represents isopeptidase T. The specification also  
CC describes arginyl tRNA protein transferase polypeptides and  
CC polynucleotides. Both these enzymes are involved in the N-end rule  
CC pathway of protein degradation. The polynucleotides are useful to isolate  
CC cDNAs and genes encoding homologous proteins from the same or other plant  
CC species. They are also useful for creating transgenic plants in which  
CC arginyl tRNA protein transferase and isopeptidase T polypeptides present  
CC at higher or lower levels than normal or in cell types or in  
CC developmental stages in which they are not normally found. All or  
CC substantial portion of the polynucleotides may also be used as probes for  
CC genetically and physically mapping the genes that they are a part of and  
CC used as markers for traits linked to those genes. This information is  
CC used in plant breeding in order to develop lines with desired phenotypes  
XX  
SQ Sequence 795 AA;

Query Match 3.3%; Score 86; DB 5; Length 795;  
Best Local Similarity 20.5%; Pred. No. 2.8e+02;  
Matches 94; Conservative 57; Mismatches 168; Indels 140; Gaps 25;

QY 84 TLQRLGARVASVDMGPQQ-----LPDQGSLLPIPPVILAE---LGSDPT----- 123  
Db 87 TLLAIGVEGGFGDQPEYDETFEIVILPDPFICLPFPSPVDLPEKVRLAVDKVLAEADRK 146  
QY 124 -----KGTVCFYGHLDVQPADRG-----DGW-----LTPDVPVTEVDGK-LYGRG 162  
Db 147 EQLAAWVADKKNISAYA-MDLQQLDNGVIVPPTGWKCKDKTENLWNLTDGMILCGRK 205  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEE-----LVEKEKD 215  
Db 206 LWDGSG--GNNHAIEHYEQTKYPLAVKLGTITADLEAADVFSYPEDSDSVEDPLLAQHLS 262  
QY 216 RFFSGVDYIVIS-----DNLWISQRKPAITYG-----TRGNSYF 249  
Db 263 HF--GIDFSSLQKTEMTTAERELDANTYDWNRIQESGKDAELLFGPGYTGLANLGNCSY 320



XX (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA53370.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 77424; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 881 AA;

Query Match 3.3%; Score 86; DB 6; Length 881;

Best Local Similarity 20.2%; Pred. No. 3.3e+02;

Matches 85; Conservative 59; Mismatches 176; Indels 100; Gaps 19;

QY 151 LTEVDGKLYRGATD-----NKGpVLAWI-NAVSaFRALEQDLpVNIkFIIEGME 199

Db 77 LVAVGg--YGRGELHPLSDIDLlVLSQQpLSEqVANKISQFLTLlWDLKLEIGHAVRTVE 134

QY 200 ---EAGSVAlEELVEKEKDRFFSGVD-----YIVISDNLWISQRKPAITYGTRGNSYF 240

Db 135 QCAEIGKADLTvATNLQEARLLCGCEETfHRLKwVHSEsFWPSE----IFyQAK----- 185

QY 250 MVEVKCRDQDFHSGTfGGILHEPMAdlVALLGSLVD-----SSGH 289

Db 186 VREQERHARyHDTTYN---LEP--DIKSTPGGLRDIHTLSwARRHFGATSLYEMsRFG 240

QY 290 ILVPGIYDEVVPLTEEEINTYKAIHLDLEeYRNSSRVEKfLEFDTKIEILMHLWRyPSLSI 349

Db 241 FLTDAEYRELVECDfLWRVRfALHIELKRYDN-----RLTfAHQVQVARHL-GYfGEGN 294

QY 350 HGIEGAFDEPGTKtVIPGRVIGKfSIRLVPhMNVsAVEKQVTRHLEDVfSKRNSSNKwVV 409

Db 295 RGIEMMMKE-fFRTLRRVAELNKMlLKIFDKAILNNGEEAEAVIIDDfDfQRRGNMIEARK 353

QY 410 SMTlGLHPwIANIDdTQYLAAKRAIRtVFGTEpDMIRdG-----STIPIAK-MFQEI 460

Db 354 PALFQARPEtI-LDMFLHMASDStIESVAPATMRQlRtARRRlNKfLHTLPAAREKfIEL 412

QY 461 V-----HKSVVLiPLGAVDdGHSQNEKIN-----RWNYIEGTkLFAAFfLEMAQLH 507

Db 413 VRHPNALHKA-----FSQMHKLGVLAAyLPQwNIqVGMQfDLfHVYtTVDEH 459

RESULT 1074

ABR41754

ID ABR41754 standard; protein; 902 AA.

XX

AC ABR41754;

XX

DT 02-JUN-2003 (first entry)

XX

DE Human DITHP biochemical pathway protein.

XX

KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;

KW cancer; cell proliferative disorder; autoimmune disorder;

KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;

KW neurological disorder; gastrointestinal disorder; transport disorder;

KW connective tissue disorder; drug screening; proteome analysis;

KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;

KW disease model; toxicological testing; transcript imaging;

KW biochemical pathway.

XX

OS Homo sapiens.

XX

PN WO200297031-A2.

XX

PD 05-DEC-2002.

XX

PF 27-MAR-2002; 2002WO-US010056.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-030001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-129518/12.

DR N-PSDB; ACC46691.

XX

PT Novel human diagnostic and therapeutic polypeptide useful for identifying

PT test compound which specifically binds to a polypeptide encoded by human

PT diagnostic and therapeutic polynucleotide, and to induce antibodies.

XX

PS Claim 27; SEQ ID NO 1289; 591pp; English.

XX

CC The invention relates to novel human diagnostic and therapeutic

CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded

CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to

CC polynucleotide sequences at least 90% identical to the dithp cDNA

CC sequences of the invention; recombinant vectors, host cells and

CC transgenic organisms comprising a dithp nucleic acid sequence; the

CC recombinant production of DITHP proteins; antibodies specific for DITHP

CC proteins; microarrays comprising dithp nucleic acid sequences; methods of

CC detecting dithp nucleotide and protein sequences; methods of screening

CC for compounds which specifically bind a DITHP protein; and methods of



CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a DITHP protein which is involved in a  
CC biochemical pathway. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 902 AA;

Query Match 3.3%; Score 86; DB 6; Length 902;  
Best Local Similarity 18.7%; Pred. No. 3.4e+02;  
Matches 109; Conservative 80; Mismatches 197; Indels 198; Gaps 27;

QY 29 SPPPALLEKVFQYIDLHQ--DEFVQTLKEWVAIESDSQVPPRFRQEL-----FRMMAVAA 82  
Db 349 TPAEQALEKALAILTLRSALPGVWHCLQEVLDKYVTLVDRVPTLLQLHLSMDFSTVVEE 408  
QY 83 DTLQRL--GARVASVD-----MGQQQLPDGQSLRIP-----PVILAEIGSDPT--K 124  
Db 409 DLVTKLNAGLQAASEDRLLVRAIGPTETP---SWPAPDAAEDSPGVAPELPEDEAIRQ 465  
QY 125 GTVCFYGHLDVQPADRG---DGW-----LTDPPVLTVEVDGKL-----YGRG 162  
Db 466 ALVDSVFQVSVLPNGVGLRFDSPADASVLGLVAPVLRQVWEPLQDTEHLMDLRNPG 525  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGNEEAGSVALEELVEKED---RFFS 219  
Db 526 GPSSAVPLL-----LSYFQG-----PEAGPVHLFTTYDRRNTITQEHFS 564  
QY 220 GVD-----YIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGG 267  
Db 565 HMEPLGPRYSTQRGVYLLTSHRTATAAEFAFLMQSLGWATLVGEI-----TAGN 614  
QY 268 ILHE---PMAD-----LVALLGSLVDSSGHI-LVPGIYDEVVPLTEEEINTYKAHLD 316  
Db 615 LLHTRTVPLDTPEGSLALTVPVLTFDINHGAEWLGGGVVDPDAIVLAEAL----- 665  
QY 317 LEEYRNSRVEKFLFTKKEILMHLWRYPVLSIHGIEGAFDEPGTKTVIPG-----RVIG 371  
Db 666 -----DKAQEV-----LEFQSLGALVE-GTGHLLLEAHYARPEVVG 700  
QY 372 KFSIRLVPHM-----NVSAREKQVTRHLEDVFSKR-----NSSNMVVSMTLGLHP 417  
Db 701 QTSALLRAKLAQGAVRTAVDLESLASQLTADLQEVSGDHRLLLVFHSPEGELVVEEAPPPP 760  
QY 418 WIANIDDTQYLA-----AKRAIRTVFGTEPDMIRDGSTIPIAKMFQ 458  
Db 761 AVPSPEELTYLIEALFKTEVLPQGLYLRFDMAAELETVKAQGPQLVR-----LVWQ 812  
QY 459 EIVHKSIVLIPLGAVDDGHSQNEKINRWNYIEGFKLFAAFFLE 502  
Db 813 QLVDTAALVIDL-----RYNPGSYSTAIPLLCSYFFE 844

RESULT 1075  
AAR10333  
ID AAR10333 standard; protein; 911 AA.  
XX  
AC AAR10333;  
XX

DT 25-MAR-2003 (revised)  
DT 08-APR-1991 (first entry)  
XX  
DE Deduced sequence of tomato nitrate reductase.  
XX tomato nitrate reductase; nitrogen assimilation.  
KW Lycopersicon esculentum.  
XX  
PN EP409730-A.  
XX  
PD 23-JAN-1991.  
XX  
PF 18-JUL-1990; 90EP-00402077.  
XX  
PR 19-JUL-1989; 89FR-00009707.  
XX  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
XX  
PI Danielvede F, Caboche M;  
XX  
DR WPI; 1991-024287/04.  
DR N-PSDB; AAQ10280.  
XX  
PT New DNA encoding tomato nitrate reductase - and related cloning and  
PT expression vectors, used to improve nitrogen assimilation in plants.  
XX  
PS Claim 2; Fig 1; 27pp; French.  
XX  
CC An EcoRI digest of tomato DNA was screened with labelled tobacco nitrate  
CC reductase cDNA under low stringency conditions. A 6.5kb fragment  
CC contained part of the tomato nitrate reductase gene and was used, under  
CC high stringency, to screen a Hind III library. A 7kb fragment was  
CC isolated, having 1.5kb in common with the EcoRI fragment. Restriction  
CC fragments were subcloned and sequenced. The deduced protein sequence is  
CC encoded by four exons. Comparison with known nitrate reductases from  
CC other plants, e.g. Nicotiana, Solanum, Trifolium pratense, Cucumis  
CC sativus, etc., shows conserved regions. These have structural and/or  
CC functional importance and tend to be separated by variable regions, often  
CC hydrophilic, which are possibly specific surface epitopes of the enzyme.  
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX  
SQ Sequence 911 AA;

Query Match 3.3%; Score 86; DB 2; Length 911;  
Best Local Similarity 17.9%; Pred. No. 3.5e+02;  
Matches 99; Conservative 80; Mismatches 179; Indels 196; Gaps 27;

QY 92 VASVDMGPQQLPDGQSLPIPPVILAEIGSD-----PTKGTVCFY-----GH 132  
Db 275 VAYMQNGEMLSPD-HGFPVRMIIPGFIGRGMVKWLKRIVVTTQESYHYKDNRLVPPH 333  
QY 133 LDVQPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVN-- 190  
Db 334 VDAELANAEAWYKPEYIINELN-----INSVITTPCHEELPINAW 375  
QY 191 -----IKFIIEGMEEAGSVALEE-----LVEK 212  
Db 376 TTQRPYTLRGYAYSGGKKVTRVEVTLDDGETWSVCTLDHPEKPTYKYKWCWCFWSLEV 435  
QY 213 EKDRFFSGVDYIVISDNLWISQRKPAITYGTRG---NSYFMVEVK-CRDQDFHSGTGGI 268  
Db 436 EVLDLLSAKEIAVRATDETTLNTOPEKLIWNVGMNMNCWFRVGMNVCKP---HKGEIGIV 492  
QY 269 LHEP-----MADL----- 276  
Db 493 FEHPTQPGNQSGGWMakerHLEISAVAPPTLKKISITPFMTASKMYSMEVRKHNSSDS 552  
QY 277 --VALLGSLVDSSGHIL-VPGIYDEVV-----PLTEEEINTYKAHLD-----LEEYRNS 323  
Db 553 AWIIVHGHYDASRFLKDHPPGGVDSILINAGTDCTEE---FDAIHSKAKXLLJEDFRIG 608







Db 178 ALPAASEPVPSSAEKIMDLMEQPGNTVSSGQEDFPSPVILETAASLPSLSPLSTVS-FK- 235

Qy 183 LEQDLPVNIKFI--IEG-MEEAGSVALEELVEKEKDRF-----FSGVDYIVISDNLWI 232

Db 236 -EHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY----- 285

Qy 233 SQRKPAITYGTRGNSYFMV-----EVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSS 287

Db 286 SEMGSSFKGSPKGESAILVENTKBEVIVRSKDKEDLVCSAALHSPQE-----SPVGKE 338

Qy 288 GHILVP-----GIYDE-----VVPLTEEEIINTYKAHLDLEEYRNSRVEKFLFDTKBEIL 338

Db 339 DRVVSPEKTMDIFNEMQMSVVAVPREE-----YADFKPFEQAWEVK-----DTYE--- 383

Qy 339 MHLWRYPYLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRH-LEDV 397

Db 384 -----GSRDVLAA-----ANVESKVDKCLEDS 407

Qy 398 FSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGS 449

Db 408 LEQK-----SLGKDSSEGRNEDAS-----FPSTPEPVKDSS 437

RESULT 1079

ABB07586

ID ABB07586 standard; protein; 1509 AA.

XX

AC ABB07586;

DT 08-MAY-2002 (first entry)

DE Human Zneu2 polypeptide.

DE Zneu2; human; placental polypeptide; epidermal growth factor; EGF;

KW vulnerary; cellular differentiation; gene therapy; vaccine.

XX

OS Homo sapiens.

XX WO200204599-A2.

PN 17-JAN-2002.

XX

PD 09-JUL-2001; 2001WO-US021865.

PF 12-JUL-2000; 2000US-0218004P.

XX

PR (ZYMO ) ZYMOGENETICS INC.

PA Holloway JL, Heffernan JK, Taft DW;

XX

PI WPI; 2002-179703/23.

XX

DR N-PSDB; ABA94934, ABA94935.

XX Novel placental polypeptides comprising multiple epidermal growth factor-  
PT like domains, designated as Zneu2 polypeptides, useful for stimulating  
PT epidermal tissue growth e.g. in burn treatment and wound healing.

XX

PS Claim 1; Page 2-3; 91pp; English.

XX The invention provides a human placental polypeptide (I), designated  
CC Zneu2 polypeptide, having multiple epidermal growth factor (EGF)-like  
CC domains. The Zneu2 polypeptide can be expressed by standard recombinant  
CC methodology. (I) is useful for constructing Zneu2 variants and to  
CC identify Zneu2 analogues. (I) is useful as a component of defined cell  
CC culture media, alone or in combination with other bioactive agents, to  
CC replace serum that is commonly used in cell culture. (I) is also useful  
CC to identify and isolate Zneu2 receptors. The Zneu2 polynucleotides are  
CC useful for detecting the expression of Zneu2 gene in a biological sample.  
CC It is also useful in linkage-based testing for various diseases, and to  
CC determine whether a subject's chromosomes contain a mutation in the Zneu2  
CC gene. Zneu2 is useful to stimulate epidermal tissue growth (e.g. burn  
CC treatment, skin graft production and administration, wound healing, and  
CC corneal transplant healing). The present sequence represents the human

CC Zneu2 polypeptide

XX

SQ Sequence 1509 AA;

Query Match 3.3%; Score 86; DB 5; Length 1509;

Best Local Similarity 18.3%; Pred. No. 7.6e+02;

Matches 90; Conservative 68; Mismatches 151; Indels 184; Gaps 25;

Qy 81 AADTLQRLGARVASVDMGP-----QQLPDQSLPIPPVILAEELGSDPTKGTVCIFYG 131

Db 224 AVTDFSRDGDVSNIVVQPIVNEDFLWNNYIPDSIQIKVKDV-----PT--AYCY-- 271

Qy 132 HLDVQPADRGDGLTDPYVLTEVDGKLYGRGAT-----DNKGPVLAWINAVSAF 180

Db 272 -----TFIDPHIIT-FDGRVYDNFKTGTFTVLYKMSRDFEVHVRQW-----DC 313

Qy 181 RALEQDLPVNIKFIIEGMEEAGSVAL-----EELVEKEKDRFFSGVDYIVISDNLWISQ- 234

Db 314 RSLHYVPVSCNCGFV---AQEGGDIVTFDMCNGQLRESQPYLFIKSQD---VTRNIKISES 367

Qy 235 ---RKPAITYGT-----RGNSYFMVEVKCRDQDFHS--GTFFGGILHEPMADLVALLGS 282

Db 368 YLGRKVTIWFSSGAFIRADLGEWGMSLTIRAPSVDYRNTLGLCGTFDENPENDFHDKNGM 427

Qy 283 LVDSSGH-----ILVPG--IYDEV-VPLTEEEIINTYKAHLDLEEYRNSRVEKFL 330

Db 428 QIDQNFNNYVAFINERILPGKSMFDTLPVSMTLPGKPSYCSCLDTAAYPSSEDLDSV- 486

Qy 331 FDTKEEI-----LMHLWRYPYLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 384

Db 487 --SRSEIALGCKDLNHV---SLS-----SLIPELDDVT 513

Qy 385 A-----VEKQVTRH-----LEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLA 430

Db 514 SEYINSDTLVREINKHTSPBEYNLNLFLQEKKHINLTGLNVQKHGPNKEKEDSLQYLAN 573

Qy 431 KRAIRTVFGTEPDMIRDSGTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQN---EKINRW 487

Db 574 KKYTQ-----GRGSHSQEMRYNRQNRW 595

Qy 488 ---NYIEGTKLFA 497

Db 596 KRQNFHEFPPLFA 608

RESULT 1080

ADI39291

ID ADI39291 standard; protein; 3896 AA.

XX

AC ADI39291;

XX

DT 22-APR-2004 (first entry)

XX

DE S. hygroscopicus geldanamycin gene cluster-encoded protein, SEQ ID:133.

XX Polyketide biosynthesis; benzoquinone ansamycin; polyketide synthase;

KW PKS; geldanamycin; herbimycin; chimeric PKS; antitumour; cytostatic;

KW geldanamycin gene cluster.

XX

OS Streptomyces hygroscopicus; var. geldanus NRRL 3602.

XX

PN WO2003106653-A2.

XX

PD 24-DEC-2003.

XX

PF 16-JUN-2003; 2003WO-US019069.

XX

PR 14-JUN-2002; 2002US-0389255P.

PR 03-JUL-2002; 2002US-0393929P.

PR 12-JUL-2002; 2002US-0395275P.

PR 05-AUG-2002; 2002US-00212962.

PR 30-SEP-2002; 2002US-0415326P.

PR 24-OCT-2002; 2002US-0420820P.

PR 13-DEC-2002; 2002US-0433130P.  
PR 13-JUN-2003; 2003US-00461194.  
XX (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
XX Hutchinson CR, Hu Z, Rascher A, Schirmer A, Mcdaniel R;  
XX WPI; 2004-071556/07.  
DR N-PSDB; ADI39159.  
XX  
PT Producing a polyketide such as progeldanamycin from a cell transfected  
PT with a recombinant polynucleotide encoding the geldanamycin or herbimycin  
PT polyketide synthase.  
XX  
PS Example 1; SEQ ID NO 133; 332pp; English.  
XX  
CC The invention relates to a method for producing polyketides by culturing  
CC a cell comprising a recombinant polyketide synthase (PKS)-encoding region  
CC of the geldanamycin gene cluster (ADI39159) of Streptomyces hygroscopicus  
CC var. geldanus NRRL 3602 or the herbimycin gene cluster (ADI39160) of  
CC Streptomyces hygroscopicus AM-3672. The invention also relates to a  
CC method of producing a polyketide other than geldanamycin by modification  
CC of a gene in the geldanamycin gene cluster; a method of producing a  
CC polyketide other than herbimycin by modification of a gene in the  
CC herbimycin gene cluster; recombinant DNA molecules encoding a domain of a  
CC geldanamycin or a herbimycin PKS, a geldanamycin or herbimycin  
CC modification enzyme involved in the conversion of progeldanamycin to  
CC geldanamycin or proherbimycin to herbimycin, or a chimeric PKS comprising  
CC a portion of geldanamycin or herbimycin PKS fused to a portion of a  
CC different PKS; and host cells comprising the recombinant DNA molecules.  
CC The invention further discloses a PCR-based method to rapidly query the  
CC genomic DNA for the presence of type I modular PKS genes, and isolated  
CC and purified herbimycin and geldanamycin PKS domains expressed from  
CC nucleic acids of the invention. The methods of the invention are useful  
CC for producing geldanamycin and herbimycin, both compounds with antitumour  
CC activity, on a commercially useful scale, and to produce geldanamycin  
CC analogues. Sequences ADI39273-ADI39304 represent proteins encoded by the  
CC geldanamycin gene cluster of Streptomyces hygroscopicus var. geldanus  
CC NRRL 3602.  
XX  
SQ Sequence 3896 AA;

Query Match 3.3%; Score 86; DB 8; Length 3896;  
Best Local Similarity 21.8%; Pred. No. 3.3e+03;  
Matches 117; Conservative 48; Mismatches 177; Indels 194; Gaps 26;  
QY 32 PALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPV--RFRQELFRMMVAADTLQ--- 86  
Db 1149 PALLDAA-----LHAGSF-----CLPSPDPARQVTLPLFAWNTVRLHAGGASAVRVHV 1195  
QY 87 -----RL----GARVASVD-----MGPPQLPDG-----QSLPIPPV 113  
Db 1196 RPVGDDAFSVRLTDGSGQTVASVDSLTLRAVDPAQLKIGTADDALWTVRWSETSLPDGAV 1255  
QY 114 ILAELGSDPTKGTVCFYGHLDVQPADRGDGLWTDPPVLTVDGKLYGRGAT-DNKGPVLA 172  
Db 1256 SWAPLGESAT-----GATGGYGATGDDGGPGGA 1283  
QY 173 WINA-VSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLW 231  
Db 1284 LPDVLVADTRAWAEDL-----TGPPTARARELTGRLLLEEIQRW-----VADDAM 1327  
QY 232 ISQRKPAITYGTRGNSYFMVEVKCRDQ-----DFHSGTFFGILHEPMADLVALLGSLVDSS 287  
Db 1328 AGTRLAVVTRGA-----VAVHDDTEVTDPAATALWGLVRSQAEPGRV-ALVDAD 1377  
QY 288 G--HILVPGIY--DE-----VVPLTEEE-----INTYKAHLDLLEEYRNSRVEK 328  
Db 1378 GACEELPAGVSGDEPQLAVRGAVVWVPLRTRVEPGLRVPAQASWHLDSAIEYGTLDNL-A 1436  
QY 329 FLFDTKE-----EILMHLWRYPSLSIHGIEGA--FDEPG---TK 362

Db 1437 LLPDEAEPAPPAACQVRIEVRAGLNFDRDVLVALGMYPGRSVIGTEGAGVVTVTEVGPVTG 1496  
QY 363 TVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVSVMTLGLHPWIANI 422  
Db 1497 LAVGDRVMGLFSGSGPLATADA-----RTVIRMPEGWSFCTAAG 1536  
QY 423 DDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEH 478  
Db 1537 VPVAYLTALYALQDLGRVQP-----GETV-----LVHAAAGGVGMAAVQLAQH 1579  
RESULT 1081  
AAE31506  
ID AAE31506 standard; protein; 131 AA.  
XX  
AC AAE31506;  
XX  
DT 24-FEB-2003 (first entry)  
XX  
DE Latex Hev b8 profilin III protein.  
XX  
KW Profilin; therapy; allergy; immunoassay; latex.  
XX  
OS Hevea brasiliensis.  
XX  
PN WO200270005-A1.  
XX  
PD 12-SEP-2002.  
XX  
PF 27-FEB-2002; 2002WO-US005911.  
XX  
PR 28-FEB-2001; 2001US-0272149P.  
XX  
PA (IMMV-) IMMVARX INC.  
XX  
PI Babich M;  
XX  
XX WPI; 2003-046731/04.  
XX  
PT Purified multimeric forms of plant profilin, for use in a diagnostic test  
PT for allergies and to hyposensitize a mammal, comprises plant profilin  
PT monomers each comprising a sequence containing a cysteine.  
XX  
PS Claim 10; Page 15-16; 37pp; English.  
XX  
CC The invention relates to purified multimeric forms of plant profilin used  
CC in diagnosis and treatment of allergies. Multimeric profilin, or a  
CC functional equivalent of it, is used in a diagnostic test for allergies  
CC and is used to hyposensitize a mammal. It is also used in immunoassays  
CC and for screening patients to determine profilin allergenicity. The  
CC present sequence is latex Hev b8 profilin protein  
XX  
SQ Sequence 131 AA;  
Query Match 3.3%; Score 85.5; DB 6; Length 131;  
Best Local Similarity 24.3%; Pred. No. 19;  
Matches 41; Conservative 22; Mismatches 47; Indels 59; Gaps 9;  
QY 144 WLT--DPYVLTEVDG-KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEE 200  
Db 3 WQTYVDEHLMCDIDGHHLTAAAIIGHDGSVWQAQSSFPQFK-----PEEVAAIMKDFDE 56  
QY 201 AGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP-AITYGTRGNSYFMVEVKCRDQD 259  
Db 57 PGSLAPTGL-----HLGGTKYMWI-----QGEPAVIRKKGS----- 89  
QY 260 FHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN 308  
Db 90 -----GGI-----TVKKTQALIIIGIYDE--PLTPGQC 116  
RESULT 1082  
AAB11959







[illegible]

CC	on expression of the CA gene. The CAP proteins are useful for detecting
CC	cancer associated with expression of a CAP protein in a test cell sample
CC	and for screening for a bioactive agent capable of modulating the
CC	activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC	cancer, involving determining the expression of a CA nucleic acid in a
CC	tissue. This sequence represents a human CAP of the invention. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 259 AA;
	Query Match            3.3%; Score 85.5; DB 8; Length 259;
	Best Local Similarity 19.9%; Pred. No. 55;
	Matches 60; Conservative 52; Mismatches 96; Indels 93; Gaps 15
QY	159 YRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEGAGSVALE-ELVEKEKD RF 217
Db	: ::: : :  :         : : : :
D b	11 HGEA WNKENR FCSWVDQ-----KLNSEGMEEEARNCGQLKALNFEFDLV 55
QY	218 FSGV-----DYIVISDNLWISQRKPAITYGTRGN SYFMVEVKCRDQDFHSGTGGILH 270
Db	:  : : : : : : : :  :  :  :  :
D b	56 FTSVLNRSIHTAWLILEE-----LGQEWVPV ESWRLNERHYGALIGLNR 100
QY	271 EPMA-----DLVALGLSLVDSSGHILVPGIYDEVVPLTEEEIN--TYKA IHL DLEEYRNS 323
Db	: :  : :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
D b	101 EQMALNHGEEQVR LW-----RRSYNVTPPPIEESHPPYQEIYNDRRYKVCDVPLDQLPRS 155
QY	324 SRVEKFLFDTK EEILMHLWRYP SLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN V 383
Db	::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
D b	156 ESLKDV L-----ERLLPYW-----NERIAPEVLR GK-TILISAHGNS 191
QY	384 SAVEKQVTRHLEDVF SKRNSSNMKVSM TL--GLHPWTIANIDDT-----QYLAAKRAI 434
Db	: : :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
D b	192 S---RAL LKHLEGI-----SDEDI INITLPTGV-PILLELDENLR A VGPHQFLGDQEI 241
QY	435 R 435
D b	242 Q 242
 RESULT 1087	
ABO84886	
ID	ABO84886 standard; protein; 259 AA.
XX	
AC	ABO84886;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human cancer-associated protein (CAP) HP07-057.1.
XX	
KW	Human; cancer-associated protein; CAP; cancer; cytostatic.
XX	
OS	Homo sapiens.
XX	
PN	WO2004058146-A2.
XX	
PD	15-JUL-2004.
XX	
PF	15-DEC-2003; 2003WO-US040081.
XX	
PR	17-DEC-2002; 2002US-00322281.
XX	
PA	(SAGR-) SAGRES DISCOVERY INC.
XX	
PI	Morris DW, Malandro MS;
XX	
DR	WPI; 2004-499109/47.
DR	N-PSDB; ABD33320.
XX	
PT	Novel human cancer associated protein encoded within open reading frame
PT	of cancer associated gene, useful as targets for diagnosing cancer.
XX	

PS Claim 18; SEQ ID NO 390; 182pp; English.  
XX The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 259 AA;

Query Match 3.3%; Score 85.5; DB 8; Length 259;  
Best Local Similarity 19.9%; Pred. No. 55;  
Matches 60; Conservative 52; Mismatches 96; Indels 93; Gaps 15;  
QY 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALE-ELVEKEKDRF 217  
Db 11 HEGAWNKENRFCSWVDQ-----KLNSEGMEEARNCCKQLKALNFEFDLV 55  
QY 218 FSGV-----DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILH 270  
Db 56 FTSVLNRSIHTAWLILEE-----LQGEWVPVLESSWRLNERHYGALIGLNR 100  
QY 271 EPMA-----DLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN--TYKAIHLDLEEYRNS 323  
Db 101 EQMALNHGEEQVRLW-----RRSYNVTPTPIEESHYPYQEIYNDRRYKVCDDVPLDQLPRS 155  
QY 324 SRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNV 383  
Db 156 ESLKDVL-----ERLLPYW-----NERIAPEVLRGK-TILISAHGNS 191  
QY 384 SAVEKQVTRHLEDVFSKRNSNKMVWSMTL--GLHPWIANIDDT-----QYLAAKRAI 434  
Db 192 S---RALLKHLEGI-----SDEDIINITLPTGV-PILLELDENLRAVGPHQFLGDQEI 241  
QY 435 R 435  
Db 242 Q 242

RESULT 1088  
ABO84888  
ID ABO84888 standard; protein; 259 AA.  
XX  
AC ABO84888;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human cancer-associated protein (CAP) HP07-057.3.  
XX  
KW Human; cancer-associated protein; CAP; cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004058146-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 15-DEC-2003; 2003WO-US040081.  
XX  
PR 17-DEC-2002; 2002US-00322281.  
XX  
PA (SAGR-) SAGRES DISCOVERY INC.

XX PI Morris DW, Malandro MS;  
XX WPI; 2004-499109/47.  
DR N-PSDB; ABD33322.  
XX  
PT Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.  
XX  
PS Claim 18; SEQ ID NO 394; 182pp; English.  
XX  
CC The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 259 AA;

Query Match 3.3%; Score 85.5; DB 8; Length 259;  
Best Local Similarity 19.9%; Pred. No. 55;  
Matches 60; Conservative 52; Mismatches 96; Indels 93; Gaps 15;  
QY 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALE-ELVEKEKDRF 217  
Db 11 HEGAWNKENRFCSWVDQ-----KLNSEGMEEARNCCKQLKALNFEFDLV 55  
QY 218 FSGV-----DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILH 270  
Db 56 FTSVLNRSIHTAWLILEE-----LQGEWVPVLESSWRLNERHYGALIGLNR 100  
QY 271 EPMA-----DLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN--TYKAIHLDLEEYRNS 323  
Db 101 EQMALNHGEEQVRLW-----RRSYNVTPTPIEESHYPYQEIYNDRRYKVCDDVPLDQLPRS 155  
QY 324 SRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNV 383  
Db 156 ESLKDVL-----ERLLPYW-----NERIAPEVLRGK-TILISAHGNS 191  
QY 384 SAVEKQVTRHLEDVFSKRNSNKMVWSMTL--GLHPWIANIDDT-----QYLAAKRAI 434  
Db 192 S---RALLKHLEGI-----SDEDIINITLPTGV-PILLELDENLRAVGPHQFLGDQEI 241  
QY 435 R 435  
Db 242 Q 242

RESULT 1089  
ABB97202  
ID ABB97202 standard; protein; 270 AA.  
XX  
AC ABB97202;  
XX  
DT 28-JUN-2002 (first entry)  
XX  
DE Novel human protein SEQ ID NO: 470.  
XX  
KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;  
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
KW neuroprotective; antiparkinsonian; protein therapy; EST;  
KW expressed sequence tag.



XX OS Homo sapiens.  
XX PN WO200222660-A2.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US026015.  
XX PR 11-SEP-2000; 2000US-00659671.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX WPI; 2002-292408/33.  
DR N-PSDB; ABN32388.  
XX An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis.  
PT  
XX Example 2; SEQ ID NO 470; 509pp; English.  
XX The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibit e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke  
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.  
CC rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention  
XX  
SQ Sequence 270 AA;  
Query Match 3.3%; Score 85.5; DB 5; Length 270;  
Best Local Similarity 19.9%; Pred. No. 58;  
Matches 60; Conservative 52; Mismatches 96; Indels 93; Gaps 15;  
QY 159 YGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALE-ELVEKEKDRF 217  
Db 22 HGEGAWNKENRFCSSWDQ-----KLNSEGMEEARNCGKQKALNFEFDLV 66  
QY 218 FSGV-----DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILH 270  
Db 67 FTSVLNRSIHTAWLILEE-----LGQEWVPVSESWRLNERHYGALIGLNR 111  
QY 271 EPMA-----DLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN--TYKAHLDLEEYRNS 323  
Db 112 EQMALNHGEEQVRLW-----RRSYNVTPPIEESHPIYQEIYNDRYKVCDDVPLDQLPRS 166  
QY 324 SRVEKFLFDTKKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 383  
Db 167 ESLKQVL-----ERLLPYW-----NERIAPEVLRGK-TILISAHGNS 202  
QY 384 SAVEKQVTRHLEDVFSKRNSNKMVSMTL--GLHPWIANIDDT-----QYLAAKRAI 434  
Db 203 S---RALLKHLEGI-----SDEIINITLPTGV-PILLELDENLRAVGP HQFLGDQEA I 252  
QY 435 R 435  
Db 253 Q 253  
RESULT 1090  
ADM25679  
ID ADM25679 standard; protein; 322 AA.  
XX  
AC ADM25679;  
XX  
DT 20-MAY-2004 (first entry)

XX Hyperthermophile Methanopyrus kandleri protein #285.  
DE  
XX  
KW hyperthermophile; protein stability enhancement;  
XX protein activity enhancement.  
OS Methanopyrus kandleri.  
XX WO2003076575-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 04-MAR-2003; 2003WO-US006664.  
XX  
PR 04-MAR-2002; 2002US-0361742P.  
PR 14-MAY-2002; 2002US-0380423P.  
PR 16-SEP-2002; 2002US-0410974P.  
XX (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
PA  
XX Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;  
PI  
XX WPI; 2003-748383/70.  
DR N-PSDB; ADM27081.  
DR  
XX New isolated nucleic acids encoding any of about 1700 Methanopyrus  
PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
PT as diagnostic agents.  
PT  
XX Claim 31; SEQ ID NO 285; 1023pp; English.  
PS  
XX The invention comprises the amino acid sequence of proteins from the  
XX hyperthermophile Methanopyrus kandleri, the invention also comprises the  
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
CC proteins of the invention are useful for enhancing the stability and/or  
CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
CC a variety of diagnostic and analytical methods. The present amino acid  
CC sequence represents a Methanopyrus kandleri protein of the invention.  
XX  
SQ Sequence 322 AA;  
Query Match 3.3%; Score 85.5; DB 7; Length 322;  
Best Local Similarity 23.5%; Pred. No. 77;  
Matches 70; Conservative 36; Mismatches 91; Indels 101; Gaps 17;  
QY 170 VLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELV-----EKEKDRFFSGVD 222  
Db 4 VLAVAGTDGALVAGDR-----RTLVARMDDEKMRKVEEKLYSGEIRTEEELESFLKDLD 57  
QY 223 ----YIVISDN---LW-----ISQRKPAITYGTRGNSYFMVEVKCRD 257  
Db 58 VEDGYFEFHDDRRKKWKVNDEVVAGEVGVRSAGVRRRR---VYATPG-AHAIVELE--G 111  
QY 258 QDFHSGTGG---ILHEPMA-----DLVALLGSLVD-----SSGHILV 292  
Db 112 EKVLKSNFGGPPALIVEGPKVVKELVIEFVNSELGGKPDLESRLNALDDDLFEYVSSGTILV 171  
QY 293 PGIYD-----EVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKKEEILMHLWRYPS 346  
Db 172 SSEYDAYEVKGKADPLARLQ--KAIDEDIERLREHRR-----RLAEEMLKHIREGYD 223  
QY 347 LSIHGIEGAFDEPGT-----KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV 397  
Db 224 ILKEGVVGEVVEVGTETEEKGKVEDVPPER-----RIV-----VRLAEDVDARHMGDV 270  
RESULT 1091  
ABU29969  
ID ABU29969 standard; protein; 364 AA.  
XX  
AC ABU29969;  
XX

DT 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #15496.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
KW Enterococcus faecium.  
XX WO200277183-A2.  
PN 03-OCT-2002.  
PD 21-MAR-2002; 2002WO-US0009107.  
PF 21-MAR-2001; 2001US-00815242.  
XX 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA33839.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 57893; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 364 AA;  
Query Match 3.3%; Score 85.5; DB 6; Length 364;  
Best Local Similarity 19.0%; Pred. No. 93;  
Matches 74; Conservative 51; Mismatches 129; Indels 135; Gaps 17;  
QY 30 PPPALLEKFQYIDL-HQDEFVQTLKEWVAIESDSVQVPRFRQ----- 72

Db 10 PERSTFEKDKAYLDLAHKYGYQRVLTSLWQLINDDKKVLSEFKEVVDYANSLGMEVMVDI 69  
QY 73 --ELFRMMAVAADTL---QRLGARVASVDMGPQQLPDGQSLPIPPVILAE----- 118  
Db 70 NPALFEQLEISYDDLFFHKMGAYGVRLDIGFTGABEAKMTRNPFGIKIEINNSSGTYV 129  
QY 119 -----GSDPTKGTVCFYGLDVQPADRGDWLTDPYVLTVDGKLYGRGATDNKGPV 170  
Db 130 DNIMSYSPNTDNLGSHNFYPH-----RYSGLGYEHFVFCSEKFRKYNLN-----T 175  
QY 171 LAWINAVSA-----FRALEQDLPVNIKF-----IIEGMEEAGSVALEEL 209  
Db 176 MAFVNSQSAEFGPWPTQDGLCTLEDHRDLE--IATQVKHLILTGLIDDISIGNAYASEE 233  
QY 210 VEKEKDRFFSGVDY-----IVISDNLWISQKPAITYGTRGNSYFMVEV 253  
Db 234 LKEMAEAF--NADYPTLKVDTEEGITENERICLFDNLH-SYRGDRSEYILRST---MTRV 287  
QY 254 KCRDQDFHSGTGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA- 312  
Db 288 YYKDKDFPHNTRDMHGDV-----LIDNEG-----GQYKGE 320  
QY 313 IHLDLLEYRNSRV-----EKFLFD 332  
Db 321 TQIALXDMKNDGRVNVVGRISDDELFLD 349  
RESULT 1092  
ABO62697  
ID ABO62697 standard; protein; 388 AA.  
XX  
AC ABO62697;  
XX  
DT 29-JUL-2004 (first entry)  
XX Klebsiella pneumoniae polypeptide seqid 9214.  
DE Klebsiella pneumoniae polypeptide seqid 9214.  
XX  
KW Recombinant expression vector; transcription regulatory element;  
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.  
XX  
OS Klebsiella pneumoniae.  
XX  
PN US6610836-B1.  
XX  
PD 26-AUG-2003.  
XX  
PF 27-JAN-2000; 2000US-00489039.  
PR 29-JAN-1999; 99US-0117747P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA Breton GL, Osborne M;  
PI WPI; 2003-895346/82.  
XX N-PSDB; ACH96248.  
DR  
DR  
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
PS Disclosure; SEQ ID NO 9214; 932pp; English.  
XX  
CC The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention  
XX  
SQ Sequence 388 AA;

Query Match 3.3%; Score 85.5; DB 7; Length 388;  
Best Local Similarity 19.5%; Pred. No. 1e+02;  
Matches 70; Conservative 57; Mismatches 135; Indels 97; Gaps 17;

QY 25 FSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVA-- 82  
Db 63 FGGIEPNPS-YETLMNAVKLAREEKVTF--LAVGGSVLDGTFK-----IAAAHY 111

QY 83 -----DTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAELGSDPTKGTVC----- 128  
Db 112 DADIDPWEILETYGSKIASA-----IPMGSVLTLPAT-----GSESNKGAVISRKTITGD 160

QY 129 -----FYGHLDVQPADRGDWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALE 184  
Db 161 KRAFMSSHVPQFA-----ILDPPVYTYTLPPRQVANGVVD-----AFVHTVEQY----- 204

QY 185 QDLPVNIKPIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTR 244  
Db 205 -----VTYPVDG-----KIQDRFAEGILLTLIEDGPKALQEP--NYNVR 242

QY 245 GNSYFMVEVKR-----DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYD 297  
Db 243 ANIMWAATQALNGLIGAGVPQDWATHMLG---HE---LTAMHGLDHAQTIAIVLPALWN 295

QY 298 EVVPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPS-LSIHGIEGA 355  
Db 296 EKRDAREKLLQYAERVWNITEGSDQORIDAAIAATRQ--FFEQMGVPTRLSDYGLDGS 352

RESULT 1093  
ADS12038  
ID ADS12038 standard; protein; 412 AA.  
XX  
AC ADS12038;  
XX  
DT 16-DEC-2004 (first entry)  
DE Human therapeutic contig protein - SEQ ID 2275.  
XX  
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
KW aplastic anaemia; cancer; wound healing; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..412  
FT /label= Unknown, OTHER  
FT /note= "OTHER = In-frame STOP codon"  
XX  
PN WO2004080148-A2.  
XX  
PD 23-SEP-2004.  
XX  
PF 30-SEP-2003; 2003WO-US030720.  
XX  
PR 02-OCT-2002; 2002US-0416186P.  
XX  
PA (NUVE-) NUVELO INC.  
XX  
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
XX  
DR WPI; 2004-668857/65.  
DR N-PSDB; ADS11440.  
XX  
PT New polynucleotide, useful in preparing a composition for diagnosing or  
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
XX  
XX aplastic anemia or cancer for promoting wound healing.  
PS Example 2; SEQ ID NO 2275; 718pp; English.  
XX  
CC The invention relates to a novel isolated polynucleotide and the encoded

CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic contig  
CC protein of the invention.  
XX  
SQ Sequence 412 AA;  
Query Match 3.3%; Score 85.5; DB 8; Length 412;  
Best Local Similarity 19.4%; Pred. No. 1.1e+02;  
Matches 72; Conservative 67; Mismatches 140; Indels 93; Gaps 17;

QY 82 ADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAELG-----SDPTKGTVCFYGHLDVQ 136  
Db 36 SDIYQATESEVGDVLD--TRLPEG---PVDSEDDDEEIDEIDRTDPLQGRDLVRECLEKE 90

QY 137 PADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNI--KFI 194  
Db 91 PADKTD-----DDIEQLLEFMEHQLPAPANMTMSVRRELCSVMI 128

QY 195 IEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVK 254  
Db 129 FEVVEQAGAIILED--GQELDSW-----YVILNGTVEISHPDGKVENLFMGNSFGITPT- 180

QY 255 CRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKA-- 312  
Db 181 -LDKQYMHG-----IVRTKVDDCCQFVCI-AQQDYWRILNHVEKNTHKVEE 223

QY 313 -----IHLDLLEEYRNSRVEKFLFD-TKEEILMHLWRYPSLSIHGIEGAFDEP---GTK 362  
Db 224 EGEIVMVHEHRELDMSGTRKGHIVIKATPERLIMHLIEHSI---VDPTYIEDFLLTYSR 279

QY 363 TVIPGRVIGKFSIRLVPHNMVSAVEKQVTR-----HLEDVFSKRNSNMVSVMTLG 414  
Db 280 TFLSPPL--DVGIKLLEWFKIDSLRDKVTRIVLLWNHNFNDFEGD-----PAMTRF 329

QY 415 LHPWIANIDDTQ 426  
Db 330 LEEFEKNLEDTK 341

RESULT 1094  
ADS12039  
ID ADS12039 standard; protein; 412 AA.  
XX  
AC ADS12039;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Human therapeutic contig protein - SEQ ID 2276.  
XX  
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
XX  
XX aplastic anaemia; cancer; wound healing; gene therapy.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..412  
FT /label= Unknown, OTHER  
FT /note= "OTHER = In-frame STOP codon"  
XX  
PN WO2004080148-A2.  
XX  
PD 23-SEP-2004.  
XX  
PF 30-SEP-2003; 2003WO-US030720.  
XX  
PR 02-OCT-2002; 2002US-0416186P.  
XX





Db 261 KEDTYLSEINKDIEEC--NAIEQFIDYLRGTQEMPMEFCELNSI----- 304  
QY 362 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIAN 421  
Db 305 -----LKEVISAENGYEQDIEN-HLSLHPITVN 331  
QY 422 IDDTQYLAAKRAI 434  
Db 332 ANP---ISIKRAL 341  
RESULT 1096  
AAY14049  
ID AAY14049 standard; protein; 544 AA.  
XX  
AC AAY14049;  
XX  
DT 15-JUL-1999 (first entry)  
XX  
DE G. oxydans D-sorbitol dehydrogenase.  
XX  
KW D-sorbitol dehydrogenase; L-sorbose; 2-keto-L-gulonic acid; precursor;  
KW L-ascorbic acid production.  
XX  
OS Gluconobacter oxydans.  
XX  
PN WO9920763-A1.  
XX  
PD 29-APR-1999.  
XX  
PF 13-OCT-1998; 98WO-JP004612.  
XX  
PR 17-OCT-1997; 97JP-00285280.  
XX  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
XX  
PI Saito Y, Ishii Y, Noguchi Y, Yoshikawa K, Soeda S;  
XX WPI; 1999-302741/25.  
DR N-PSDB; AAX57909.  
XX  
PT Gene group for D-sorbitol dehydrogenase, useful for simple large-scale  
PT production of L-sorbose or 2-keto-L-gulonic acid as precursor for L-  
PT ascorbic acid.  
XX  
PS Claim 7; Page 52-54; 83pp; Japanese.  
XX  
CC This sequence represents the D-sorbitol dehydrogenase of the invention.  
CC Cells transformed with a vector containing DNA encoding the dehydrogenase  
CC can be used to produce L-sorbose or 2-keto-L-gulonic acid as precursor  
CC for simple large-scale L-ascorbic acid production  
XX  
SQ Sequence 544 AA;  
Query Match 3.3%; Score 85.5; DB 2; Length 544;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
Matches 106; Conservative 65; Mismatches 165; Indels 205; Gaps 27;  
QY 79 AVAADTLQRLGARVASVDMGPQ-----QLPDGQSLPIPPVILAEGLSDPTKG 125  
Db 20 ASIANELARAGLSVIVLEAGPRIDRQHILENFRRTTENKGAYQLPYPPVPA----- 70  
QY 126 TVCFYGLDVPADRG--DGWL--TDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFR 181  
Db 71 -----MHPFDQGSNGYLHTTGP-----DGAAYQQGYLRFVVGTT-TWHWAGCAWR 114  
QY 182 ALEQDLPVNKIFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITY 241  
Db 115 YLPDSDFELH-----SRYGVRDWAIXYDDLEPFYYQAEVMM 150  
QY 242 GT-----RGSYFMVEVKC---RDQD---FHSGTFGILHEPMAD----- 275

Db 151 GVAGPNMVDVDDLGSPRSHNYPMKEVPLSYGADQFRKLIHEKTNRYRVVHEPQARNTRPYDK 210  
QY 276 -----LVALLGSL---VDSSGHILVPG---IYDEVVPLTEEEINTYKAHLDD-L 317  
Db 211 RPTCEGNNNCMPICPIGAMYNGIHSVNHAEEAGARIIPNAVYRLETASNKKVVPVNY 270  
QY 318 BEYRNSSRVEKFLFDTK---EEILMHLWRYPSLSIHGIEGAFDE----- 358  
Db 271 DPKNSHRVTGKFFVVAACHIESAKLLLLSADDKNPRGIANSSDQVGRNMDHTGVQLSF 330  
QY 359 -PGTKTVIPGR-----VI-----GKFSIRLVPHMNV-----SA 385  
Db 331 MSGNDSLWPGRGPLLTSLIDSFRDGPWRSERGAYLVHMVDDNQVDFATGLAIAKGYVGKE 390  
QY 386 VEKQV---TRHLEDVFSKR---NSSNMVVSMT-----LGL-HP-----WIANIDD 424  
Db 391 LEEQIRYGSASHAVRLFSSHNEGIADPDNRLTLSTKHKDVLGIPHPEVYKLPETVTKSCDH 450  
QY 425 TOYLAAKRAIRTVFGTEPDMIR-----DGSTPIAKMFQEIIVHKSVVLIPLGAVDDG 476  
Db 451 TKEL-FKELMALMSGTDPOWTKGYFPQCHPSGSTI-----MGTDPTNSVVVDG 496  
QY 477 E 477  
Db 497 E 497  
RESULT 1097  
ABG16690  
ID ABG16690 standard; protein; 594 AA.  
XX  
AC ABG16690;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #16681.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS80877.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 47049; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a





XX PD 03-AUG-2000.  
XX PF 28-JAN-2000; 2000WO-GB0000263.  
XX PR 28-JAN-1999; 99GB-00001902.  
XX PA (ROYA-) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
XX PI Bramley PM, Harker M;  
XX DR WPI; 2000-505979/45.  
XX PT Manipulating isoprenoid expression in cells or organisms and identifying  
PT modulators of the expression, for use in antibacterials and herbicides  
PT and to produce transgenic plants with improved properties.  
XX PS Claim 26; Fig 3; 52pp; English.  
XX CC The present invention describes a method for manipulating isoprenoid  
CC expression in cells or organisms having a mevalonate independent  
CC isopentenyl diphosphate (IPP) synthesising pathway. The method comprises  
CC altering the activity of 1-deoxy-D-xylulose-5-phosphate synthase (DXPS),  
CC or a functional equivalent, derivative, or bioprecursor of it. The  
CC isoprenoid activity or expression modulators are used as medicaments to  
CC treat bacterial diseases, and as herbicides. The method can be used to  
CC produce transgenic plants which have higher levels of isoprenoids, and  
CC which have health care benefits when consumed. The present sequence  
CC represents the DXPS protein from *Synechocystis* sp. 6803, which is used in  
CC the exemplification of the present invention. (Updated on 12-SEP-2003 to  
CC standardise OS field)  
XX SQ Sequence 633 AA;

Query Match 3.3%; Score 85.5; DB 3; Length 633;  
Best Local Similarity 21.8%; Pred. No. 2.2e+02;  
Matches 63; Conservative 37; Mismatches 84; Indels 105; Gaps 16;  
QY 271 EPMADLVA--LLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSSRVEK 328  
Db 21 EKLSDEIRQFLITSLASGGHI--GPNLGVVELT-----VALHKEF-----NSPKDK 65  
QY 329 FLFDTKKEILMH-----LWR--YPSLSIHGIEG- 354  
Db 66 FLWDVGHQSYVHKLLTGRGKEFATLRQYKGLCGFPKRSESHDVWETGHSSTLSGAMGM 125  
QY 355 --AFDEPGT-KTVIP---GRVIGKFSIRLVPHM-----NVSARE 387  
Db 126 AAARDIKGTDEYIPIIGDGALTGGMALEALNHIGDEKKDMIVILNDNEMSIAPNVGAIH 185  
QY 388 KQVTRHLEDVFSKRNSNKMVSMVLGLHPWIANIDDTQYLAAK-RAIRTVFGTEPDMIR 446  
Db 186 SMLGR-----LRTAGKYQWVK--DELEYLFKKIPAVGGKLAATAERVK 226  
QY 447 DG-STIPIAKMFQEIHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTK 494  
Db 227 DSLKYMVLVSGMFFE----ELGFTYLGPDVG--HSYHELIENTLYQAKKTK 269

RESULT 1100  
AAO21848  
ID AAO21848 standard; protein; 633 AA.  
XX  
AC AAO21848;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Isoprenoid related protein sequence SEQ ID No 19.  
XX  
KW Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS; DDS;  
KW decaprenyl diphosphate synthase.  
XX  
OS *Bacillus subtilis*.

XX PN WO200226933-A2.  
XX PD 04-APR-2002.  
XX PF 28-SEP-2001; 2001WO-US030328.  
XX PR 29-SEP-2000; 2000US-0236580P.  
XX PA (CRGI ) CARGILL INC.  
XX PI Gokarn R, Jessen H, Zidwick MJ;  
XX DR WPI; 2002-416480/44.  
XX PT Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate  
PT synthase activity, useful for the production of isoprenoids, especially  
PT CoQ(10).  
XX PS Disclosure; Fig 6; 246pp; English.  
XX CC The invention relates to methods and materials for the production of  
CC isoprenoids. More particularly the invention provides isolated nucleic  
CC acids, substantially pure polypeptides, host cells, and methods for  
CC producing various isoprenoid compounds. The polypeptides are useful for  
CC the production of isoprenoids, especially CoQ(10). Expressing the pure  
CC polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS)  
CC activity or decaprenyl diphosphate synthase (DDS) activity, is useful for  
CC increasing production of CoQ(10) in a cell having endogenous DDS  
CC activity. This sequence represents a protein relating to the isoprenoid  
CC production of the invention  
XX SQ Sequence 633 AA;

Query Match 3.3%; Score 85.5; DB 5; Length 633;  
Best Local Similarity 21.8%; Pred. No. 2.2e+02;  
Matches 63; Conservative 37; Mismatches 84; Indels 105; Gaps 16;  
QY 271 EPMADLVA--LLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNSSRVEK 328  
Db 21 EKLSDEIRQFLITSLASGGHI--GPNLGVVELT-----VALHKEF-----NSPKDK 65  
QY 329 FLFDTKKEILMH-----LWR--YPSLSIHGIEG- 354  
Db 66 FLWDVGHQSYVHKLLTGRGKEFATLRQYKGLCGFPKRSESHDVWETGHSSTLSGAMGM 125  
QY 355 --AFDEPGT-KTVIP---GRVIGKFSIRLVPHM-----NVSARE 387  
Db 126 AAARDIKGTDEYIPIIGDGALTGGMALEALNHIGDEKKDMIVILNDNEMSIAPNVGAIH 185  
QY 388 KQVTRHLEDVFSKRNSNKMVSMVLGLHPWIANIDDTQYLAAK-RAIRTVFGTEPDMIR 446  
Db 186 SMLGR-----LRTAGKYQWVK--DELEYLFKKIPAVGGKLAATAERVK 226  
QY 447 DG-STIPIAKMFQEIHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTK 494  
Db 227 DSLKYMVLVSGMFFE----ELGFTYLGPDVG--HSYHELIENTLYQAKKTK 269

RESULT 1101  
ADS44770  
ID ADS44770 standard; protein; 633 AA.  
XX  
AC ADS44770;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #23200.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;



Db 265 VYLPFIASYFEMSEWSLPAQQAFLVEFEVK-----LKELNMFERYRVF-----VRGGI 312

QY 231 W-----ISQKPAITYGTRGN---SYFMVEVKCRDQDFHSGTGGILHEPMAD 275

Db 313 WKNFFYKYPEANYMHKRMMLSLRLLRDNPSARRFVLAQCNDAVWH-GVFGGIYLPHLRR 371

QY 276 LVALLGSLVDSSGH-----ILVPGIYDEVVPLTEEE-- 306

Db 372 --AIWSNLIKAHSHLEPKNKILDVDFDGRREVFLENDNFIIIVKPHYGGSIFELSSKRA 429

QY 307 INTYKAIHLDLEEYRNSRVE-----KFLFDTKBEILMHLWRYPSLS 348

Db 430 VNYADVIARRWEHYHNLGESESDDNENQEGVSSIHEIGKRIPEDIRKELAYDRYRRGILQ 489

QY 349 IH-----GIEGAFD-EPGKTVPGRVIGKFSIRLVPHMNVSAV 386

Db 490 DHFFSANETLDRYRLAKYWELGDFIEGVYNYEVGNGLVLWRR--GKV-----LNVTV 540

QY 387 EKQVTRHLEDVFSKRNSSNMVSMVMTGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIR 446

Db 541 VKKSIEVREDGFSVRYT-----VLSEEDIEALFGIELNI-- 574

QY 447 DGSTIPIAKMFQEIYVHKSVLPLGAVDDGEHSQNEKINRWNY 489

Db 575 --AVHSIKESPEELIGKRIKVNCKYGVGFEIVLNKKARIWKY 615

RESULT 1103

ABU241188

ID ABU241188 standard; protein; 696 AA.

XX AC ABU241188;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #9715.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

KW Clostridium acetobutylicum.

OS WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US0009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA28058.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 52112; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 696 AA;

Query Match 3.3%; Score 85.5; DB 6; Length 696;

Best Local Similarity 21.2%; Pred. No. 2.5e+02;

Matches 99; Conservative 64; Mismatches 174; Indels 129; Gaps 26;

QY 47 DEFVOTLKEWVAIESDSVQVPFRFRQELFRMMAVAADT-LQRLGARVASVDMGPQQL--- 102

Db 46 DEIAKVMKEW-AIEKGATHFTHWF-QPLTGLTAEKHDAFIDPEGSGKVLKFSKELIKG 103

QY 103 -PDGQSLPIPPVILAEELGSDPTKGTVCFYGHL---DVQPADRGDGLWLTDPYVLTEVDGKL 158

Db 104 EPDASSFP-----SGGURATCAARGYTIWDCTSPAFIKDGTLCIPTVFCSYTGEI 153

QY 159 YRGATDNKGPVLAWINAVS--AFRAL-----EQDLPVNIKFIIEGMEEAGSVALEEL 209

Db 154 -----LDTKGPLLRSDALSRAIRVLRCLGNTTSQKVFENV-----GPEQYFIVDKKS 203

QY 210 VEKEKDRFFSGVDYIVISDNLWISQKKAITYGTRGNSYFMVEVKCRDQDFHSGTFGGIL 269

Db 204 YDEREDLIFTG-----RTLFGA-----PSPKGQELDDH---YFGVL 236

QY 270 HEPMADLVALLGSLVDSSGHILVPGI-----YDEVVPLTTEEINTYKAIHLDLEEYRNS 324

Db 237 KERVS-----AFMKDVKELWALGITAKTKHNEVAPAQHEIATITYSGNLATD---NNQ 287

QY 325 RVEKFLFDTKKEILMH-----LWRYPSLSIHGIEGAFD-----EPGKTVPGRVIGKF 373

Db 288 LVMEIL---KKIALKHGLVCLLHEKPPFAGING-SGKHNNWSMGTDGDLNLEPTD----- 338

QY 374 SIRLVPHMN-----VSAVEKQVTRHLEDV-FSKRNSN-----KMWVSMTLG-- 414

Db 339 ----MPHDNKQFLFFFTATIKAVDKYADLLRFSASNAGNDHRLGANEAPPAIISVFVG 394

QY 415 LHPWIANIDDTQYLAAK-----RAIRTVEGTEPDMIRDCSTIPIA 454

Db 395 LEDILEQLEKKGKATSTKGN SKLDLAISTVPAVEKDATDRNRTSPFA 440

RESULT 1104

ADM25891

ID ADM25891 standard; protein; 724 AA.

XX AC ADM25891;

XX DT 20-MAY-2004 (first entry)





Matches 64; Conservative 59; Mismatches 136; Indels 103; Gaps 16;

QY 164 TDNKGVLAWINAVS--AFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGV 221

Db 300 SSNPPLMFHLGQLVALNYQTDDPLHLN---AAMFEAN-----GGC 340

QY 222 DYIVISDNLW-----ISQRKPAI-----TYGTRGNSYFMVEV 253

Db 341 GYVLKPPVLWDKNCMPYQKFSPLERDLDSMDFAVYSLTIVSGQNVCPNSMGSPCIEVDV 400

QY 254 -----KC--RDQDFHSGTFGG-----ILHEPMADLVALLGSLVDSSG----- 288

Db 401 LGMPLDSCHFRTKPIHRNTLNPMMWNEQFLFHVHFDLVFLRFAVVENNSSAVTAQRIIPL 460

QY 289 -----HILVPGIYDEWVPLTEEEINTYKAHLDLEEYRNSSRVE-KFLFDTKEEILM 339

Db 461 KALKRGYRHLQLRNHLHNEVLEISSLFINSRR-----MEENSSGNTMSASSMFNTEERKCL 515

QY 340 HLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIR--LVPHMNVSAVEKQVTRHLEDV 397

Db 516 QTHR---VTVHGVPG--PEPFTVFTINGGTAKQLLQOILTNEQDIKPVTTDYFLMEEKY 570

QY 398 F--SKRNSSNMVMSMTLGLHPWIANIDDTQYLAAKRAIRTVFGT-----EPDMIRDGS 449

Db 571 FISKEKNECRKQPFQRAIGPEEEIMQILSSWFPPEGYMGRIVLTKQENLEEKNIQVDGK 630

QY 450 TI 451

Db 631 EV 632

RESULT 1106

ADH22554

ID ADH22554 standard; protein; 812 AA.

XX

AC ADH22554;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human transporter & ion channel (TRICH) protein SeqID52.

XX

KW human; transporters and ion channel; TRICH; cell proliferative;

KW arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;

KW neurological; epilepsy; stroke; developmental; Cushing's syndrome;

KW hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;

KW immunosuppressive; antiasthmatic; anticonvulsant; nootropic;

KW neuroprotective; single nucleotide polymorphism; SNP.

XX

OS Homo sapiens.

XX

PN WO2003093444-A2.

XX

PD 13-NOV-2003.

XX

PF 02-MAY-2003; 2003WO-US014026.

XX

PR 03-MAY-2002; 2002US-0377435P.

PR 03-MAY-2002; 2002US-0377444P.

PR 05-JUN-2002; 2002US-0386497P.

PR 11-JUN-2002; 2002US-0388180P.

XX

PA (INCY-) INCYTE CORP.

XX

PI Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;

PI Emerling BM, Griffin JA, Hafalia AJA, Ison CH, Jackson AA, Jiang X;

PI Jin P, Kable AE, Khare R, Lee SY, Lee S, Mason PM, Marquis JP;

PI Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Chawla NK;

PI Wilson AD;

XX

DR WPI; 2004-022655/02.

DR N-PSDB; ADH22620.

XX

PT New human transporters and ion channels (TRICH), useful for diagnosing,

PT treating and preventing diseases or conditions associated with the

PT aberrant TRICH expression e.g. cancer, AIDS, arteriosclerosis, epilepsy,

PT or infections.

XX

PS Claim 1; SEQ ID NO 52; 448pp; English.

XX

CC This invention relates to novel isolated polynucleotides identified as

CC human transporters and ion channels (TRICH), and the encoded polypeptides

CC thereof. Specifically, it describes using these TRICH molecules, as well

CC as agonists, antagonists, antibodies, expression vectors and host cells,

CC in appropriate screening and toxicity assays to assess the effects of

CC exogenous compounds on TRICH expression. The present invention describes

CC TRICH compositions that are useful in the diagnosis, treatment and

CC prevention of various disorders such as cell proliferative (e.g.

CC arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma),

CC neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's

CC syndrome hypothyroidism) and for infections. Accordingly, these TRICH

CC molecules can be used for gene therapy purposes and exhibit various

CC activities such as cytostatic, antiinflammatory, immunosuppressive,

CC antiasthmatic, anticonvulsant, nootropic and neuroprotective.

CC Furthermore, a microarray is useful in monitoring or measuring protein-

CC protein interactions, drug-target interactions and gene expression

CC profiles. This polypeptide sequence is a human TRICH protein of the

XX invention.

SQ Sequence 812 AA;

Query Match 3.3%; Score 85.5; DB 8; Length 812;

Best Local Similarity 21.5%; Pred. No. 3.2e+02;

Matches 114; Conservative 70; Mismatches 179; Indels 167; Gaps 29;

QY 34 LLEKV-----FQYIDLHQDEFVQTLKEWVAIESDSVQVPV-RF----- 70

Db 209 LLEKIPEDAEATVVLVGCVPFLEQPAAFVR-LNEAVLLESVLEVPVRFVLMGFSH 267

QY 71 -----RQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVI 114

Db 268 TSTDYHELGRSIATLMSDKLFHEAAYQADRDLLSAIS-----EFLDG-SIVIPP-- 317

QY 115 LAEL-GSDPTKGTVCFYGHLDVQPADRGD-----GWLTDPPVLTEDVGKLYGRGATD 165

Db 318 -SEVEGRDLLRSVAAFQRELLRKRREEQTKVEMTTRGGYTAPG--KELSLELGGSEATP 374

QY 166 NKGPVLAWINAVSAFRALEODL-----PVNIKFIEGMEEAGSV-----ALEELVE-- 211

Db 375 EDDPLL---RTGSVFGGLVRDVRRRYPHYPSDLRDALHSQCVAAVLFIYFAALSPAITFG 431

QY 212 ---KEKDRFFSGVDYIVISDNLW-----ISQRKPAITYGTRG-----NSYFMVEVKCRD 257

Db 432 GLLGEKTEGLMGVSELIVSTAVLGVLFSLLLGAQPLLVVGFSGPLLVFEAEFFKF---CRA 488

QY 258 QDFHSGT---FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAH 314

Db 489 QDLEYLTGRVWVGLW-----LVVFLALVAAGSFLV----RYISPFTQEIF----AFL 534

QY 315 LDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIPGRVIGKFS 374

Db 535 ISL-----IFYETFYKLYKVFTTEHPLLLPFVPEGALE-----GSLA 571

QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVMSMTLGLHP-----WIANIDDTQYLA 429

Db 572 AGLEP--NGSALPP-----TEGPPSPRNQPNNTALLSLMLGTFFIAFFLRKFRNSRPLG 624

QY 430 AK-RAIRTVFGTEPDMIRDSSTIPIAKMFQEI VHKSV-----VLIPLG 471

Db 625 GKARRIIGDFG-----IPISILVMVLVDYSITDTYTKLTVP TG 663

RESULT 1107

AAR67760

ID AAR67760 standard; protein; 843 AA.

XX

AC AAR67760;

XX 25-MAR-2003 (revised)  
DT 01-AUG-1995 (first entry)  
XX  
XX  
DE Lys-aminopeptidase PepN.  
XX  
XX Lys-aminopeptidase; PepN; fermented food; cheese.  
KW  
XX  
OS Lactobacillus delbrueckii subsp. lactis.  
XX  
XX  
PN EP633316-A1.  
XX  
XX  
PD 11-JAN-1995.  
XX  
XX 30-JUN-1994; 94EP-00401497.  
PF  
XX  
PR 01-JUL-1993; 93GB-00013586.  
XX  
XX (EECE-) EEC EURO ECONOMIC COMMUNITY.  
PA  
XX  
PI Klein JR, Plapp R;  
XX  
XX WPI; 1995-038513/06.  
DR  
DR N-PSDB; AAQ79913.  
XX  
XX Purified Lys-aminopeptidase PepN enzyme and PepN gene - useful for prepn.  
PT of fermented foodstuff, esp. cheese.  
PT  
XX  
XX Claim 3; Page 17-21; 4lpp; English.  
PS  
XX A new Lys-aminopeptidase, PepN, was isolated from L. delbrueckii subsp.  
CC lactis WS87 (DSM 7290) and had the sequence given in AAR67760. The pepN  
CC gene (AAQ79913) was isolated from a library of DSM 7290 chromosomal DNA  
CC by screening for peptolytic activity in Escherichia coli ER1562  
CC transformants. The isolated gene is used for recombinant PepN production.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 843 AA;  
Query Match 3.3%; Score 85.5; DB 2; Length 843;  
Best Local Similarity 22.8%; Pred. No. 3.4e+02;  
Matches 59; Conservative 37; Mismatches 112; Indels 51; Gaps 14;  
QY 48 EFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGP--QQLPDG 105  
Db 519 KYDQTLMDDIMKEAKDLDPVSQL--QLLQDLRLLAEE-----GKQASYADVVPVLELFKNS 571  
QY 106 QSLPIPPVI-----LAELGSDPTKGTVCFYGHLDVQPADRGDGLW----- 145  
Db 572 ESHVNDALYTTADKLQRFAPAGSEADKNLRALYNLDSKDQVAR-LGWLPKAGESDEDIQ 630  
QY 146 TDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVA 205  
Db 631 TRPYVLS---ASLYGRNADSEKQAHEIYVEYADKLAEISADIRPYV--LINEVENYGS-- 683  
QY 206 LEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYG-TRGN-----SYFMVEVKCRDQD 259  
Db 684 -SELTDK-----LIGL-YQATSDPSFKMDLEAAIVKSKDEGELKKIVSWFKNAEIVKPD 736  
QY 260 FHSQTFGGILHEPMADLVA 278  
Db 737 LR-GWFSGVLSNPAGEQLA 754  
RESULT 1108  
ADF05476  
ID ADF05476 standard; protein; 849 AA.  
XX  
AC ADF05476;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Bacterial polypeptide #1589.

XX Proteus mirabilis infection; bacterial infection; antibacterial;  
KW immunostimulant.  
XX  
XX Proteus mirabilis.  
OS  
XX  
PN US6605709-B1.  
XX  
PD 12-AUG-2003.  
XX  
PF 05-APR-2000; 2000US-00543681.  
XX  
PR 09-APR-1999; 99US-0128706P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton GL;  
XX  
DR WPI; 2003-895291/82.  
DR N-PSDB; ADF01304.  
XX  
XX New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.  
XX  
PS Disclosure; SEQ ID NO 5761; 870pp; English.  
XX  
XX The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis, a  
CC method for evaluating a compound for the ability to bind a P. mirabilis  
CC polypeptide and a method for screening test compounds for anti-bacterial  
CC activity. The polypeptides and polynucleotides are useful as molecular  
CC targets for diagnosing, preventing and treating pathological conditions  
CC resulting from bacterial infection, as reagents for diagnosis of  
CC bacterial diseases, as components of antibacterial vaccines, as targets  
CC for antibacterial drugs or as bio-control agents for plants. This  
CC sequence represents a Proteus mirabilis polypeptide of the invention.  
XX  
SQ Sequence 849 AA;

Query Match 3.3%; Score 85.5; DB 7; Length 849;  
Best Local Similarity 20.2%; Pred. No. 3.5e+02;  
Matches 89; Conservative 72; Mismatches 153; Indels 127; Gaps 23;  
QY 15 VLLLLLERGMFSPSPPPALLEKFQYIDLHQDEFVQTL--KEWVAIESDSVQVPRFRQ 72  
Db 2 VIRCLSRQFHHSDSLEIVMSKDPFQ--DREAKEYASPIASREFI-LEEMKRPAPMSRE 58  
QY 73 ELFRMMAVAA-DTLQRLGARVASVDMGPQQLPDQSL-----PIPPVILABELGSDPTK 124  
Db 59 DIAQALKISGEENLEALRRRLRAMER-----DQQLVFTRRQCYALPERL-----DLWK 106  
QY 125 GTVCIFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE 184  
Db 107 GKV--IGHRDGYGFLRAEGQKDDLYLSQDEMCKTM-----HGDVI-----LA 146  
QY 185 QDLPVNIKFIIEGMEEAGSV-ALEELVEKEKDRFF--SGVDYIV-----ISDNLWISQK 236  
Db 147 QPLGMDRK---GRREGVRVVRVLEPRNSQIVGRYFIESGMGFVVPDDSRLSFDILIPKED 202  
QY 237 PAITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMADLVALGSLVDSSGHILVPGIY 296  
Db 203 ---IMGARMGNVVVVEVTTTR-----PTRRTQA-VGRIVEILGETMTGTGIA 243  
QY 297 DEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGEGAF 356  
Db 244 VEIALRTHEIPHTW-----PPKVEKEIADLKEDV----- 272  
QY 357 DEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLED-VFSKRNSNKMVVMSTLGL 415







CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins

XX  
SQ Sequence 906 AA;

Query Match 3.3%; Score 85.5; DB 6; Length 906;  
Best Local Similarity 19.4%; Pred. No. 3.8e+02;  
Matches 111; Conservative 87; Mismatches 170; Indels 203; Gaps 36;

QY 42 IDLHODEF-VQTL--KEW-VAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDM 97  
Db 190 VELFQPEFFIEKLSQKWEKRRRLQVSWQ-----FAGIAILADWIGS-DSHYFTYQS 239  
QY 98 GPQQLPD----GQSLPIPPVILAEGLSDPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTE 153  
Db 240 KPMLPTDYWKHAQAMAKKAVMAINLGRPP-----VVKPFISIQ 277  
QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIIE-----GMEEGSVALEE 208  
Db 278 ---EYVGFAAT----PLQQAESIPV-----DDSPQ--LFILEDTGAGKTEAALALTHR 323  
QY 209 LVE-KEKDRFFSGVDYIVISDNLW--ISQR-----KP--AITYGTRG-NSYFMV 251  
Db 324 LMQAKAADGFYGLPTIASSNAIFSRIAQHYQQMLLTEDDSKPNIVLAHGTWGMNQF-- 381  
QY 252 EVKCRDQDFHSGTGGILHEPMADLVALGLSLVDSSGH-----IL 291  
Db 382 -----HEP----VLALGHPRDNDGKTDIAASAQCQNLADPRKQALL 419  
QY 292 VP---GIYDE----VVLPTTEEEINTY----KATHLDLEEYRNSRVEKFLDFTKEEIL-M 339  
Db 420 APAGIGAIQDQALLAVLPTRYQSLRFLGKLNKVLIVD-----EVHAADBFMFNLLLENLAL 474  
QY 340 HLWRYPSLSIHGEGAFDEPGTKTVI-----PGRVIGKFSIRLVPHMNVSAV----- 386  
Db 475 HLYQGGSAVLLTATLTFKQQRQLTDIWLNVGGLSSQLLQKNDFFPLATKISLNAILPVIEQ 534  
QY 387 ----EKQVTRHLEDVF--SKRNSNKMVVSMTLG-LHPWIAN-IDDTQYLAAKRAIRTVF 438  
Db 535 PLSSRKQDVSREIKVDFLNSVGSCEKVLAAIVQGCQVWIRNTVDDA--IEAYQTLRSLL 592  
QY 439 GTEPDM-----IRDGSTIPIAKMFQEIIV--HKSV 465  
Db 593 -TEPERCLLFHSQFIIQHRKEIEDHVLTFIDKNSHGELRRGKALITTIQIFQASLTDADV 651  
QY 466 VLIPLGAVDD-----GEHSQ-NEKINRW 487  
Db 652 MISDLCPIDDLIQRAGRLHRHTRDSGDIYRW 682

RESULT 1113  
AAG90902  
ID AAG90902 standard; protein; 1014 AA.  
XX  
AC AAG90902;  
XX  
DT 26-SEP-2001 (first entry)

XX  
DE C glutamicum protein fragment SEQ ID NO: 4656.  
XX  
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
XX organic acid synthesis.  
OS Corynebacterium glutamicum.  
XX EP1108790-A2.  
XX 20-JUN-2001.  
XX 18-DEC-2000; 2000EP-00127688.  
XX 16-DEC-1999; 99JP-00377484.  
XX 07-APR-2000; 2000JP-00159162.  
XX 03-AUG-2000; 2000JP-00280988.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX WPI; 2001-376931/40.  
XX N-PSDB; AAH66121.  
DR  
XX Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analyzing  
PT expression profile or pattern of a gene and identifying homologous gene.  
XX  
PS Claim 17; SEQ ID NO 4656; 246pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of coryneform bacterium, measuring expression amount and analysing  
CC the expression profile or expression pattern of a gene derived from  
CC Coryneform bacterium, and identifying a homologue of a gene derived from  
CC coryneform bacterium. Coryneform bacteria are useful for producing amino  
CC acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a protein described in the  
CC exemplification of the invention. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the European Patent Office  
XX  
SQ Sequence 1014 AA;

Query Match 3.3%; Score 85.5; DB 4; Length 1014;  
Best Local Similarity 18.7%; Pred. No. 4.5e+02;  
Matches 116; Conservative 104; Mismatches 216; Indels 183; Gaps 30;  
QY 9 AASLLAVLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPV 68  
Db 256 SATRLPVLLAVL-HAVFTS-----AIV--VILYLLGTGSFAIT-DESILVQATTIQ--- 303  
QY 69 RFRQELFRMMA-----VAADTLQRLGARVASVDMGPQQLPD-----GQSLPIPPVIL 115  
Db 304 -----LFVLMCILLSLVSTTVQTSALVEELEVVAKTLPDALFVNKNGTAFPVNAGAK 358  
QY 116 AELGSDPTKGTVCFYGH-----LDVQPAD-----RGDGWLTDPYVLTEVDGK 157  
Db 359 NFVKQSPD-----GHYSMPKLQNIIDCEPMDEKESPPSMALRGQVEGVLAKLGEVLGE 411  
QY 158 -----LYGRGATDNKGPVLAWINAVSAF-----RALEQDLPV 189  
Db 412 DPDLARRIFEISASPMYLRGETEPGHALVIWHDSTNEYTMQQLTLAYEESRLLFEKAPQ 471  
QY 190 NIKFIEGMEEGSVALE-----ELVEKEKDRFFS-----GV-----DYI---VISD--- 228  
Db 472 GIAM-----LDPSGEIVMANRSFGDLVGTTPVRLLRNLEDFGVEGMEYVTPVLSDEA 527  
QY 229 -----NLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM-----A 274



Db 528 VVHLDRSLETLRGKQKNVAMSPSSMGNV-----GGRIGTLLVNVVDVTERQ 573

Qy 275 DLVALLGSLVDSSGHILVPGI-----YDEVVPLTEEEINTYKAIHLDLEEYRNSR 325

Db 574 ELIELVEHLAD---HDSLTGLVNRRLSDIEELILKNERDSTDSALLLLDLDFYKEVN- 629

Qy 326 VEKFLFTKEEILMHLWRYPSSLIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSA 385

Db 630 -DSLGEAGDQLLIEFAEILKDSVRDSD-----IVGRIGGDEFVIVLPDTRDRG 677

Qy 386 VEKQVTRHLEDVFSKRNSNKMV--VSMTL-----GLHPWIANIDDTQYLAAGR 432

Db 678 AEAIGIRIIELVNQHFKGKGLSRVSVSIGGTLFSDARAQGVNPF--LADQLLYDAKH 735

Qy 433 AIR---TVFGTEPDMIRGDTIPIAKMFQEIIVHKSUV---LIPLGAVDDGEHSQNEKINR 486

Db 736 AGRNRVAVRRAENTIVRSAPKAFSVEELSEILSHSIRLELOPILELETGRVGAAGEGLR 795

Qy 487 WNYIEGTKLFAAFFLEMAQ 505

Db 796 IN-LDGTDTVPTGQFVQSVE 813

RESULT 1114

ADN20163

ID ADN20163 standard; protein; 1105 AA.

XX AC ADN20163;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #2816.

XX KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

OS Bacteria.

PN US2003233675-A1.

XX PD 18-DEC-2003.

PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

XX PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX DR New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 2816; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.

XX SQ Sequence 1105 AA;

Query Match 3.3%; Score 85.5; DB 8; Length 1105;

Best Local Similarity 21.6%; Pred. No. 5.2e+02;

Matches 72; Conservative 46; Mismatches 105; Indels 111; Gaps 20;

Qy 183 LEQDLPVNI-KFIIEGME-----EAGSVALEELVEK-EKDRFFSG-----VDYIVIS 227

Db 775 IEPDHPILIDKFLENAIEVDVDSLTDSTGKVVIGSIMEHIEAGIHSGDSACSIPYTSLS 834

Qy 228 DNL-----WISQRKPA-----ITYGTRGNSYFMVEVK---CRDQDFHSGTGGILH 270

Db 835 DNVLTITRQWTEQLARALNVVGLMNIQYAVQGDQVILEANPRASRTVPYVSKATG---- 890

Qy 271 EPMADLVALLGSLVDSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFL 330

Db 891 RPLAKIASLV-----MSGKTL-----EELGVTEEFIPQHVAV----- 922

Qy 331 FDTKEEILMHLWRYPSSL-----SIHGIEGAFDEPGTKVIPGRVI-----GKFS 374

Db 923 ----KEAVLPFSKFPFGADTLLGPEMRSTGEVMGIDSDFGKAFAKAELGAGVILATGTGVF 978

Qy 375 IRLVPHMNVSAVEKQVTRHLEDVFSK---RNSSNKMV-----VSMTLGLH-----P 417

Db 979 VMSMDRTKEAAV--PVVRELIDLGFKVVATSGTQKVLREHGIEGVEVVLKHEGRPHVID 1036

Qy 418 WIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTI 451

Db 1037 WIKN-GQIQFI-----INTPSGEESQL--DGRTI 1062

RESULT 1115

ABU40048

ID ABU40048 standard; protein; 1162 AA.

XX AC ABU40048;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #25575.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Pseudomonas putida.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA43918.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 67972; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1162 AA;

Query Match 3.3%; Score 85.5; DB 6; Length 1162;  
Best Local Similarity 20.1%; Pred. No. 5.6e+02;  
Matches 75; Conservative 46; Mismatches 113; Indels 139; Gaps 17;  
QY 18 LLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQEL--- 74  
Db 422 LVEEREQLGSDPDQAAMLEAEQ---LASSEML--LEELQCEEQVIERLESAREQLQQA 476  
QY 75 FRMMAVAADTLQRLGARVASVD-----MGPPQLPDGQSLPIPPVILAE----- 117  
Db 477 TQAQQAQGDQLQRLGRLASLEALQQAALPEPGAGAAQWLHGQGLEQP-RLAEGRLRVEPG 535  
QY 118 -----LGSDDTKGTVCYFYLHLDVQPADRGD-----GWLTDPPYLVTEVDGKLYG 160  
Db 536 WELAVETVLGADLQAVLVDDFNDLDFAGLEQGEQLRLLLAVGAGATLPGSLLEKVEGRI-- 593  
QY 161 RGATDNKGPVLAWINAVSAFRALEQDLPVNITKFIIEGMEEAGSVALEBELVEKEKDRFFSG 220  
Db 594 -----DLAPWLGQV---RPVED-----LAQALEQRGSLGEGQ----- 622  
QY 221 VDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVALL 280

Db 623 --SLVSRDGYWV-----GRHFLRVR-----RGG----- 643  
QY 281 GSLVDSSGHILVPGIYDEVVPLTEEEINTYKAI-----HLDLEEYRNSSRVE 327  
Db 644 ----EAEGGVLARG--QETIERLGQEQLEQEAALQDLQALREQQLDLEEQRQLRRR 697  
QY 328 KFLFDTKKEEILMH 340  
Db 698 -----TQDENRLH 705  
RESULT 1116  
ABO69149  
ID ABO69149 standard; protein; 1179 AA.  
XX  
AC ABO69149;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #1324.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
XX 18-FEB-1999; 99US-00252991.  
PF  
XX 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
DR WPI; 2003-615309/58.  
DR N-PSDB; ABD02720.  
XX  
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 17895; 455pp; English.  
XX  
CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 1179 AA;

Query Match 3.3%; Score 85.5; DB 7; Length 1179;  
Best Local Similarity 19.9%; Pred. No. 5.7e+02;  
Matches 107; Conservative 60; Mismatches 195; Indels 175; Gaps 26;  
QY 6 GRMAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQ 65  
Db 230 GRRGARLTA----LTSGGTIPTDGTYSVLEP-----QGLLVGTVNEFAVES----- 273

QY 66 PVRFRQELFRMMAVAADTLQ--RLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPT 123  
Db 274 -----LAGDFVQLGNTSYRIIRIEPRGRVVEDAQGQ--PPNIPFWLGEAP- 316  
QY 124 KGTVCIFYGHLVQPADRGWLTDPYVLTEVDGKLYGRGATDNKG----PVLAMINAV-- 177  
Db 317 -----GRSDELSASVARLRTDLDELGEGQALPEGQRLPAIAWLGATLG 361  
QY 178 ---SAFRALEQDLPVNIKFIEGMEEGSV-ALEELVEKEKDRFF---SGVDYIVISDNL 230  
Db 362 LDDGAARQI-----VEYLARARQALGGLPGSRLV---MERFFDESGBMQLIHS--- 408  
QY 231 WISQRKPAITYGTRGNSYFMVEVK---CRDQDFH---SGTFGGIL-----HE-PMADLV 277  
Db 409 -----PHGSRNLRAWGLARKRFCRSFNFEQLQAAATEDAILSLSTSHSFFLDEVW 459  
QY 278 ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLLEEYRNSRVEKFLPDTKEEI 337  
Db 460 RYLHSA--SAEHLVQAVLD--APLFGVRWRWNLTTSLGLPRYAGGRKVPPLRMKSED 515  
QY 338 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDV 397  
Db 516 LL-----ASVFPDQV-----ACLENI 531  
QY 398 FSKRNSNMVWSMTLG--LHP-----WIANIDTQYLAAKRAIRTVFGTFPDMIRDS 449  
Db 532 VGERVPDHPVLAQTLLDCLHEAMDCEGWLALLRDMESGAV-----DLLARDL 579  
QY 450 TIPIAKMFQEIIVHKSVVLIPLGAVDDG---EHSQNEKINRWNYIEGKLFPAFFLE 502  
Db 580 PAPSA-----LAAEILTARPYAYLDDAPLEERTQAVQNRWSDPESADDLGALDLE 631

RESULT 1117  
ABR52808  
ID ABR52808 standard; protein; 1230 AA.  
XX ABR52808;  
XX AC  
XX XX  
DT 20-JUN-2003 (first entry)  
XX  
DE protein sequence #SEQ ID 481.  
XX  
KW Multiprotein complex; eukaryote; drug target; diagnosis.  
XX  
OS Saccharomyces cerevisiae.  
XX PN  
XX EPI258494-A1.  
XX  
PD 20-NOV-2002.  
XX  
PF 20-DEC-2001; 2001EP-00130253.  
XX  
PR 15-MAY-2001; 2001EP-00111774.  
XX  
PA (CELL-) CELLZOME AG.  
PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;  
PI Marzioch M, Schultz JD, Superti-Furga GD;  
XX  
DR WPI; 2003-250078/25.  
DR N-PSDB; ACC60850.  
XX

New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease or disorder.  
XX  
PS Disclosure; SEQ ID NO 481; 17pp + Sequence Listing; English.  
XX  
CC The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records

CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM  
XX  
SQ Sequence 1230 AA;

Query Match 3.3%; Score 85.5; DB 6; Length 1230;  
Best Local Similarity 22.0%; Pred. No. 6.1e+02;  
Matches 116; Conservative 61; Mismatches 189; Indels 161; Gaps 30;  
QY 21 ERGMFSSPPPPALLEKVFQYIDLHQDE-----FVQTLKEWVAIE----- 60  
Db 694 EEGVASTEEDDKALLETV-SFLDLFIEEYPYELQFLNKLKEASLISKAQLDDELISTIRT 752  
QY 61 -----SDSVQPV--PRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPP 112  
Db 753 NLPELTGGIEPVFATDNKSNLLFVKSYPHTQKLLGFGHFAVNQ-LQQLSD-----ISA 806  
QY 113 VILAEIGSDPTKGTVCIFYGHLVQPADRGDWL-----TDPYVLTEVDGKLYGRG 162  
Db 807 IIEDSISSNE---KLTFYE--EVQPGTINEIYNKETIYDADIDTGDIVSFEVPG-----A 856  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFI-IEGMEEAGSVALEELVEKEKDRFFSGV 221  
Db 857 VLPDTFPVYATIKDFYSYLYR---VKLFKSKFDGSSEYGVSN----- 898  
QY 222 DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALL- 280  
Db 899 --IPESFEFWISAYAPYDDLARMVSKYAHVKPE-----YDKIIALYS 938  
QY 281 -GSLVDSSGHIL-----VPGIYDEV--VPLTEEE-----INTYKAIHL 315  
Db 939 NGRFVLKSTSLNDYLLKDFNCDDQIPPFAPFVLSVPLKELERLRPIKLYWLKNSY--IHY 996  
QY 316 D-----LEEYRNSRVEK-----FLDFTKEEILMHLWRYPSLSIHGI---EGAFDEPG 360  
Db 997 QCFEFEVANDYTESQFLEKQVHKIGFTDEKENIL--LWTNTNFQFQGLLSDQNTFKDVS 1054  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNK-MVVSMTLGLHPWI 419  
Db 1055 KHSLLFGRIIPES-KLFKELN--RLENVQTSSEDFMDDENATDRPMDDEQDLGMA--I 1109  
QY 420 ANIDD-----TQY---LAAKRAIRTVFGTFPDMIRDGSTIPIAK 455  
Db 1110 EHSEDMKGRIVVVVQYFKDLENRHGISFLNLIIPD-----ETFPKTK 1151

RESULT 1118  
ADK62206  
ID ADK62206 standard; protein; 1230 AA.  
XX ADK62206;  
XX AC  
XX XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Disease treating protein complex-derived protein #229.  
XX  
KW protein complex; drug target; diagnosis.  
XX  
OS Unidentified.  
XX  
PN EP1338608-A2.  
XX  
PD 27-AUG-2003.  
XX  
PF 20-DEC-2002; 2002EP-00102902.



XX 20-DEC-2001; 2001EP-00130253.  
XX (CELL-) CELLZONE AG.  
XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;  
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
PI Michon A, Leutwein C, Rick J;  
XX WPI; 2003-638460/61.  
DR N-PSDB; ADK62207.  
XX New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.  
XX Disclosure; SEQ ID NO 457; 13pp; English.  
XX The invention relates to novel protein complexes comprising a first and a  
CC second protein, or its derivative, fragment, homologue or variant. The  
CC proteins are selected from given protein complexes, which are not defined  
CC in the specification. The variants are encoded by nucleic acids that  
CC hybridize to the nucleic acids encoding the proteins under low stringency  
CC conditions. The protein complexes are useful as targets for an active  
CC agent of a pharmaceutical. These protein complexes are particularly  
CC useful as drugs targets for the treatment or preventing of a disease or  
CC disorder. The complexes and methods above are useful in diagnosing or  
CC screening for the presence of a disease or disorder or a predisposition  
CC for developing a disease or disorder in a subject. These are also useful  
CC in screening for a drug for treatment or prevention of a disease or  
CC disorder. The molecule that modulates the amount, activity or protein  
CC components of the complex is useful for the manufacture of a medicament  
CC for the treatment or prevention of a disease or disorder. This sequence  
CC corresponds to a protein of the invention. (Note: the sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained from the EPO in electronic format).  
XX SQ Sequence 1230 AA;  
Query Match 3.3%; Score 85.5; DB 7; Length 1230;  
Best Local Similarity 22.0%; Pred. No. 6.1e+02;  
Matches 116; Conservative 61; Mismatches 189; Indels 161; Gaps 30;  
QY 21 ERGMFSSPPFALLKVFQYIDLHQDE-----FVQTLKEWVAIE----- 60  
DB 694 EEGVASTEEDDKALLETV-SFLDLFIEEPYLEQLFLNKLKEASLSKAQLDELISTIRT 752  
QY 61 -----SDSVQPV--PRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPP 112  
DB 753 NLPELTKGIEPVFATDNKSNLLFVKSYDPHTQKLLGFHFAVNO-LQQLSD-----ISA 806  
QY 113 VILAELGSDPTKGTVCIFYGHLDVQPADRGDGL-----TDPYVLTEVDGKLYGRG 162  
DB 807 IIEDSISSNE---KLTFYE--EVQPGTINEIYMKETIYDADIDTGDIVSFEVPG-----A 856  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFI-IEGMEEAGSVALEELVEKEKDRFFSGV 221  
DB 857 VLPDTPFPVYATIKDFYSYLYR---VKLKFSKFDGSSEYGVNE----- 898  
QY 222 DYIVISDNLMTSQRPKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMDLVALL- 280  
DB 899 --IPESFEFWSAYAPYDDLARMVSKYAHVKPE-----YLKIIALYS 938  
QY 281 -GSLVDSSGHIL-----VPGIYDEV--VPLTEEE-----INTYKAHL 315  
DB 939 NGRFVLKSTSLNDYLLKDFNCDOIPPPAFEVLSVPLKELERLRPIKLYWLKNSY--IHY 996  
QY 316 D-----LEEYRNSRVEK-----FLDFTKEEILMHLWRYPSSIHG I---EGAFDEPG 360  
DB 997 QCFEFEVANDYTESQFLEKVQHKGIGFTDEEKENIL--LWTNTNEFQQLSDQNTFKDVS 1054  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNK-MVVSMTLGLHPWI 419

Db 1055 KHSLLFGRLPEES-KLFKELN--RLENVQTSLSLEDFMDDENATDRPMDDEQDLGMA--I 1109  
QY 420 ANIDD-----TQY---LAAKRAIRTVFGTEPDMIRDGSTIPIAK 455  
Db 1110 EHSEDMKGRIVVQQYFKDLENRHGISFLFNLPD-----ETFPKTK 1151  
RESULT 1119  
ADN19276  
ID ADN19276 standard; protein; 1230 AA.  
XX  
AC ADN19276;  
XX 02-DEC-2004 (first entry)  
XX Bacterial polypeptide #1929.  
DE  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX US2003233675-A1.  
PN 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
PF 21-FEB-2002; 2002US-0360039P.  
PR  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI WPI; 2004-061375/06.  
DR New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
PT Claim 1; SEQ ID NO 1929; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the



Db 868 AGLEP--NGSALPP-----TEGPPSPRNQPNNTALLSLMLGTFFIAFFLRKFRNSRFLG 920

QY 430 AK-RAIRTVFGTEPDMIRDGSTIPIAKMFQIIVHKSIV-----VLIPLG 471

Db 921 GKARRIIGDFG-----IPISILVMVLVDYSITDTYTTQKLTVP TG 959

RESULT 1121

ABP74021

ID ABP74021 standard; protein; 1262 AA.

XX

AC ABP74021;

XX

DT 30-JAN-2003 (first entry)

XX

DE Candida albicans essential protein SEQ ID NO 7858.

XX

KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;

KW signal transduction; DNA replication; cell division; growth;

KW proliferation; Candida albicans; fungicide; antifungal.

XX

OS Candida albicans.

XX

PN WO200253728-A2.

XX

PD 11-JUL-2002.

XX

PF 26-DEC-2001; 2001WO-US049486.

XX

PR 29-DEC-2000; 2000US-0259128P.

PR 20-FEB-2001; 2001US-00792024.

PR 22-AUG-2001; 2001US-0314050P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX

DR WPI; 2002-566694/60.

DR N-PSDB; ABZ32571.

XX

Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.

XX

PS Claim 44; SEQ ID NO 7858; 167pp + Sequence Listing; English.

XX

CC The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance and/or pathogenicity of a fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention.

CC Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

XX

SQ Sequence 1262 AA;

Query Match 3.3%; Score 85.5; DB 5; Length 1262;

Best Local Similarity 18.5%; Pred. No. 6.4e+02;

Matches 90; Conservative 61; Mismatches 140; Indels 195; Gaps 23;

QY 147 DPYVLTEVDGKLYGRGAT-----DNKGPVL-- 171

Db 551 DPYVRVLMNGKLRAKTVTFAETVNPQWNSVYFLPVANEHQHVLLQIMDAEPEGKDRSLGT 610

QY 172 AWINAVSAFR-----ALEQDLPVNIKFIIEGMEEGSV----- 204

Db 611 AAINVADILRKNEEGYVLGYDGSDEIIEQVLFNTK-----EAGSIFYSVSFFPAIPT 663

QY 205 -----ALEELVEKEKDRFFSGVDYIVISDN-----LWISQRKPAITYGTRGN 246

Db 664 YLSQLHNFETYQKELKEQEREKERY--ARDEKMFKENPDEFIEWIEIENEQMKVPPK-- 719

QY 247 SYFMVEVKCRDQ-DFHSGTF-----GGILHEPMDLVALLSGLVDSSGHILVPGIYDE-- 298

Db 720 ----VELKLQDAIKYRAGNMIVHLKGGQFEKP-----DVYVHTLFDEHA 759

QY 299 ----VVPLTE-EEINTYKAHLDLEEYRNS--RVEKFLFDTKEEILMHLWRYPSLSIH 350

Db 760 YPSGISPISEGKLTITASVGETFIRDLPNSNLIFRVAKVAEVTKSSEVIVEKMYNTLDIY 819

QY 351 GIEGAFDEP-----GTKIV-----IPGRV-----IGKFSIRLVPHMNVSAVEK 388

Db 820 --EKSFEKPIKLNIGNRNTIEVQLEFIPSTVKLAPLDTILDVGKIKLEIIGGENLRSVDS 877

QY 389 Q-----VTRHLEDVFSKRNSNKMVVS-----MTLGLHPW----- 418

Db 878 NGKSDPLCTVNLGDGVEIYKTDKKRKTLDPIWNESVEFPMTSRQVLLVEYDWDYTHDD 937

QY 419 ----IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVH----KSVVLIP 469

Db 938 ELLGVANIDLSNIPAL-----TTTPFSVDLDTQGVNLRATFFPEYIRPPLDAKSAIPID 992

QY 470 LGAVDD 475

Db 993 LGAVSD 998

RESULT 1122

ABB92830

ID ABB92830 standard; protein; 1780 AA.

XX

AC ABB92830;

XX

DT 31-MAY-2002 (first entry)

XX

DE Herbicidally active polypeptide SEQ ID NO 2041.

XX

KW Herbicidal; plant; agriculture; herbicide.

XX

OS Arabidopsis thaliana.

XX

PN WO200210210-A2.

XX

PD 07-FEB-2002.

XX

PF 28-AUG-2001; 2001WO-EP009892.

XX

PR 28-AUG-2001; 2001WO-EP009892.

XX

PA (FARB ) BAYER AG.

XX

PI Tietjen K, Weidler M;

XX

DR WPI; 2002-269010/31.

XX

PT Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant



PT organisms.  
XX Claim 5; SEQ ID NO 2041; 261pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 1780 AA;  
  
Query Match 3.3%; Score 85.5; DB 5; Length 1780;  
Best Local Similarity 20.6%; Pred. No. 1.1e+03;  
Matches 33; Conservative 26; Mismatches 76; Indels 25; Gaps 4;  
  
QY 196 EGMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRP-----AITYGT 243  
Db 113 DNIDSLDSAVVRRFRKLLANYSSWCSYLGKKSNIWISDRNPDSSRELLYVGLYLLIWGE 172  
QY 244 RGNYSFMVEVKCRDQDFHSGTGGILHEPMDLVALGSLVD-SSGHILVPGIYDEVVPL 302  
Db 173 AANLRFMPECICY-----IFHNMASELNKKILEDCLDENTGQPYLPSSLGSENAFL 221  
QY 303 TEEEINTYKAHLDLEEVNRRSRVEKFLFDTTKEEILMHLW 342  
Db 222 TGVVKPIYDTIQAEIDESKNGT-VAHCKWRNYDDINEYFW 260  
  
RESULT 1123  
ABU62068  
ID ABU62068 standard; protein; 2011 AA.  
XX  
AC ABU62068;  
XX  
DT 04-SEP-2003 (first entry)  
XX  
DE Mouse kidney alpha-kinase (KK).  
XX  
KW Mouse; mammalian kinase; melanoma alpha-kinase; MK; HK; KK; SK; LK;  
KW heart alpha-kinase; kidney alpha-kinase; skeletal muscle alpha-kinase;  
KW lymphocyte alpha-kinase; alpha-kinase catalytic domain; murine;  
KW ion channel domain; enzyme.  
XX  
OS Mus sp.  
XX  
PN US2002177205-A1.  
XX  
PD 28-NOV-2002.  
XX  
PF 10-APR-2001; 2001US-00832292.  
XX  
PR 03-AUG-2000; 2000US-00632131.  
XX  
PA (RYAZ/) RYAZANOV A.  
XX  
PI Ryazanov A;  
XX  
DR WPI; 2003-352609/33.  
DR N-PSDB; ACD26090.  
XX  
PT Novel mammalian alpha-kinase proteins, including melanoma, kidney, heart,  
PT skeletal muscle or lymphocyte alpha-kinase protein useful for treating an  
PT animal in need of increased activity of mammalian alpha-kinase.  
XX  
PS Claim 22; Fig 9B; 69pp; English.  
XX  
CC The present invention relates to the isolation of novel mammalian kinases  
CC designated melanoma alpha-kinase (MK), heart alpha-kinase (HK), kidney

CC alpha-kinase (KK), skeletal muscle alpha-kinase (SK), and lymphocyte  
CC alpha-kinase (LK), and the polynucleotide sequences encoding them. The  
CC alpha-kinase proteins are characterised by the presence of at least two  
CC domains, one being an alpha-kinase catalytic domain and other being an  
CC ion channel domain. The proteins are useful for treating an animal in  
CC need of increased activity of melanoma, kidney, heart, skeletal muscle or  
CC lymphocyte alpha-kinase. An antibody to the kinase is useful for  
CC detecting the presence of an melanoma, kidney, heart, skeletal muscle or  
CC lymphocyte alpha-kinase in a sample. ABU62065-ABU62072 represent the  
CC alpha-kinases of the invention  
XX  
SQ Sequence 2011 AA;  
  
Query Match 3.3%; Score 85.5; DB 6; Length 2011;  
Best Local Similarity 22.0%; Pred. No. 1.3e+03;  
Matches 44; Conservative 39; Mismatches 80; Indels 37; Gaps 11;  
  
QY 303 TEEEINTYKAHLDLEEVNRRSRVEKFLFDTTKEEILMHL-----WR--YPSL--SIHGIEG 354  
Db 78 TKSPTDTFGTINFQDGEHTTHAKYIRTSYDTKLDHLLHMLKEWKMLPKLVISVHG--- 134  
QY 355 AFDEPGTKT-VIPGRVIGKFSIRLVPHMNVSAV-----EKQVTRHLEDVFSKRNSNKM 407  
Db 135 -----GIONFTMPSEKFEIFSQGLVKAETTGAWITGINTVSKHVGDAL-KSHSSHSL 188  
QY 408 VVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMRDGSTIPIAKMFQ-EIVHKSVV 466  
Db 189 RKIWTVGIPPW--GVLENQ-----RDLIGKDVVCLYQTLNPLSKLTTLNSMHSHPFI 238  
QY 467 LIPLGAVDDGEHSQNEKINR 486  
Db 239 L5DDGTV--GKYGNEMKLR 256  
  
RESULT 1124  
ABU62067  
ID ABU62067 standard; protein; 2011 AA.  
XX  
AC ABU62067;  
XX  
DT 04-SEP-2003 (first entry)  
XX  
DE Human kidney alpha-kinase (KK).  
XX  
KW Human; mammalian kinase; melanoma alpha-kinase; MK; HK; KK; SK; LK;  
KW heart alpha-kinase; kidney alpha-kinase; skeletal muscle alpha-kinase;  
KW lymphocyte alpha-kinase; alpha-kinase catalytic domain;  
KW ion channel domain; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN US2002177205-A1.  
XX  
PD 28-NOV-2002.  
XX  
PF 10-APR-2001; 2001US-00832292.  
XX  
PR 03-AUG-2000; 2000US-00632131.  
XX  
PA (RYAZ/) RYAZANOV A.  
XX  
PI Ryazanov A;  
XX  
DR WPI; 2003-352609/33.  
DR N-PSDB; ACD26089.  
XX  
PT Novel mammalian alpha-kinase proteins, including melanoma, kidney, heart,  
PT skeletal muscle or lymphocyte alpha-kinase protein useful for treating an  
PT animal in need of increased activity of mammalian alpha-kinase.  
XX  
PS Claim 22; Fig 9B; 69pp; English.  
XX  
CC The present invention relates to the isolation of novel mammalian kinases







PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.



Qy 201 AGSVALBELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDF 260  
Db 224 LDLIRIRNAARK---RGYKPMELVKIP-----VEVALQDEK- 256  
Qy 261 HSGTGGILHEPMADLV-----ALLG-----SLVDSSGHILVPGIYDEV-VPLTE----- 304  
Db 257 -----GFPHKGTLDVNTGLNASTGTMEFRALLPNKGYPVPLVGLFVQVRVPISEPSPKL 310  
Qy 305 -----EEINTYKAJHLDLLEEYRNSSRV 326  
Db 311 TIPDTSVQVDQIGPYVLV-VDKDNYVLTGRV 340

RESULT 1128  
ABP70996  
ID ABP70996 standard; protein; 385 AA.  
AC ABP70996;  
XX  
DT 06-AUG-2003 (first entry)  
XX  
DE Epoxide hydrolase #40 SEQ ID 80.  
XX  
KW Epoxide hydrolase; enzyme; epoxide; arene oxide.  
XX  
OS Unidentified.  
XX  
PN WO2003012126-A2.  
XX  
PD 13-FEB-2003.  
XX  
PF 05-AUG-2002; 2002WO-US025070.  
XX  
PR 03-AUG-2001; 2001US-0309478P.  
PR 03-JUL-2002; 2002US-0393978P.  
XX  
PA (DIVE-) DIVERSA CORP.  
XX  
PI Zhao L, Mathur E, Weiner D, Richardson T, Milaln A, Burk M;  
PI Han B;  
XX  
WPI; 2003-332731/31.  
DR N-PSDB; ACC42725.  
XX

New isolated or recombinant epoxide hydrolase polypeptides, useful for catalyzing hydrolysis of epoxides and arene oxides to their corresponding diols.

Claim 67; Page 399-400; 400pp; English.  
The present invention relates to novel epoxide hydrolases (I, ABP70957-ABP70996), which catalyze the hydrolysis of epoxides and arene oxides to their corresponding diols, and their coding sequences (II, ACC42686-ACC42725). (I) are useful for isolating or identifying a polypeptide having an epoxide hydrolase activity, for identifying an epoxide hydrolase substrate, for determining whether a test compound specifically binds to (I), and for identifying a modulator of an epoxide hydrolase activity. (I) or nucleic acid (II) encoding (I) are useful for making an antiepoixide hydrolase antibody and for generating a humoral immune response. (I) or a nucleic acid (III) that hybridises to (II) is useful for isolating or recovering a nucleic acid encoding (I) from an environmental sample, for generating a variant of a nucleic acid encoding (I), and for modifying codons in a nucleic acid encoding (I) to increase or decrease its expression in a host cell. (I) and (II) are useful for modifying a small molecule, for determining a functional fragment of an epoxide hydrolase enzyme, for hydrolysing an epoxide, for producing a chiral diol, for producing a chiral epoxide and for increasing thermostolerance or thermostability of an epoxide hydrolase polypeptide

Sequence 385 AA;

Query Match 3.2%; Score 85; DB 6; Length 385;

Best Local Similarity 21.4%; Pred. No. 1.1e+02;  
Matches 75; Conservative 44; Mismatches 100; Indels 132; Gaps 18;  
Qy 138 ADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAW-----INAVSAFRALEQ 185  
Db 31 APEGGGW-----AYGTELSTMKEIVEYWLHGYDWMYREQELINRLPHFKARVR 77  
Qy 186 DLPVNIKFI-IEGMEE-----AGSV-----ALEELVEKEKDRFFSG-----VDY 223  
Db 78 DL--DIHFIHIKSGEKRRLIISHGWPGSFYEFMSVIEPLAQPK---FGGSKDDAFDI 132  
Qy 224 IVISDNLWISQRKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTGGIL 269  
Db 133 VVPSLPGYGFSSKPAKPMSPRTVAGYFDELMTGTLGYTRYLAQ---GGDWGSSITGWL 188  
Qy 270 HEP---MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE-----I 307  
Db 189 YEGRCQAIHINMLG-----WRSPG-----VVPETDEKAEAAKFAAGAYFRL 236  
Qy 308 NTYKAJHL-----LBEYRNSSRVEKFLD---TKEEILMHLWRYPSLSIH 350  
Db 237 QSTKPLTLSYGMMDSPVGAANAIIIEKFKGWSLDLDDGQLESVYTKDQLLTNVMYLVTRTF 296  
Qy 351 G-----IEGAFDEPGTKTVIPG-----RVIGKFSIRLVPHMNVSAVEKQV 390  
Db 297 GTATWMYRGLFEDPGGAPIQPGSIRKPTAIARFPVDLIPFPFPRSMVEKGM 347

RESULT 1129  
ADN47224  
ID ADN47224 standard; protein; 397 AA.  
XX  
AC ADN47224;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1102.  
XX  
KW gene disruption; gene targeting; marker gene; transformation;  
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;  
KW gene structure; gene function; enzyme activity; medicine;  
KW forensic science; food; drug inspection; molecular biology; immunology.  
XX  
OS Thermococcus kodakaraensis.  
XX  
PN WO2004022736-A1.  
XX  
PD 18-MAR-2004.  
XX  
PF 29-AUG-2003; 2003WO-IB003597.  
XX  
PR 30-AUG-2002; 2002JP-00319011.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Imanaka T, Atomi H;  
XX  
WPI; 2004-257583/24.  
XX  
PT Method for disrupting targeted gene in genome of organism particularly  
PT thermostable bacterium and with genome chips for analysis, applicable in  
PT studying gene structure and functions.  
XX  
PS Claim 9; SEQ ID NO 1102; 598pp; Japanese.  
XX  
CC This invention relates to a novel method for targeting disruption of an  
CC arbitrary gene in a genome of an organism which comprises providing the  
CC whole sequential data of the genome of such organism, selecting at least  
CC 1 arbitrary region in the sequence, providing a vector that contains a  
CC sequence homologous with the selected region and a marker gene,  
CC transformation, and homologous recombination. The genome is preferably  
CC the genome of a hyperthermostable archaeobacterium, particularly  
CC Thermococcus kodakaraensis KOD1. The method is for targeting the







PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
PS Disclosure; SEQ ID NO 7944; 932pp; English.  
XX

CC The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention  
XX  
SQ Sequence 426 AA;

Query Match 3.2%; Score 85; DB 7; Length 426;  
Best Local Similarity 18.7%; Pred. No. 1.3e+02;  
Matches 80; Conservative 52; Mismatches 122; Indels 174; Gaps 20;

QY 156 GKLYGRG-ATDNKGPVLAWINAV-----SAFRALEQDLPVNIKFIEGMEEA 201  
Db 37 GLRYMRGRAADRFRFVSWLSTIGITLGVMAVTVLSVMNGFERELQNNILGL--MPQA 93  
QY 202 -----GSVALEELVEKEK-----DRFFSGVDYIVISDNLWI--SQKPAI 239  
Db 94 ILSAKQGSVNPQQLPERAKLNGVTRVAPITTDVVLQARSVAVGVMLGIDPAQNPLT 153  
QY 240 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSG---HILVPGIY 296  
Db 154 PY-----LVNVK--QSDLQAGKYNVILGEQLA-----GQLGVNVRGDKIRVMVPSA- 196  
QY 297 DEVVPLTE-----BEINTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSI 349  
Db 197 SQFTPMGRVPSQRLFTVIGTFAA-----NSEVDGYQMLTNIDDASRLMRYPLGNI 246  
QY 350 HGIEGAFDEP-----GTKTVIPGR-----VIGKFS 374  
Db 247 TGWRLWLDQPLQVDTLSQQTLPFGTQWDWRERKGELEFQAVRMEKNMGLLSLIVAVAA 306  
QY 375 IRLVPHMNVSAVEKQTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 307 FNIITSLGMVMMEKQ-----GEVAILQTQGLTP-----RQI 337  
QY 435 RTVF---GTEPDMI-----RDGSTIPIAKMFQEIIVHKSV 465  
Db 338 MAVFMVQASAGIVGALLGAVLGALLASQLNNLMPIIGAFLDGAALPVA-----IEPLQV 392  
QY 466 VLIPLGAV 473  
Db 393 IVIALVAM 400

RESULT 1133  
AAE30470  
ID AAE30470 standard; protein; 451 AA.  
XX  
AC AAE30470;  
XX

DT 24-FEB-2003 (first entry)

XX H. influenza pmBA protein.

DE Virulence; veterinary; infection; pneumonia; antimicrobial drug; vaccine;  
XX antibiotic; gene therapy; antibacterial; pmBA protein.

OS Haemophilus influenzae.

XX WO200277020-A2.

XX 03-OCT-2002.

XX 18-MAR-2002; 2002WO-GB001305.

PR 22-MAR-2001; 2001GB-00007234.  
PR 23-MAR-2001; 2001GB-00007360.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Herbert MA, Deadman ME, Hood DW, Moxon ER;  
XX  
DR WPI; 2003-029913/02.  
DR N-PSDB; AAD47838.  
XX  
PT New virulence gene from Hemophilus influenzae, useful for producing  
PT vaccines or antibiotics for preventing or treating pneumonia.  
XX  
PS Claim 4; Page 83-85; 132pp; English.  
XX

CC The present invention relates to Hemophilus influenzae virulence genes  
CC and proteins encoded by them. The microorganisms or the peptides of the  
CC invention are useful for manufacturing a medicament for treating  
CC (veterinary) or preventing a condition associated with H. influenzae  
CC infection, particularly pneumonia or for identifying an antimicrobial  
CC drug. Sequences of the invention are useful in the production of vaccines  
CC or antibiotics to prevent or treat H. influenzae infection. They are also  
CC used in gene therapy. The present sequence is H. influenzae pmBA protein  
XX  
SQ Sequence 451 AA;

Query Match 3.2%; Score 85; DB 6; Length 451;  
Best Local Similarity 20.8%; Pred. No. 1.4e+02;  
Matches 54; Conservative 37; Mismatches 86; Indels 82; Gaps 12;

QY 79 AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPA 138  
Db 263 AISGGSLYRKSSFLLD-HLGKQVLPDWFISERPHLLRRLASTP-----FDSEGVRTQ 314  
QY 139 DRG--DGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWI---NAVSAFRALEQDLPVNIKF 193  
Db 315 DREIVENGILQTYLVTSYSGKLGMSSTGHAGIHNWLVKPNLTGGLTAL----- 364  
QY 194 IIEGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEV 253  
Db 365 ---LRQMGTLGL-----VTDVMGQGVN-IVTGDY-----SRGASGFWE- 399  
QY 254 KCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEETINTYKAI 313  
Db 400 -----NGEIQYPVAE-ITIAGQLQDMLKQML--AVADDI----- 430  
QY 314 HLDLEEYRNSRVEKFLFD 332  
Db 431 -----EHRSNIQTSILLD 444

RESULT 1134  
ABU15862  
ID ABU15862 standard; protein; 485 AA.  
XX  
AC ABU15862;  
XX

DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #1389.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus aureus.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.





Db 59 FRRWLWDEVTOPTKEITLEAARYEDESNLGDYVEDQIESVTFDRITTTAKQVIVQKV 118

QY 244 RGNYSFVMEVKCRDQDFHSG-TFGGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVP 301

Db 119 REAERAMVVDQFRE---HEGEIITGVVKKVNRDNISLDLGNNA-----EAVI 162

QY 302 LTHEEINTYKAHLDLBEYRNSRVEKFLFD-----TKEEILMHLWR--YP 345

Db 163 LRED-----MLPRENFRPGDRVRGVLYSRPEARGAQLFVTRSKPEMLIELFRIEVP 214

QY 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371

Db 215 EIGEEVIEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274

QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGL 415

Db 275 LWDDNPAQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAIGRNGQNVRLASQLSGW 334

QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRDSSTIPIAKMFQEIHKSVVLIPL 470

Db 335 ELNVMVTVDLQAKHQAHAHAIDTFTKYLDIDEDFATVLVEEGFSTL--EELAYVPM 389

RESULT 1136

AAU33544

ID AAU33544 standard; protein; 495 AA.

XX

AC AAU33544;

XX

DT 14-FEB-2002 (first entry)

XX

DE Klebsiella pneumoniae cellular proliferation protein #9.

XX

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX

OS Klebsiella pneumoniae.

XX

PN WO200170955-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009180.

XX

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-020727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX

DR WPI; 2001-611495/70.

DR N-PSDB; AAS51403.

XX

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX

PS Example 3; SEQ ID NO 5040; 51lpp; English.

XX

CC The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 495 AA;

Query Match 3.2%; Score 85; DB 4; Length 495;

Best Local Similarity 18.1%; Pred. No. 1.7e+02;

Matches 77; Conservative 61; Mismatches 138; Indels 150; Gaps 16;

QY 170 VLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKE----- 213

Db 5 ILAVVEAVSNEKALPREK-----IFEALESALATATKKKYEQIDVRVEIDRKSQDFDT 58

QY 214 -----KORFFSGVDYI-----VISDNLWISQKPAITYGT 243

Db 59 FRRWLWVEEVTQPTREITLEAARFEDESVMVGDYVEDQIESVTFDRITTTAKQVIVQKV 118

QY 244 RGNYSFVMEVKCRDQDFHSG-TFGGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVP 301

Db 119 REAERAMVVDQFRE---HEGEIITGVVKKVNRDNITLDLGNNA-----EAVI 162

QY 302 LTHEEINTYKAHLDLBEYRNSRV-----EKFLFDTKEEILMHLWR--YP 345

Db 163 LRED-----MLPRENFRPGDRIRGVLYAVRPEARQAQLFVTRSKPEMLIELFRIEVP 214

QY 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371

Db 215 EIGEEVLEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274

QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGL 415

Db 275 LWDDNPAQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAIGRNGQNVRLASQLSGW 334

QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRDSSTIPIAKMFQEIHKSVV--LIP 469

Db 335 ELNVMVTVDLQAKHQAHAHAIDTFTKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLE 394

QY 470 LGAVDD 475

Db 395 IDGLDE 400

RESULT 1137

AAU36123

ID AAU36123 standard; protein; 495 AA.

XX

AC AAU36123;

XX

DT 14-FEB-2002 (first entry)

XX

DE Klebsiella pneumoniae cellular proliferation protein #11.

XX

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX

OS Klebsiella pneumoniae.

XX

PN WO200170955-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009180.

XX

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS53982.  
XX  
PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 11716; 511pp; English.  
XX  
CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 495 AA;

Query Match 3.2%; Score 85; DB 4; Length 495;  
Best Local Similarity 18.1%; Pred. No. 1.7e+02;  
Matches 77; Conservative 61; Mismatches 138; Indels 150; Gaps 16;

Qy 170 VLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKE----- 213  
Db 5 ILAVEAVSNEKALPREK-----IFEALESALATATKKKVEQEIDVRVEIDRKSGDEFT 58  
Qy 214 -----KDRFFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 59 FRRWLVEEVTQPTREITLEAARFEDESMMVGDYVEDQIESVTFDRITTQTAKQVIVQKV 118  
Qy 244 RGNsyMVEVKCRDQDFHSG-TFGGILHEPMDLVAL-LGSLVDSSGHILVPGIYDEVVP 301  
Db 119 REAERAMVVDQFRE---HEGEIITGVVKKVNRDNITLDLGNA-----EAVI 162  
Qy 302 LTEEEINTYKAHLDLEEYRNSSRV-----EKFLFTKEEILMHLWR--YP 345  
Db 163 LRED-----MLPRENFRPGDRIRGVLYAVRPEARGAQLFVTRSKPEMLIELFRIFVP 214  
Qy 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371  
Db 215 EIGEEVLEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274  
Qy 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGL 415  
Db 275 LWDDNPAQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAGRNGQVRLASQLSGW 334  
Qy 416 HPWIANDDTQ--YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVKHSV---LIP 469  
Db 335 ELNVMTVDDLQAKHQAEAAHAIIDFTFKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLE 394  
Qy 470 LGAVDD 475

Db 395 IDGLDE 400  
RESULT 1138  
ABU15338  
ID ABU15338 standard; protein; 495 AA.  
XX  
AC ABU15338;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #865.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Escherichia coli.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA19208.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
PS Claim 25; SEQ ID NO 43262; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained



CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 495 AA;

Query Match 3.2%; Score 85; DB 6; Length 495;  
Best Local Similarity 18.2%; Pred. No. 1.7e+02;  
Matches 76; Conservative 59; Mismatches 134; Indels 148; Gaps 16;  
QY 170 VLWINAVSAFRALEQDLVPNIKFIIEGMEAGSVALEELVEKE----- 213  
Db 5 ILAVVEAVSNEKALPREK-----IFEALESALATATKKYEQEIDVRVQIDRKSGDFDT 58  
QY 214 -----KDRFFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 59 FRRWLVDVETQPTKEITLEAARYEDESINLGDYVEDQIESVTFDRITTTQAKQVIVQKV 118  
QY 244 RGNYSFMVEVKCRDQDFHSG-TFGGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVWP 301  
Db 119 REAERAMVVDQFRE---HEGEIITGVVKVNRDNISLDLGNA-----EAVI 162  
QY 302 LTEEEINTYKAIHLDLEEYRNSRV-----TKEEILMHLWR--YP 345  
Db 163 LRED-----MLPRENFRPGDRVGVLYSVRPEARGAQLFVTRSKPEMLIELFRIEVP 214  
QY 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371  
Db 215 EIGEEVIEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274  
QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNMVVSMTLGL 415  
Db 275 LWDDNPAQFVINAMAPADVASIVVDKHTMDIAVEAGNLAQAIGRNGQNVRLASQLSGW 334  
QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRGSGTIPIAKMFQEIIVHKSVVLIPL 470  
Db 335 ELNVMVTVDLQAKHQAEAAHAIDTFTKYLDIDEDFATVLVEEGFSTL--EELAYVPM 389

RESULT 1139  
ABU31460  
ID ABU31460 standard; protein; 495 AA.

XX AC ABU31460;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #16987.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Klebsiella pneumoniae.

XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA35330.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

PT  
XX  
PS  
XX

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 495 AA;

Query Match 3.2%; Score 85; DB 6; Length 495;  
Best Local Similarity 18.1%; Pred. No. 1.7e+02;  
Matches 77; Conservative 61; Mismatches 138; Indels 150; Gaps 16;

QY 170 VLWINAVSAFRALEQDLVPNIKFIIEGMEAGSVALEELVEKE----- 213  
Db 5 ILAVVEAVSNEKALPREK-----IFEALESALATATKKYEQEIDVRVDRKSGDFDT 58  
QY 214 -----KDRFFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 59 FRRWLVDVETQPTKEITLEAARFEDESMNVGDYVEDQIESVTFDRITTTQAKQVIVQKV 118  
QY 244 RGNYSFMVEVKCRDQDFHSG-TFGGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVWP 301  
Db 119 REAERAMVVDQFRE---HEGEIITGVVKVNRDNITLDGNA-----EAVI 162  
QY 302 LTEEEINTYKAIHLDLEEYRNSRV-----EKFLEDTKEEILMHLWR--YP 345  
Db 163 LRED-----MLPRENFRPGDRIRGVLYAVRPEARQAQLFVTRSKPEMLIELFRIEVP 214  
QY 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371  
Db 215 EIGEEVLEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274  
QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNMVVSMTLGL 415  
Db 275 LWDDNPAQFVINAMAPADVASIVVDKHTMDIAVEAGNLAQAIGRNGQNVRLASQLSGW 334  
QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRGSGTIPIAKMFQEIIVHKSVV---LIP 469  
Db 335 ELNVMVTVDLQAKHQAEAAHAIDTFTKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLE 394  
QY 470 LGAVDD 475  
: :|:



CC for elucidating biological pathways and their reactions that occur either  
CC simultaneously or sequentially, disease processes, inhibitors and  
CC enhancers of a molecular system or for understanding receptor-signal  
CC recognition. In particular, it enables assaying one or more biological  
CC samples having one or more targets per sample on a single array, such  
CC that it is cost effective and specific. This polypeptide sequence is an  
CC exemplary tag of a binding partner e.g. a monoclonal antibody that binds  
CC to capture agents of the invention.

XX Sequence 495 AA;

Query Match 3.2%; Score 85; DB 8; Length 495;  
Best Local Similarity 18.2%; Pred. No. 1.7e+02;  
Matches 76; Conservative 59; Mismatches 134; Indels 148; Gaps 16;

QY 170 VLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKE----- 213  
Db 5 ILAVVEAVSNEKALPREK-----IFEALESALATATKKKYEQEI DVRVQIDRKSGDFDT 58  
QY 214 -----KORFFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 59 FRRWLVDDEVTPQTKETILEAARYEDESINLGDYVEDQIESVTFDRITTTQAKQVIVQKV 118  
QY 244 RGN SYFMVEVKCRDQDFHSG-TFGGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVP 301  
Db 119 REAERAMVVDQFRE---HEGEIITGVVKKVNRDNISLDLGNNA-----EAVI 162  
QY 302 L TEE EINTYKA IHL DLE EYRNSRVEKFLFD-----TKEEILMHLWR--YP 345  
Db 163 LRED-----MLPRENFRPGDRVRGVLYSVRPEARGAQLFVTRSKPEMLIELFRIEVP 214  
QY 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371  
Db 215 EIGEEVIEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274  
QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGL 415  
Db 275 LWDDNPAQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAGRNGQNVRLASQLSGW 334  
QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEI VHKSVVLIPL 470  
Db 335 ELNVMTVDDLQAKHQAEAAHAIDTFTKYLDIDEDFATVLVEEGFSTL--EELAYVPM 389

RESULT 1142  
ABO67190  
ID ABO67190 standard; protein; 498 AA.

XX ABO67190;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Klebsiella pneumoniae polypeptide seqid 13707.

XX Recombinant expression vector; transcription regulatory element;  
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

DR N-PSDB; ABD00761.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
XX Disclosure; SEQ ID NO 13707; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention

XX Sequence 498 AA;

Query Match 3.2%; Score 85; DB 7; Length 498;  
Best Local Similarity 18.1%; Pred. No. 1.7e+02;  
Matches 77; Conservative 61; Mismatches 138; Indels 150; Gaps 16;

QY 170 VLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKE----- 213  
Db 8 ILAVVEAVSNEKALPREK-----IFEALESALATATKKKYEQEI DVRVEIDRKSGDFDT 61  
QY 214 -----KORFFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 62 FRRWLVDDEVTPQTKETILEAARFEDESMNVGDYVEDQIESVTFDRITTTQAKQVIVQKV 121  
QY 244 RGN SYFMVEVKCRDQDFHSG-TFGGILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVP 301  
Db 122 REAERAMVVDQFRE---HEGEIITGVVKKVNRDNITLDLGNNA-----EAVI 165  
QY 302 L TEE EINTYKA IHL DLE EYRNSRV-----EKFLDFTKKEILMHLWR--YP 345  
Db 166 LRED-----MLPRENFRPGDRIRGVLYAVRPEARGAQLFVTRSKPEMLIELFRIEVP 217  
QY 346 SL--SIHGIEGAFDEPGTKTVIP-----GRVIG----- 371  
Db 218 EIGEEVLEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 277  
QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGL 415  
Db 278 LWDDNPAQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAGRNGQNVRLASQLSGW 337  
QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQEI VHKSVV---LIP 469  
Db 338 ELNVMTVDDLQAKHQAEAAHAIDTFTKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLE 397  
QY 470 LGA VDD 475  
Db 398 IDGLDE 403

RESULT 1143  
AAU77470  
ID AAU77470 standard; protein; 500 AA.

XX AAU77470;

XX 05-JUN-2002 (first entry)

XX Euphorbia lagascae cytochrome P450 enzyme.

XX Cytochrome P450 enzyme; synthesis of delta 12-epoxy fatty acid; epoxide;  
KW vernolic acid; modified fatty acid; oil; commercial crop; plasticiser;  
KW crosslinking coating application; setting printing ink; transgenic;  
KW plant; enzyme.

XX Euphorbia lagascae.

XX WO200208269-A2.

XX 31-JAN-2002.



XX 19-JUL-2001; 2001WO-US022790.  
XX PF  
XX PR  
XX 21-JUL-2000; 2000US-0219833P.  
XX PA  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX PI  
XX Cahoon EB;  
XX  
XX WPI; 2002-257331/30.  
XX N-PSDB; ABK11137.  
XX  
XX Novel isolated polynucleotide encoding plant cytochrome P450 enzyme  
PT associated with synthesis of Delta12-epoxy fatty acids, useful for  
PT creating transgenic plants with higher or lower level expression of the  
PT enzyme.  
XX  
XX Claim 2; Fig 1; 53pp; English.  
XX  
XX The present invention relates to the isolation of the polynucleotide and  
CC polypeptide sequences for a plant cytochrome P450 enzyme associated with  
CC the synthesis of delta 12-epoxy fatty acids from Euphorbia lagascae. The  
CC polynucleotide sequence of the invention can be used to produce epoxide  
CC containing fatty acids such as vernolic acid. The sequences of the  
CC invention can be used to manipulate modified fatty acids to produce oils  
CC in commercial crops. They can also be used to produce plasticisers, for  
CC crosslinking coating applications, and setting printing inks. The  
CC polynucleotide can also be used for creating transgenic plants in which  
CC the enzyme is present at higher or lower levels than normal, in cell  
CC types or in developmental stages in which they are not normally found.  
CC The present sequence represents the E. lagascae cytochrome P450 enzyme of  
CC the invention  
XX  
XX Sequence 500 AA;  
SQ  
  
Query Match  
Best Local Similarity 3.2%; Score 85; DB 5; Length 500;  
Matches 97; Conservative 63; Mismatches 167; Indels 200; Gaps 22;  
  
QY 11 SLLAVLLLLLBERGMFSSPPPP-----ALLEKVFQYIDLHDEF---VQTLKEWVAI 59  
Db 14 SFLLVILVVMRLWKQNPFGPKFPIIGNLPHLLTSDLGHERFRALAQIYGPVMSL 73  
QY 60 ESDSVQVPFRFQELFR-MMAVAADTL-QRLGARVASVDMGPPQLPDGQSLPIPPVILAE 117  
Db 74 QIGQVSADVVISABAAKEVMKTOADAFAGR-----PIVL-- 107  
QY 118 LGSDPKTGTCFYGHLDVQPADRGDW--LTDPPVLTVDGKLYGRGATDNKGPVLAWIN 175  
Db 108 -----DAQIVFYNRKDVLFASYGDHWRQMCKIWILEFLSAK----- 143  
QY 176 AVSAFRALEQD-----LPVNIKFIIEGMEEAGSVALEELVE--KEKDRFFS 219  
Db 144 KVQSSRLIREEMEDAITFLRSKAGSPVNIKIYGI--IISIMRTSVGNCKQKERLLS 201  
QY 220 GVDYIVISDNLWISQRPKPAITYGTRGN-----SYFMVEVKCRDQDFHSGTFCGILHEPM 273  
Db 202 VADAV-----NEAATSFGTADAFPTWKLLHYIIGAESKPRRLH----- 239  
QY 274 ADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFDT 333  
Db 240 -----QEIDDLLEEILNEHKA-----NKPFEADN 263  
QY 334 KEEILMHLWRYPSSLIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRH 393  
Db 264 LMDVLLNLQK-----NGNVPPVPVTNESIKASVLQMFT----- 295  
QY 394 LEDVFSKRNSNMVSMVMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPI 453  
Db 296 ---AGSETTSKATEWVMAELMKNP-----TELKRAQEEVRQVFGEMGKV--DESRFHD 343  
QY 454 AKMFQEIIV-----HKSVVLIP-----LGAVDDGGEHSQNEKI--NRW 487

Db 344 LKFEKLVVKETLRLHPPVVLIPRECRETTRIDGYEIHNPTRIVVNAW 390  
  
RESULT 1144  
ABM69226  
ID ABM69226 standard; protein; 535 AA.  
XX  
XX AC ABM69226;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Photorhabdus luminescens protein sequence #2323.  
XX  
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX  
XX Photorhabdus luminescens.  
XX  
XX WO200294867-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 07-FEB-2002; 2002WO-IB003040.  
XX  
XX 07-FEB-2001; 2001FR-00001659.  
XX  
XX (INSP ) INST PASTEUR.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
XX  
XX WPI; 2003-148459/14.  
XX  
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
PT  
XX  
PS Claim 2; SEQ ID NO 2323; 1205pp; French.  
XX  
XX The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
SQ Sequence 535 AA;  
  
Query Match  
Best Local Similarity 3.2%; Score 85; DB 6; Length 535;  
Matches 55; Conservative 41; Mismatches 91; Indels 58; Gaps 11;  
  
QY 235 RKPAITYGTRGNSYFMVEVKCRDQD---FHSGTFGG----ILHEPMDLVALLGSLVDSS 287  
Db 276 RTPDLTNGRNRYAYGLIIIEQREGQRIIQHNGTFAGFRANICILPDKLGMAWTSATDA- 334

QY 288 GHILVPGIYDEVVPLTEEEINTYKAHLDLEE-----YRNSSRVEKELF-DT 333  
Db 335 -----DVDQWTNYMDILFNTHIEPEKPYCLTSDIDITGIFRG---IBPYPIIT 381  
QY 334 KBEI--LMHLWRYPSSLIHGIEGAFDEPGTKTVIPGR-VIGKFSIRLVPHMNVSAVEKQV 390  
Db 382 KEDIYFLGDLFKKGNPIIFNSDGTFOEKGSK--IQRPVIENDSVIALEHIDENG----- 434  
QY 391 TRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST 450  
Db 435 -----NVFYLLKMNNESSVDINL-----LSGRYYSHETEAINIISGDDIYIDGII 481  
QY 451 IPIAK 455  
Db 482 HPVKK 486

RESULT 1145  
AAY06394  
ID AAY06394 standard; protein; 547 AA.  
XX AC AAY06394;  
XX 20-SEP-1999 (first entry)  
XX DB Bacillus subtilis metalloprotease YqjN.  
XX DE Metalloprotease; protease; YqjN; detergent; surfactant; cleaning;  
KW textile; feedstuff; animal feed; host cell.  
KW XX Bacillus subtilis.  
OS XX WO9934001-A2.  
PN XX 08-JUL-1999.  
PD XX 17-DEC-1998; 98WO-US026971.  
PF XX 30-DEC-1997; 97GB-00027470.  
PR XX (GEMV ) GENENCOR INT INC.  
PA XX Estell DA;  
XX PI WPI; 1999-419110/35.  
XX DR N-PSDB; AAX59331.  
XX DR A Bacillus subtilis metalloprotease, designated YqjN, useful in cleaning  
PT compositions, animal feed and for treating textiles.  
PT XX Claim 9; Fig 1A-H; 35pp; English.  
PS XX The present sequence represents a novel metalloprotease (MP), designated  
XX YqjN, of Bacillus subtilis. YqjN DNA (see AAX59331) was identified via a  
CC BLAST search of B. subtilis genomic DNA. The deduced protein sequence  
CC shows identity to the MP succinyl- diaminopimelate desuccinylase from  
CC Escherichia coli. An expression vector including YqjN DNA and a host cell  
CC comprising the vector are claimed. Also claimed are a cleaning  
CC composition, an animal feed and a composition for the treatment of a  
CC textile, all comprising YqjN. Gram positive microorganisms having a  
CC mutation or deletion of all or part of YqjN DNA are used as host cells  
CC for expression of a homologous or heterologous protein, such as a  
CC hormone, growth factor, cytokine or enzyme, especially a protease, kinase  
CC carboxydase, lipase, isomerase, oxidase, reductase, transferase, kinase  
CC or phosphatase (all claimed). Also claimed is a method for detecting a  
CC Gram positive microorganism MP using a probe comprising all or part of  
CC the YqjN DNA  
XX SQ Sequence 547 AA;

Query Match 3.2%; Score 85; DB 2; Length 547;  
Best Local Similarity 21.8%; Pred. No. 1.9e+02;  
Matches 65; Conservative 39; Mismatches 108; Indels 86; Gaps 12;

QY 96 DMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCYGHLDV-----QPADRG 141  
Db 51 DVTPHPMDDGRSF-----LTALVKKKNVKKTVLLLSHFDVVDIEDYGEFFKHMACKPAELL 105  
QY 142 DGWLTDPPYVL-----TEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI 194  
Db 106 SSFLEKKELLPERVRRDAESGDWLFGRGTMDKAGLCIQLSMLE--RAMNGHFEGNLLJI 163  
QY 195 IEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVK 254  
Db 164 TVPDEEVNSRGMIEAVPALKE-----MEKKHDITLTACLNABPMFEKF 206  
QY 255 CRDQD--FHSGTFFGIL-----HEPNADLVALLGSLVDSSGHIL----- 291  
Db 207 PGDQQQYFYTGSIQKVLAGFFCKGIETHVGEPSGLNANL--MVSEINRLLELNADYCEK 264  
QY 292 VPGIYDEVVP-----LTEEEI-----NTYKAHLDLEEYRNSSRVEKFLFTKBE 336  
Db 265 VDG---EVTPTPPVNLQKDLKEAYSVQTPHTAVTLFNVLSMKRSASELHQLMLKTAEQ 319

RESULT 1146  
ADO58596  
ID ADO58596 standard; protein; 555 AA.  
XX AC ADO58596;  
XX 26-AUG-2004 (first entry)  
XX DE Nusa protein, SEQ ID NO:17.  
XX KW Fusion protein; Notch protein; Nusa; NICD; Notch-1 intracellular domain;  
KW Notch-1 signalling; haematopoiesis; immunodeficiency; anaemia;  
KW gamma-secretase cleavage; APP; amyloid precursor protein;  
KW CT-100 cleavage; epsilon cleavage; S3 cleavage; Alzheimer's disease;  
KW adverse effect; side effect; drug screening.  
XX OS Unidentified.  
XX PN WO2004048578-A1.  
XX PD 10-JUN-2004.  
XX PF 17-NOV-2003; 2003WO-IB005233.  
XX PR 26-NOV-2002; 2002US-0429206P.  
XX PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX PI Rank KB, Sharma SK;  
XX XX WPI; 2004-450388/42.  
DR N-PSDB; ADO58595.  
XX PT Novel soluble fusion protein comprising a recombinant Notch protein fused  
PT to C-terminus of Nusa protein sequence, useful for screening modulators  
PT of gamma secretase mediated cleavage of Notch protein.  
XX XX Claim 14; SEQ ID NO 17; 89pp; English.  
XX CC The invention relates to a soluble fusion protein comprising a  
CC recombinant Notch protein fused to the C-terminus of a Nusa protein  
CC sequence. The Nusa protein allows the fusion protein to remain soluble.  
CC The Notch protein component of the fusion protein is preferably mouse  
CC .Notch-1 (ADO58587) and especially residues 1703-1860 of this protein  
CC (ADO58592). Notch-1 is an integral membrane protein which is  
CC proteolytically processed within its ectodomain upon ligand-mediated  
CC activation. Notch-1 processing is similar to the processing of amyloid  
CC protein precursor (APP), undergoing two presenilin-dependent  
CC intramembraneous gamma-secretase cleavages. The first cleavage is between  
CC residues 1731-1732 (numbering is that of mouse Notch-1) and is akin to  
CC the Abeta-like (CT-100) gamma-secretase cleavage of APP, while the

CC second, referred to as S3 or epsilon cleavage, is between 1743-1744 and  
CC is akin to epsilon cleavage of APP. It is S3 (epsilon) cleavage of Notch-  
CC 1, occurring towards the end of the transmembrane domain, that releases  
CC the intracellular domain (NICD) which then translocates to the nucleus to  
CC form a transcriptional regulatory complex with a protein called CSL.  
CC Notch-1 signalling is important in haematopoiesis in adults, as well as  
CC being required in embryonic development. Because Notch-1 is processed in  
CC a similar fashion to APP, it can be used in identifying compounds that  
CC specifically inhibit CT-100 gamma-secretase cleavage of APP but which do  
CC not inhibit the S3 (epsilon) cleavage-mediated release of NICD from Notch  
CC -1. Such compounds would be useful in the treatment of Alzheimer's  
CC disease, without producing the deleterious effects of inhibition of NICD  
CC production, such as immunodeficiency and anaemia. The invention also  
CC relates to nucleic acids encoding the Notch/Nusa fusion protein;  
CC expression vectors comprising the nucleic acid; recombinant production of  
CC the fusion protein; methods of assaying for and identifying modulators of  
CC gamma-secretase-mediated epsilon cleavage of Notch proteins; a kit for  
CC performing a gamma-secretase assay comprising the fusion protein; a  
CC method of screening for selective inhibitors of gamma-secretase-mediated  
CC APP cleavage; and a Notch transmembrane domain-containing fusion protein  
CC comprising 90-95% sequence identity with the Nusa sequence of (ADO58596).  
CC The fusion proteins, methods and kits permit the identification of  
CC compounds for the treatment of Alzheimer's disease which inhibit gamma-  
CC secretase-mediated cleavage of APP, but which do not inhibit Notch-1  
CC cleavage and NICD production. The present sequence represents a Nusa  
CC protein which is specifically claimed for use in the fusion proteins of  
CC the invention.

XX SQ Sequence 555 AA;

Query Match 3.2%; Score 85; DB 8; Length 555;  
Best Local Similarity 18.2%; Pred. No. 2e+02;  
Matches 76; Conservative 59; Mismatches 134; Indels 148; Gaps 16;

QY 170 VLWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKE----- 213  
Db 5 ILAVEAVSNEKALPREK-----IFEALESALATATKKYQEIDVRVQIDRKSGDFT 58  
QY 214 -----KDRFSGVDYI-----VISDNLWISQRKPAITYGT 243  
Db 59 FRRWLVDVETQPTKEITLEAARYEDESINLGDYVEDQIESVTFDRITTTAKQVIVQKV 118  
QY 244 RGNYSFMVEVKCRDQDFHSG-TFGGILHEPMDLVAL-LGSLVDSSGHILVPGIYDEVVP 301  
Db 119 REAERAMVVDDQFRE---HEGEIITGVVKKVNRDNISLDLGNNA-----EAVI 162  
QY 302 LTHEEINTYKAHLDLEEYRNSRVEKFLFD-----TKEEILMHLWR--YP 345  
Db 163 LRED-----MLPRENFRPGDRVRGVLYSVRPEARGAQLFVTRSKPEMLIELFRIEVP 214  
QY 346 SL--SIHGEGAFDEPGTKTVIP-----GRVIG----- 371  
Db 215 EIGEEVIEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIV 274  
QY 372 -----KFSIRLVPHMNVSAVEKQVTRHLEDVFSK-----RNSSNKMVVSMTLGL 415  
Db 275 LWDDNPAQFVINAMAPADVASIVVDEDKHTWMDIAVEAGNLAQIENGQNVRLASQLSGW 334  
QY 416 HPWIANIDDTQ--YLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVLIP 470  
Db 335 ELNVMTVDDLQAKHQAEAAHAAIDTFTKYLDIDEDFATVLVEEGFSTL--EELAYVPM 389

RESULT 1147  
ADS25316  
ID ADS25316 standard; protein; 574 AA.

XX AC ADS25316;  
XX AC  
DT 02-DEC-2004 (first entry)  
XX DE  
DE Bacterial polypeptide #14349.

KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 14349; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 574 AA;

Query Match 3.2%; Score 85; DB 8; Length 574;  
Best Local Similarity 21.9%; Pred. No. 2.1e+02;  
Matches 118; Conservative 67; Mismatches 194; Indels 160; Gaps 30;

QY 35 LEKVFOYIDLHQDE-FVQTLKEWVAIESDSVQVPRFRQELPFMMVAADTLQRLGARVA 93

Db 25 LQSVAVYADPDQDALFVRLADEAYALE--GVRPAETY-LDISKLIATA----KRAGA--D 75

QY 94 SVDMGPOQLPDGQSLPIPPVILABELGSDPTKGTVCFYGLHDVQP-----ADRGDGL-T 146

Db 76 AVHPG-----YGLSERAEFAQAVIDAGLIWIGP 104



QY	147	DPYVLTEVDGKLYGRG-ATDNKGPVLAWINA-----VSAFRALEQDLPVNITKFIIEGM	198
Db	105	DPDVEIALGDKWMARRIATGVGAPLVAGSDGPVSSAAEVTAFAEQHGLPVAIKAAHGGG	163
QY	199	EEAGSVA--LEELVEKEK-----DRFFSGVDYI---VISDNLWISQRK	236
Db	164	GRGLKVANKMEEIAELYESAVREATVAFGRGECFLERFLDRPRHIEAQVIAD-----KHG	218
QY	237	PAITYGTRGNSYFMVEVKCRDQ---DFHSGTGGILHEPMADLVALLGSLVDSSGHI-LV	292
Db	219	NVLVLGTRDCSLORRNQKLEAPAPFLSDEQRQKIHDAKAICAAG--YSGAGHVFFL	276
QY	293	PGIYDEWV-----PLTEEEINTYKAIHLDLEEYRNSRRVEKFLPDTKEEILMH	340
Db	277	LGVDGTISFLEVNTPPQVEHPVTEET-----TGIDLVEIQFRIAECHKLRVLETPEP----	328
QY	341	LWRYPSLSIH-----GIEGAFDEPG-----TKTVIPGRVITGKFSIRLVPH	380
Db	329	--RGHSMEFRINAEDPGRGFLPTPGLISVEDAPSGPGIRMDSGVISGSSIPGVFDSLMAK	386
QY	381	MNVSAVEK-QVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAA-----KRA	433
Db	387	LIVTGVDRDQVLRARRALREFRIEG---IATVLPFHR--AAIETEDFIGTDGFKVHTRW	441
QY	434	IRTVFGTEPDMIR-----DGSTIPIAKMFOEIVHK-----SVLLPLGAVDDEHS	479
Db	442	IETDFAAMPDAMERPAPADPPS---ITRTYLEIDGKRVSUGLPSILLSSLTGTVSGGNAS	497

**RESULT 1148**

ADN17371

ID ADN17371 standard; protein; 592 AA.

AC ADN17371;

DT 02-DEC-2004 (first entry)

Bacterial polypeptide #24.

Recombinant DNA construct; transformed plant; improved plant property;  
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
pathogen tolerance; pest tolerance; plant disease resistance;  
cell cycle pathway modification; plant growth regulator;  
homologous recombination; seed oil yield; protein yield; carbohydrate;  
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
bacterial polypeptide.

**OS Bacteria.**

PN US2003233675-A1.

PD 18-DEC-2003.

20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

PA (CAOY//) CAO Y.  
PA (HINK//) HINKLE G J.  
PA (SLAT//) SLATER S C.  
PA (CHEN//) CHEN X.  
PA (GOLD//) GOLDMAN B S.

Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR · WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 24; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

Sequence 592 AA;

Query Match 3.2%; Score 85; DB 8; Length 592;

Best Local Similarity 21.6%; Pred. No. 2.2e+02;

Matches 80; Conservative 52; Mismatches 127; Indels 112; Gaps 16;

```
QY      16 LLLLLRGMFSSPPALLEKVFQYIDLHQDEFVOTLKEWVAIESDSVQPVR----- 69
```

```
QY      70 -----FRQLERMMVAADTLQRLLGARVASVDMGPQQLPDQGSLPIPPVIL 115  
       ::: ||| :: | | | | | :  
Db     238 WDLVSAEKGKGFHFMUKETYEOPKAINDTLKGF---LSTEDAIPFKLKDFRR-----VL I 289
```

Qy	:       :	116 AELGSDPTKGTVCYFYGHLDVQPADRGDGLTD-PYVLTEVDKLYGRGATDNKG PVLAWI 174
Db	:       :	290 IACGTSYHAGFV-----GKYWIERFAGVPTEV---IY----- 318

QY	175	NAVS	A	F	R	A	L	E	O	D	P	V	N	T	K	F	I	E	G	M	E	E	A	G	S	V	A	L	E	E	L	V	--EKEKDRFFSGVDYIVISDNLM	231																			
						:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																			
D6	319	--A	S	E	F	R	--Y	A	D	V	P	V	S	D	K	D	I	V	I	G	I	S	Q	S	G	E	T	A	T	K	F	A	L	Q	S	A	K	E	G	A	F	T	V	G	L	V	N	V	V	G	S	---	370

QY	232	ISQRKPAITYGTRGNSYFMVEVKCRDQDF	---	HSGTGGILHEP	--	MADLVALLG	SLV	284
Db	371	-----AID-----	RESDFSLH	THAGPEIGVAATKFTFAQLTALYALSVR	409			

[illegible]

Qy 345 PLSIHGIEGA 355

Db 458 LNYPI-ALEGA 467

RESULT 1149

ABM64825

.ID ABM64825 standard; protein; 626 AA.

AC ABM64825;

DT 20-OCT-2003 (first entry)

DE Propionibacterium acnes immunogenic polypeptide #29501.

KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;  
KW immunostimulant; immune response; vaccine; immunogenic.



Best Local Similarity 16.7%; Pred. No. 2.4e+02;  
Matches 82; Conservative 64; Mismatches 130; Indels 216; Gaps 18;  
QY 102 LPDQSLPIPPVILAEGLSDPTKGTVCYFYLHGVADRGDGLTDPYVLTVDGKLYGR 161  
Db 97 MPDNCVFLP---LRQLTKPIVEHYLEFMGGVETQ-----FADVGLAEPD---GR 141  
QY 162 GATDNKGPVLAWINAVSAFRALEDLPVNIKFIEGMEHAGSVALEELVEKEKDRFFSGV 221  
Db 142 GRFD-----LMIRLCIEMLEKCG-----KLNNAKIAYTVDV 173  
QY 222 DYIVISDNLWISQKPAITYTRGNSYFMVEVKCRDQ-----DFHSGTFGGILHEPMADL 276  
Db 174 -----REP---HPSNSNHFAALQKASDLGKKEFEH----- 202  
QY 277 VALLGSLVDSGHILVPGIYD-EVVPLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKE 335  
Db 203 -----VIPMVDDFDYEPFYKEFITLSRAIELDAFQVPDAQMLREILSDRK- 247  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMNVS----- 384  
Db 248 -----LKQDFLRRLCLGHFSFYLGNLSMSVQYVYFQRRRA 282  
QY 385 -----AVEKQVTRHLEDV-----FSKRNSNNKMWVSM 411  
Db 283 YPRKVQILRRDNSVVRTKRVITVQKQKDDGSQDIEHEYQIKVTGGWYTCNVGERDLRISM 342  
QY 412 -----TLGLH-----PWIANI-----DDTQYLAAKRAIRTVFGTEPD 443  
Db 343 DQLNRVRNLHKPQMLLGFKRRSSLPEVSIYKPANFMYPDDQSIIGSKRFLRLW--ERC 400  
QY 444 MIRDGSTIPIAKMFQEIYVHKSIVLPLGAVDDGE-----HSQN 481  
Db 401 LVKDIAICLFMCKRSIPRYVALVPVEAPDNGEDKNYRSLLCGDGFKIVYLPBKAHIRH 460  
QY 482 EKINRWNYIEGT 493  
Db 461 LDLDQWNNTENT 472  
RESULT 1151  
ADRO8909  
ID ADR08909 standard; protein; 645 AA.  
XX AC ADR08909;  
XX DT 04-NOV-2004 (first entry)  
XX DE Human protein useful for treating neurological disease Seq 2415.  
XX KW human; oligo-capping method; diagnostic marker; gene therapy;  
KW osteoporosis; neurological disease; Alzheimer's disease;  
KW Parkinson's disease; dementia; short memory; cancer;  
KW sense or motor function; emotional reaction; fear response; panic;  
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
KW tranquiliser.  
XX OS Homo sapiens.  
XX PN EP1447413-A2.  
XX PD 18-AUG-2004.  
XX PF 12-FEB-2004; 2004EP-00003145.  
XX PR 14-FEB-2003; 2003JP-00102207.  
XX PR 09-MAY-2003; 2003JP-00131452.  
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX

DR WPI; 2004-583265/57.  
DR N-PSDB; ADR06953.  
XX  
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
PS Claim 1; SEQ ID NO 2415; 2686pp; English.  
XX  
CC This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded proteins thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states. In particular, they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
CC cytosstatic and tranquiliser activities. This polypeptide is a protein  
CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
CC sequence is not given in the sequence listing of the specification but  
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
CC office.  
XX  
SQ Sequence 645 AA;  
Query Match 3.2%; Score 85; DB 8; Length 645;  
Best Local Similarity 24.3%; Pred. No. 2.5e+02;  
Matches 67; Conservative 32; Mismatches 105; Indels 72; Gaps 13;  
QY 16 LLLLLLGRMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELF 75  
Db 19 LVLVPQRSVF-----PAHKGVLAAYSQFFHSLFTQN-KQLQRVLSLEALAPGGLQQIL 71  
QY 76 -----RMMVAADTLQLRGA-----RVASVDMGPQQLPDQSLPIP---PVILAEGLSDP 122  
Db 72 NFIYTSKLLVNAANVHEVLSAASLLQMAADIAASQCQLLDARSLGPPPGTVALAQPAASC 131  
QY 123 TKGTVCFYGHLDV-QPAD-----RGDGWLTDPYVLTVDGKLYGRGATDNKGPVLAW 173  
Db 132 TPAAPPY--CDIKQEADTPGLPKIYAREG--RDPYSVRVED-----GAGTAGTVPAT 181  
QY 174 INAVSAFRALEQLPVNIKFIEGMEHAGS-----VALEELVEKEKDRFFSGVDYIVISD 228  
Db 182 IGPAQPFKEEKE-----GGVEEAGGPPASLCKLEGGELEELGGSG----- 224  
QY 229 NLWISQRKPAITYTRGNSYFMVEVKCRDQDFHSGT 264  
Db 225 -----TYSRREQSQIIVEVNLNNQTLHVST 249  
RESULT 1152  
AAW99657  
ID AAW99657 standard; protein; 672 AA.  
XX AC AAW99657;  
XX DT 21-MAY-1999 (first entry)  
XX DE Staphylococcus aureus mecB ORF protein sequence.  
XX KW Staphylococcus aureus; mecB; antibacterial; infection; otitis media;  
KW conjunctivitis; toxic shock syndrome; impetigo; wound infection;  
KW septic arthritis; cancer; ulcer; gastritis.  
XX OS Staphylococcus aureus.  
XX PN EP900848-A2.  
XX



PD 10-MAR-1999.

XX

PF 20-AUG-1998; 98EP-00306683.

XX

PR 04-SEP-1997; 97US-0057535P.

PR 18-MAR-1998; 98US-00040843.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Jaworski DD, Wang M, Shilling LK, Burnham MKR, Rosenberg M;

PI Fosberry A, Lawlor E, Hodgson JE, Ward J;

XX

DR WPI; 1999-155941/14.

DR N-PSDB; AAX19481.

XX

PT New Staphylococcus aureus mecB polypeptide and polynucleotide - useful as

PT diagnostic reagents and for prevention and treatment of Staphylococci and

PT Helicobacter infections.

XX

PS Claim 23; Page 11-12; 36pp; English.

XX

CC The present sequence is the Staphylococcus aureus mecB protein, which is

CC a member of the ClpC ATPase family. MecB proteins are administered to

CC treat individuals in need of mecB proteins (directly or via a vector i.e.

CC gene therapy), and as an antigen for inducing an immunological response.

CC (administered directly i.e. vaccine). They can prevent adhesion of

CC bacteria to matrix proteins, and are useful for use on wounds and body

CC implants to prevent bacterial infection. They are also useful for

CC identifying agonists and antagonists by screening host cells expressing

CC mecB protein, and detecting the absence or presence of mecB activity.

CC Agonists and antagonists are useful for inhibition and treatment of

CC conditions associated with mecB imbalance, and are therefore potential

CC antibacterial compounds. MecB polynucleotides are useful for genetic

CC immunisation, preferably via a vector. Anti-mecB antibodies induced by

CC the polypeptide are useful for preventing or treating infections,

CC especially bacterial infections, and also for isolating clones expressing

CC mecB protein, or for purifying the polypeptide by affinity

CC chromatography. Diseases can be diagnosed by determining the presence of

CC mecB nucleic acid, and/or analysing for the presence/amount of mecB

CC polypeptide in a sample, due to infection of an organism with the mecB

CC gene. The stage and type of infection can be determined. Diseases

CC prevented, diagnosed and treated include those caused by bacterial

CC infection, especially Staphylococcus aureus infections which cause otitis

CC media, conjunctivitis, toxic shock syndrome, impetigo, wound infection

CC and septic arthritis. MecB agonists and antagonists are also useful for

CC treatment of Helicobacter pylori infections which cause stomach cancer,

CC ulcers and gastritis

XX

SQ Sequence 672 AA;

Query Match 3.2%; Score 85; DB 2; Length 672;

Best Local Similarity 18.8%; Pred. No. 2.7e+02;

Matches 102; Conservative 86; Mismatches 192; Indels 162; Gaps 25;

QY 1 MDPKLGRL--MAASLLAVL-----LLLRLGFMFSSPPPPALLEKVFQYIDLHQDEFV 50

Db :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

33 LDPVIGRDKETRVIEVLSRRTKNNPVLIGEPGVGKT-----AIAEGLAQAI--VNNEVP 85

QY 51 QTLKE--WVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQLPDGQSL 108

Db :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

86 ETLKDKRVMSLDMGTVAGTKYRGFEERLKKVMEIIQQAGNVILFID----- 133

QY 109 PIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKG 168

Db : :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

134 ----ELHTLVGAGGAEIDAASNIL--KPA-----LARGELQCIGAT---- 169

QY 169 PVLAWINAVSAFRA-LEQDLFPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFS----- 219

Db : :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

170 -----TLDEYRKNIEKDAALERRFPQVQVDEPSVVDTVAILKGLRDRYEAAHHRINISD 222

QY 220 -GVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVA 278

Db : :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

Db 223 EAIEAAVKLSNRYVSDR-----FLPDKAIDLID 250

QY 279 LLGSLVDSSGHILVPGIYDEVVPLTEEEINTYK-----AIHLDLEEYRNS-----SRV 326

Db 251 EASSKVRLLKSH-TTPNNLKEI---EQEIEKVKNKDAAVH--AQEFENAANLRDKQTKL 303

QY 327 EKFLFDTKKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAV 386

Db 304 EKQYEEAKNE-----WKNAQ---NGMSTSLSEEDIAEVIAGWT-----GIPLTKINET 348

QY 387 EKQVTRHLEDVFSKR-----NSSNKMVVSMTLGLHPWIANIDDTQYLA----- 429

Db 349 ESEKLLSLEDTLHERVIGQKDAVNSISKAVRRARAGLKDKPRPIGSFIFLPGTGVGKTEL 408

QY 430 AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLLPLGAV--DDGEHSQNEKINRW 487

Db 409 ARALAESMFGDDDAMIR-----VDMSEFMEKHAVSRVLVGAPPYVGHDDG-GQLTEKVRRK 463

QY 488 NY 489

Db 464 PY 465

RESULT 1153

AAR99797

ID AAR99797 standard; protein; 713 AA.

XX

AC AAR99797;

XX

DT 26-NOV-1996 (first entry)

XX

DE Lysine decarboxylase (W3110) of E.coli.

XX

KW Lysine decarboxylase; L-lysine; cada; transformant; deletion; mutant.

XX

OS Escherichia coli.

XX

PN WO9617930-A1.

XX

PD 13-JUN-1996.

XX

PF 05-DEC-1995; 95WO-JP002481.

XX

PR 09-DEC-1994; 94JP-00306386.

XX

PA (AJIN ) AJINOMOTO CO INC.

XX

PI Kikuchi Y, Suzuki T, Kojima H;

XX

DR WPI; 1996-287175/29.

DR N-PSDB; AAT34583.

XX

PT Production of L-lysine by culture of transformant Escherichia - in which

PT expression of new lysine decarboxylase gene and or Cada gene has been

PT partly or wholly suppressed.

XX

PS Claim 1; Page 24-27; 45pp; Japanese.

XX

CC Transformant forms of Escherichia species (e.g. E.coli), in which the

CC expression of the W3110 lysine decarboxylase gene (AAT34583), and/ or the

CC cada gene (AAT34584), have been partly or wholly suppressed by deletion

CC of part or all of the gene may be used for the efficient production of L-

CC lysine when cultured

XX

SQ Sequence 713 AA;

Query Match 3.2%; Score 85; DB 2; Length 713;

Best Local Similarity 20.9%; Pred. No. 2.9e+02;

Matches 60; Conservative 42; Mismatches 101; Indels 84; Gaps 12;

QY 169 PVLAWINAVSAFRALEQDLFPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISD 228

Db :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

78 PLYAFINTHSTMDVSVQDMRMALWFFEYALQAEADIAIR--MRQYTDEYL-----D 126



















Db 450 EKQYEEAKNE-----WKNAQ-----NGMSTSLSEEDIAEVIAGWT-----GIPLTKINET 494

Qy 387 EKQVTRHLEDVFSKR-----NSSNKMVVSMTGLHPWIANIDDTQYLA----- 429

Db 495 ESEKLLSLEDTLHERVIGQKDAVNSISKAVRRARAGLKDPKRPIGSFIFLGTGVGKTEL 554

Qy 430 AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAV--DDGEHSQNEKINRW 487

Db 555 ARALAESMFGDDDAMIR-----VDMSEFMEKHAVSRVLVGAPPYGVGHDDG-GQLTEKVRK 609

Qy 488 NY 489

Db 610 PY 611

RESULT 1162

AAU37196

ID AAU37196 standard; protein; 818 AA.

XX

AC AAU37196;

XX

DT 14-FEB-2002 (first entry)

XX

DE Staphylococcus aureus cellular proliferation protein #1366.

XX

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX

OS Staphylococcus aureus.

XX

XX WO200170955-A2.

PN

XX

XX 27-SEP-2001.

PD

XX

PF 21-MAR-2001; 2001WO-US009180.

XX

XX 21-MAR-2000; 2000US-0191078P.

PR

XX 23-MAY-2000; 2000US-0205848P.

PR

XX 26-MAY-2000; 2000US-0207727P.

PR

XX 23-OCT-2000; 2000US-0242578P.

PR

XX 27-NOV-2000; 2000US-0253625P.

PR

XX 22-DEC-2000; 2000US-0257931P.

PR

XX 16-FEB-2001; 2001US-0269308P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX

DR WPI; 2001-611495/70.

DR N-PSDE; AAS55055.

XX

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX

PS Example 3; SEQ ID NO 12789; 511pp; English.

XX

CC The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes

CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 818 AA;

Query Match 3.2%; Score 85; DB 4; Length 818;

Best Local Similarity 18.8%; Pred. No. 3.6e+02;

Matches 102; Conservative 86; Mismatches 192; Indels 162; Gaps 25;

Qy 1 MDPKLGR--MAASLLAVL-----LLLLERGMFSSPPPPALLEKVFQYIDLHQDEFV 50

Db 179 LDPVIGRDKEITRVIEVLSSRTKNNPVLIGEPGVGKT-----AIAEGLAQAI--VNNEVP 231

Qy 51 QTLKE--WVAIESDSVQPVPRFRQELFRMMAADTLQRLGARVASVDMGPPQLPDGQSL 108

Db 232 ETLKDKRVMSLDMGTIVAGTKYRGEFEERLKKVNEEIQAGNVILFID----- 279

Qy 109 PIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDWLTDPPVLTVDGKLYGRGATDNKG 168

Db 280 ----ELHTLVGAGGAIDAASNIL--KPA-----LARGELQCIGAT---- 315

Qy 169 PVLAWINAVSAFRA-LEQDLPNVNIKFIEGMEAGSVALEELVEKEKDRFFS----- 219

Db 316 -----TLDEYRKNIIEKDAALERRFPQVQVDEPSVVDTVAILKGLRDRYEAHHRINISD 368

Qy 220 -GVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVA 278

Db 369 EAIEAAVKLSNRYVSDR-----FLPDKAIDLID 396

Qy 279 LLGSLVDSSGHILVPGIYDEVVPLTEEEINTVK-----AIHLDLEEYRNS-----SRV 326

Db 397 EASSKVRLKSH-TTPNNLKEI---EQEIEKVKNEKDAAVH--AQEFENAAANLRDKQTKL 449

Qy 327 EKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPPTKTVIPGRVIGKFSIRLVPHMNVSAV 386

Db 450 EKQYEEAKNE-----WKNAQ---NGMSTSLSEEDIAEVIAGWT-----GIPLTKINET 494

Qy 387 EKQVTRHLEDVFSKR-----NSSNKMVVSMTGLHPWIANIDDTQYLA----- 429

Db 495 ESEKLLSLEDTLHERVIGQKDAVNSISKAVRRARAGLKDPKRPIGSFIFLGTGVGKTEL 554

Qy 430 AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAV--DDGEHSQNEKINRW 487

Db 555 ARALAESMFGDDDAMIR-----VDMSEFMEKHAVSRVLVGAPPYGVGHDDG-GQLTEKVRK 609

Qy 488 NY 489

Db 610 PY 611

RESULT 1163

AAU36831

ID AAU36831 standard; protein; 818 AA.

XX

AC AAU36831;

XX

DT 14-FEB-2002 (first entry)

XX

DE Staphylococcus aureus cellular proliferation protein #1001.

XX

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX

OS Staphylococcus aureus.

XX

PN WO200170955-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009180.

XX

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Haselbeck R, Ohlson KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS54690.  
XX  
PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 12424; 511pp; English.  
XX  
CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 818 AA;

Query Match 3.2%; Score 85; DB 4; Length 818;  
Best Local Similarity 18.8%; Pred. No. 3.6e+02;  
Matches 102; Conservative 86; Mismatches 192; Indels 162; Gaps 25;

Qy 1 MDPKLG--RMAASLLAVL-----LLLLRGMFSSPPPALLEKVFQYIDLHQDEFV 50  
Db 179 LDPVIGRDREITRVIEVLSRRRTKNNPVLIGEPGVGKT-----ATAEGLAQAI--VNNEVP 231  
Qy 51 QTLKE--WVAIESDSVQVPFRFQELFRMMAVAADTLQLGARVASVDMGPPQLPDGQSL 108  
Db 232 ETLKDKRVMSLDMGTVAGTKYRGFEFERLKKVMEEIQQAGNVILFID----- 279  
Qy 109 PIPPVILAEIGSDPTKGTVCFYGHLDVQPADRGDGLWLTDPVVLTEVDGKLYGRGATDNKG 168  
Db 280 ----ELHTLVGAGGAEGDAIDASNIL--KPA-----LARGELOCIGAT---- 315  
Qy 169 PVLAWNAVSAFRA-LEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFS----- 219  
Db 316 -----TLDEYKKNIEKDAALERRFPVQVDEPSVVDVTAILKGLDRDYEAAHNRINISD 368  
Qy 220 -GVDYIVISDNLWISQKPAITYTGRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVA 278  
Db 369 EAIEAAVKLSNRYVSDR-----FLPDKAIDLID 396  
Qy 279 LLGSLVDSSGHILVPGIYDEVVPLTTEEINTYK-----AIHLDLEEYRNS-----SRV 326  
Db 397 EASSKVRLLKSH--TTPNNLKEI-----EQEIEKVKNEKDAAVH--AQEFENAAANLRDKQTKL 449  
Qy 327 EKFLFDTKBEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAV 386  
Db 450 EKQVEEAKNE-----WKNAQ---NGMSTLSLSEEDIAEVIAGWT-----GIPLTKINET 494

Qy 387 EKQVTRHLEDVFSKR-----NSSNKMVVMVMTLGLHPWIANIDDTQYLA----- 429  
Db 495 ESEKLLSLEDTLHERVIGQKDAVNSISKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTEL 554  
Qy 430 AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAV--DDGEHSQNEKINRW 487  
Db 555 ARALAESMFGDDDDAMIR----VDMSEFMEKHAVSRVLVGAPPVGVGHDDG-GQLTEKVRRK 609  
Qy 488 NY 489  
Db 610 PY 611  
RESULT 1164  
ABU16354  
ID ABU16354 standard; protein; 818 AA.  
XX  
AC ABU16354;  
XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #1881.  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Staphylococcus aureus.  
OS WO200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US0009107.  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA20224.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
PS Claim 25; SEQ ID NO 44278; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of



CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 818 AA;

Query Match 3.2%; Score 85; DB 6; Length 818;  
Best Local Similarity 18.8%; Pred. No. 3.6e+02;  
Matches 102; Conservative 86; Mismatches 192; Indels 162; Gaps 25;

QY 1 MDPKLGR--MAASLLAVL-----LLLLERGMFSSPPPPALLEKVFQYIDLHQDEFV 50  
Db 179 LDPVIGRDKETRVIEVLSRRTKKNPVLIGEPGVGKT-----AIAEGLAQAI--VNNEVP 231  
QY 51 QTLKE--WVAIESDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSL 108  
Db 232 ETLKDKRVMSLDMGTVVAGTKYRGEFEERLKKVMEIIQQAGNVILFID----- 279  
QY 109 PIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKG 168  
Db 280 ----ELHTLVGAGGAEGDAIDASNIL--KPA-----LARGELQCIGAT---- 315  
QY 169 PVLAWINAVSAFRA-LEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFPS----- 219  
Db 316 -----TLDEYRKNIKDAALERRFPQVQVDEPSVVDVTVAILKGLRDRYEAHHRINISD 368  
QY 220 -GVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVA 278  
Db 369 EAIEAAVKLSNRYVSDR-----FLPKAIDLID 396  
QY 279 LLGSLVDSSGHILVPGIYDEVVPLTEEEINTYK-----AIHLDLEEYRNS-----SRV 326  
Db 397 EASSKVRLKSH-TTPNNLKEI-----EQEIEKVKNEKDAAVH--AQEFENAAANLRDKQTKL 449  
QY 327 EKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAV 386  
Db 450 EKQYEEAKNE-----WKNAQ---NGMSTSLSEEDIAEVIAGWT-----GIPLTKINET 494  
QY 387 EKQVTRHLEDVFSKR-----NSSNKMVVSMTLGLHPWIANIDDTQYLA----- 429  
Db 495 ESEKLLSLEDTLHERVIGQDAVNSISKAVRRARAGLKDPRPIGSFIFLGPTGVGKTEL 554  
QY 430 AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAV--DDGEHSQNEKINRW 487  
Db 555 ARALAESMFGDDAMIR-----VDMSEFMKEHAVSRVLVGPVGVGHDDG--QLTEKVRRK 609  
QY 488 NY 489  
Db 610 PY 611

RESULT 1165  
ABM72479  
ID ABM72479 standard; protein; 818 AA.  
XX

AC ABM72479;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Staphylococcus aureus protein #1719.  
XX  
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;  
XX enzymatic assay; antibiotic target.  
OS Staphylococcus aureus.

XX WO200294868-A2.  
PN  
XX 28-NOV-2002.  
PD  
XX 27-MAR-2002; 2002WO-IB002637.  
PF  
XX 27-MAR-2001; 2001GB-00007661.  
PR  
XX (CHIR-) CHIRON SPA.  
PA  
XX Masignani V, Mora M, Scarselli M;  
PI WPI; 2003-120786/11.  
XX N-PSDB; ACF74039.  
DR  
XX New Staphylococcus aureus protein, useful as a vaccine for treating or  
PT preventing Staphylococcal infection, specifically an infection caused by  
PT *S. aureus*, e.g. sepsis.  
XX  
PS Claim 1; SEQ ID NO 3438; 49pp; English.  
XX  
CC The invention relates to novel genes and encoded proteins from  
CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a  
CC nucleic acid encoding the protein, or an antibody to the protein, is  
CC useful as a pharmaceutical, particularly as a vaccine for treating or  
CC preventing infection due to Staphylococcus bacteria, specifically an  
CC infection caused by *S. aureus*. The composition is particularly useful for  
CC treating or preventing sepsis in a patient. The composition can also be  
CC used for diagnostics. The protein is also used in an assay for enzymatic  
CC studies and as a target for antibiotics. This sequence represents one of  
CC the novel *S. aureus* proteins of the invention  
XX  
SQ Sequence 818 AA;

Query Match 3.2%; Score 85; DB 6; Length 818;  
Best Local Similarity 18.8%; Pred. No. 3.6e+02;  
Matches 102; Conservative 86; Mismatches 192; Indels 162; Gaps 25;

QY 1 MDPKLGR--MAASLLAVL-----LLLLERGMFSSPPPPALLEKVFQYIDLHQDEFV 50  
Db 179 LDPVIGRDKETRVIEVLSRRTKKNPVLIGEPGVGKT-----AIAEGLAQAI--VNNEVP 231  
QY 51 QTLKE--WVAIESDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSL 108  
Db 232 ETLKDKRVMSLDMGTVVAGTKYRGEFEERLKKVMEIIQQAGNVILFID----- 279  
QY 109 PIPPVILAEGLSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKG 168  
Db 280 ----ELHTLVGAGGAEGDAIDASNIL--KPA-----LARGELQCIGAT---- 315  
QY 169 PVLAWINAVSAFRA-LEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFPS----- 219  
Db 316 -----TLDEYRKNIKDAALERRFPQVQVDEPSVVDVTVAILKGLRDRYEAHHRINISD 368  
QY 220 -GVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVA 278  
Db 369 EAIEAAVKLSNRYVSDR-----FLPKAIDLID 396  
QY 279 LLGSLVDSSGHILVPGIYDEVVPLTEEEINTYK-----AIHLDLEEYRNS-----SRV 326  
Db 397 EASSKVRLKSH-TTPNNLKEI-----EQEIEKVKNEKDAAVH--AQEFENAAANLRDKQTKL 449  
QY 327 EKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAV 386  
Db 450 EKQYEEAKNE-----WKNAQ---NGMSTSLSEEDIAEVIAGWT-----GIPLTKINET 494  
QY 387 EKQVTRHLEDVFSKR-----NSSNKMVVSMTLGLHPWIANIDDTQYLA----- 429  
Db 495 ESEKLLSLEDTLHERVIGQDAVNSISKAVRRARAGLKDPRPIGSFIFLGPTGVGKTEL 554  
QY 430 AKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAV--DDGEHSQNEKINRW 487  
Db 488 NY 489  
Db 610 PY 611

Db 555 ARALAESMFGDDAMIR-----VDMSEFMEKHAVSRVLGAPPGYVGHDDG-GOLTEKVRK 609

QY 488 NY 489

Db 610 PY 611

RESULT 1166

AAW99656

ID AAW99656 standard; protein; 866 AA.

XX

AC AAW99656;

DT 21-MAY-1999 (first entry)

XX

DE Staphylococcus aureus mecB protein.

XX

KW Staphylococcus aureus; mecB; antibacterial; infection; otitis media;

KW conjunctivitis; toxic shock syndrome; impetigo; wound infection;

KW septic arthritis; cancer; ulcer; gastritis.

XX

OS Staphylococcus aureus.

XX

PN EP900848-A2.

XX

PD 10-MAR-1999.

XX

PF 20-AUG-1998; 98EP-00306683.

XX

PR 04-SEP-1997; 97US-0057535P.

PR 18-MAR-1998; 98US-00040843.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Jaworski DD, Wang M, Shilling LK, Burnham MKR, Rosenberg M;

PI Fosberry A, Lawlor E, Hodgson JE, Ward J;

XX

DR WPI; 1999-155941/14.

DR N-PSDB; AAX19480.

XX

PT New Staphylococcus aureus mecB polypeptide and polynucleotide - useful as

PT diagnostic reagents and for prevention and treatment of Staphylococci and

PT Helicobacter infections.

XX

PS Claim 14; Page 8; 36pp; English.

XX

CC The present sequence is the Staphylococcus aureus mecB protein, which is

CC a member of the ClpC ATPase family. MecB proteins are administered to

CC treat individuals in need of mecB proteins (directly or via a vector i.e.

CC gene therapy), and as an antigen for inducing an immunological response

CC (administered directly i.e. vaccine). They can prevent adhesion of

CC bacteria to matrix proteins, and are useful for use on wounds and body

CC implants to prevent bacterial infection. They are also useful for

CC identifying agonists and antagonists by screening host cells expressing

CC mecB protein, and detecting the absence or presence of mecB activity.

CC Agonists and antagonists are useful for inhibition and treatment of

CC conditions associated with mecB imbalance, and are therefore potential

CC antibacterial compounds. MecB polynucleotides are useful for genetic

CC immunisation, preferably via a vector. Anti-mecB antibodies induced by

CC the polypeptide are useful for preventing or treating infections,

CC especially bacterial infections, and also for isolating clones expressing

CC mecB protein, or for purifying the polypeptide by affinity

CC chromatography. Diseases can be diagnosed by determining the presence of

CC mecB nucleic acid, and/or analysing for the presence/amount of mecB

CC polypeptide in a sample, due to infection of an organism with the mecB

CC gene. The stage and type of infection can be determined. Diseases

CC prevented, diagnosed and treated include those caused by bacterial

CC infection, especially Staphylococcus aureus infections which cause otitis

CC media, conjunctivitis, toxic shock syndrome, impetigo, wound infection

CC and septic arthritis. MecB agonists and antagonists are also useful for

CC treatment of Helicobacter pylori infections which cause stomach cancer,

CC ulcers and gastritis

XX SQ Sequence 866 AA;

Query Match 3.2%; Score 85; DB 2; Length 866;

Best Local Similarity 18.8%; Pred. No. 4e+02;

Matches 102; Conservative 86; Mismatches 192; Indels 162; Gaps 25;

QY 1 MDPKLGRL--MAASLLAVL-----LILLERGMFSSPPSPALLEKVFQYIDLHQDEFV 50

Db 179 LDPVIGRDKEITRVIEVLSRRTKNNPVLIGEPGVGKT-----AIAEGLAQAI--VNNNEVP 231

QY 51 QTLKE--WVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQLPDGQSL 108

Db 232 ETLKDKRVMSLDMGTVVAGTKYRGEFEERLKKVMEEIQQAGNVILFID----- 279

QY 109 PIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKG 168

Db 280 ----ELHTLVGAGGAEGADASNIL--KPA-----LARGELOCIGAT---- 315

QY 169 PVLAMINAVSAFRA-LEQDLVPNIKFIIEGMEEAGSVALEELVEKEKDRFFS----- 219

Db 316 -----TLDEYRKNIKDAALERRFPQVQVDEPSVVTVAILKGLDRYEAHHRINISD 368

QY 220 -GVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVA 278

Db 369 EAIEAAVKLSNRYVSDR-----FLPKAIDLID 396

QY 279 LLGSLVDSSGHILVPGIYDEVVPLTEEEINTYK-----AIHLDLEEYRNS-----SRV 326

Db 397 EASSKVRLKSH-TTPNNLKEI---EQEIEKVKNEKDAAVH--AQEFENAANLRDKQTKL 449

QY 327 EKFLFDTKEEILHLWRYPSLSIHGEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAV 386

Db 450 EKQYEEAKNE-----WKNAQ---NGMSTLSSEEDIAEVIAGWT-----GIPLTKINET 494

QY 387 EKQVTRHLEDVFSKR-----NSSNMVMSMTLGLHPWIANIDDTQYLA----- 429

Db 495 ESEKLLSLEDTLHERVIGQKDAVNSISKAVRRARAGLKDPRPIGSFIFLGPTGVGKTEL 554

QY 430 AKRAIRTVFGTEPDMIRDCSTIPIAKMFOEIVHKSVVLIPLGAV--DDGEHSQNEKINRW 487

Db 555 ARALAESMFGDDAMIR-----VDMSEFMEKHAVSRVLGAPPGYVGHDDG-GOLTEKVRK 609

QY 488 NY 489

Db 610 PY 611

RESULT 1167

ABJ72225

ID ABJ72225 standard; protein; 932 AA.

XX

AC ABJ72225;

XX

DT 06-NOV-2003 (first entry)

XX

DE Protein of Archaeoglobus fulgidus leucyl tRNA-synthetase (AFLRS) .

XX

KW Protein biosynthetic machinery; orthogonal tRNA; O-tRNA; aminoacylated;

KW orthogonal aminoacyl-tRNA synthetase; unnatural amino acid; in vivo.

XX

OS Archaeoglobus fulgidus.

XX

PN WO200286075-A2.

XX

PD 31-OCT-2002.

XX

PF 19-APR-2002; 2002WO-US012635.

XX

PR 19-APR-2001; 2001US-0285030P.

PR 06-FEB-2002; 2002US-0355514P.

XX

PA (SCRI ) SCRIPPS RES INST.







of the central nervous system and inducing regeneration of neurons.  
Example; Page; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant NiAext. The mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-974/T7-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers

Sequence 974 AA;

Query Match 3.2%; Score 85; DB 3; Length 974;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 121; Conservative 68; Mismatches 210; Indels 206; Gaps 29;

Qy	26	SSPSPPPALLEKVFQYI	-----DLHQDEFVQTLKEWVAIE-----	60
			: :   :   :	
Db	16	SPPRPPPAF	--KYQFVTEPEDEDEDEDEDEDEDELEELVLERKPAAGLSAAAVPP	72
Qy	61	-----SDSQVPVPR	-----FRQELF-RMMAVAADTLQRLGARVASVDMG	98
			:       :	
Db	73	AAAAPLLDPSSDVPPAPRGPLPAPPAAPERQPSWERSPAAPAPSLPPAAAVL	-----	126
Qy	99	PQQLPDGQSLPI	-----PPV---ILAEIGSDPTKGTVCFYGHLDVQPADRGDGLW	145
		:   :	:   :	
Db	127	PSKLPEDDEPPARPPPPAGASPLAEPAAPPS	-----TPAAPKRRGSGSVDETILF	177
Qy	146	-----TDPYV	-----LTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRA	182
		: :   :		
Db	178	ALPAASEFVIPSSAEKIMDLMEQPGNTVSSGOEDFPSVLLETAASLPSSLSTVTS-FK-	235	
Qy	183	LEQDLPVNIKFI	--IEG-MEEAGSVALEELVEKEKORF-----FSGVDYIVISDNLWI	232
		:   :	:   :	
Db	236	-EHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	-----	285
Qy	233	SQRKPAITYGTRGNSYFMV	-----EVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSS	287
		:   :	:	
Db	286	SEMGSPFKGSPKGESAILVENTKEEVIVRSKDLEDVCSAALHSPQE	-----SPVGKE	338
Qy	288	GHILVP	---GIYDE---VVPLTEE---EI-NTY-----	310
		: :   :	:   :	
Db	339	DRVVSPEKTMDFNEMQMSVAPVUREEYADFKPFQAEWEVKDTEGSRDVLAAARANVESK	398	
Qy	311	---KATHLDLEEYR	---NSSRVEKFLFDTKEEILMHLWR-----	344
		:	:	
Db	399	VDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSRAYITCASFTSATETANTF	458	
Qy	345	PSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSEKNSS	404	

QY 121 DPTKGTVCFYGHLDVQPADR-----GDGWLTDPPVLTVE--DGKL 158  
Db 102 EWTNGTAIVFDHYDVK-IDRLLSPTTFVDERDGTALVGGYGTSTTP--LTEVTGDGKY 158  
QY 159 Y-----GRGA-----TDNKGVPVLAWINAVSAFRALEQDL-----PVNIKFIIEG----- 197  
Db 159 WAPRIAAGSLIPYDDEEKEFKW-NQVASTSGVPHDLWESBRTNPKRFKQFLGGGACIK 217  
QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYG---TRGNS----- 247  
Db 218 MEDDGRYVLP--IQALKD-----DGKVVVS--LVILAKK--TSYGWEFSNGTSDEGCIQP 265  
QY 248 -----YFMVEVKCRD---QDFHSGTFGGILHEPMDLVALLGSLVDSSGHILVPGIY 296  
Db 266 AVLEWKEKELIMTSCDDGSRVRYSSTMGNLWTEEYDILSRVWGNSTRVVGHGAQGGFV 325  
QY 297 DEVVPLTSEEINTYKAHLDLEEYRNSSRVEKFLFDTKKEILMHLW----- 342  
Db 326 SAM-----IDGQKVILVSRPVVS-----EK---DKKETGRHLHLWLTDMQRIYDVGPIS 370  
QY 343 -----RYPSLSIHGIEGAFDEPGTKTVIPGRVI---GKFSI-----RLVPHM 381  
Db 371 AVGENVAASTLLYATVEAQPLKEEPEKBEKKLYCPYEVAEADGKYNIAFVGLTEKLEDMR 430  
QY 382 NVSAVEKQVTRHLEDVFSKRNSSNKM-----VVSMTLGLHPMIANID-----DTQYLAAK 431  
Db 431 KVLAAWKEKDAQIAKEYRCGNEKNWNRSGCDARELTGVLGLLSNKSKTNTWSDEYLCVN 490  
QY 432 RAIRTVFGTEPDMIRDGSTI-----PIAKMFQEI---VHKSVVLIPLGAVDDGEH 478  
Db 491 ATVHGEVESAPD---GGLTFKPGGAGAKWPVGDMGQTVPYHYFANDKFTLVATVSIDKAPE 547  
QY 479 SQNEKIN-----RWNVIEGTKLF 496  
Db 548 TGSSPIPLMGVRMNDAGQTVLF 569  
RESULT 1172  
ID AAY77728 standard; protein; 1021 AA.  
XX AAY77728;  
AC AAY77728;  
XX 15-MAY-2000 (first entry)  
DT Human G protein-conjugated receptor HK05490.  
XX G protein; guanine nucleotide binding protein; human; brain;  
KW G protein-conjugated receptor; gene therapy; HK05490.  
XX Homo sapiens.  
OS WO200005264-A1.  
XX 03-FEB-2000.  
XX 22-JUL-1999; 99WO-JP003909.  
XX 23-JUL-1998; 98JP-00207579.  
PR 07-AUG-1998; 98JP-00225060.  
PR 06-OCT-1998; 98JP-00284328.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
PA (KAZU-) KAZUSA DNA RES INST.  
XX Ohara O, Nagase T, Nomura N, Hinuma S, Fujii R, Kitahara O;  
PI Mogi S;  
XX WPI; 2000-182652/16.  
DR N-PSDB; AAZ87684.  
XX New G protein conjugated receptor protein expressed in brain tissue for

PT screening potential agonists and antagonists of its binding to ligands  
PT for use as drugs.  
XX Claim 1; Fig 7 to 15; 123pp; Japanese.  
XX The invention provides G protein (guanine nucleotide binding protein) -  
CC conjugated receptor proteins (AAY77727-29) expressed in brain tissue and  
CC nucleic acids (AAZ87683-685) encoding the polypeptides. The polypeptides  
CC and the methods are useful for identifying compounds which are agonists  
CC or antagonists to the binding of the receptor to its ligand, for use as  
CC drugs. DNA encoding all or part of the polypeptides is used for the  
CC diagnosis of diseases and in gene therapy, and for the production of  
CC transgenic animals for use as disease models. Antibodies recognizing the  
CC receptor proteins or their fragments are also useful for disease  
CC diagnosis. The present sequence represents the G protein-conjugated  
CC receptor protein HK05490  
XX  
SQ Sequence 1021 AA;  
Query Match 3.2%; Score 85; DB 3; Length 1021;  
Best Local Similarity 20.4%; Pred. No. 5.1e+02;  
Matches 89; Conservative 58; Mismatches 140; Indels 150; Gaps 22;  
QY 109 PIPPVILAELGSDPTKTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKG 168  
Db 25 PLPERFCEALDSKGIKWPQTQGMVVERPCPKTGRG-TASYLC-----MISTGTWNPKG 77  
QY 169 PVLA-----WINAVSAFRALEQDLVPNIKFIIEGNEEAGSVALEELVEKEKDRFSG--- 220  
Db 78 PDLSNCTSHWVNQLAQ-----KIRSGENAAASLA-NELAKHTKGPVFAGDVS 122  
QY 221 -----VDYIVISDNLWISQRKPAITYGTRGNSYFMV---EVKCRDQDFHSGTGGILHEP 272  
Db 123 SSVRLMEQLVDILDQAQLQELKPS-EKDSAGRSYNKLOKREKTCR----- 165  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTSEEINTYKAHLDLEEYRNSSRVEKFLFD 332  
Db 166 -----AYLKAIVDTVDNLLRP-----EALSWK--HMNSSEQAHTATM---LLD 204  
QY 333 TKEEILMHLWRYPSLSIHGIEGAFD-----EPGTXTVIPGRVIGKFSIRLVPHMNVSAV 386  
Db 205 TLE-----EGAFVLADNLLLEP-TRVSM-----TENIVLEVAVLST 239  
QY 387 EKQV-----TRHLEDVFSKRNSSNKM-----VVSMTLGLHPMIANIDDTQY 427  
Db 240 EGQIQDFKFPPLGIKGAGSSIQLSANTVVKQNSRNLAKLVFIYRSLG-----QF 288  
QY 428 LAAKRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIHVKSVVLIPLGAVDDGEH 478  
Db 289 LSTENA---TIKLGADFIGRNSTIAVNSHVISVSINKESSRVYLTDPVLTFLPHIDPDNY 345  
QY 479 SQNEKINRWNVIEGTKL 495  
Db 346 F-NANCSFWNYSSERTM 361  
RESULT 1173  
ADE55164  
ID ADE55164 standard; protein; 1021 AA.  
XX ADE55164;  
AC ADE55164;  
XX 29-JAN-2004 (first entry)  
XX Human Protein BAA34506, SEQ ID NO 969.  
DE Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX Homo sapiens.  
XX WO2003016475-A2.  
PN





CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1021 AA;

Query Match 3.2%; Score 85; DB 7; Length 1021;  
Best Local Similarity 20.4%; Pred. No. 5.1e+02;  
Matches 89; Conservative 58; Mismatches 140; Indels 150; Gaps 22;

QY 109 PIPPVILAEIGSDPTKGTVCYFYGHLVDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG 168  
Db 25 PLPERFCEALDSKGIKWPOTQGMVVERPCPKGTRG-TASYLC-----MISTGTWNPKG 77  
QY 169 PVLA-----WINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSG--- 220  
Db 78 PDLNCTSHWVNQLAQ-----KIRSGENASILA-NELAKHTKGPVFAGDVS 122  
QY 221 -----VDYIVISDNLWISQRKPAITYGTRGNSYFMV---EVKCRDQDFHSGTGGILHEP 272  
Db 123 SSVRLMEQLVDILDAQLQELKPS-EKDSAGRSYNKLOKREKTCR----- 165  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 166 -----AYLKAIVDVTVDNLLRP-----EALSWK--HMNSSEQAHTATM---LLD 204  
QY 333 TKEEILMHLWRYPSLSIHGIEGAFD-----EPGKTVPGRVIGKFSIRLVPHMNVSAV 386  
Db 205 TLE-----EGAFVLADNLLLEP-TRVSMPTENIVLEVAVLST 239  
QY 387 EKQV-----TRHLEDVFSKRNSNKM-----VVSMTLGLHPWIANIDDTQY 427  
Db 240 EGQIQDFKFLGKAGSSIQLSANTVKQNSRNLAKLVFIYRSLG-----QF 288  
QY 428 LAAKRAIRTVGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGEH 478  
Db 289 LSTENA---TIKLGADFIGRNSTIAVNSHVISINKESSRVLTDPVLTPLPHIDPDNY 345  
QY 479 SQNEKINRWNYIEGTKL 495  
Db 346 F-NANCSFWNYSERTMM 361

RESULT 1175  
ADE55172  
ID ADE55172 standard; protein; 1021 AA.

XX ADE55172;

XX 29-JAN-2004 (first entry)

XX Human Protein BAA34506, SEQ ID NO 977.

XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.  
DR GENBANK; BAA34506.

XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1021 AA;

Query Match 3.2%; Score 85; DB 7; Length 1021;  
Best Local Similarity 20.4%; Pred. No. 5.1e+02;  
Matches 89; Conservative 58; Mismatches 140; Indels 150; Gaps 22;

QY 109 PIPPVILAEIGSDPTKGTVCYFYGHLVDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKG 168  
Db 25 PLPERFCEALDSKGIKWPOTQGMVVERPCPKGTRG-TASYLC-----MISTGTWNPKG 77  
QY 169 PVLA-----WINAVSAFRALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSG--- 220  
Db 78 PDLNCTSHWVNQLAQ-----KIRSGENASILA-NELAKHTKGPVFAGDVS 122  
QY 221 -----VDYIVISDNLWISQRKPAITYGTRGNSYFMV---EVKCRDQDFHSGTGGILHEP 272  
Db 123 SSVRLMEQLVDILDAQLQELKPS-EKDSAGRSYNKLOKREKTCR----- 165  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 166 -----AYLKAIVDVTVDNLLRP-----EALSWK--HMNSSEQAHTATM---LLD 204  
QY 333 TKEEILMHLWRYPSLSIHGIEGAFD-----EPGKTVPGRVIGKFSIRLVPHMNVSAV 386  
Db 205 TLE-----EGAFVLADNLLLEP-TRVSMPTENIVLEVAVLST 239  
QY 387 EKQV-----TRHLEDVFSKRNSNKM-----VVSMTLGLHPWIANIDDTQY 427  
Db 240 EGQIQDFKFLGKAGSSIQLSANTVKQNSRNLAKLVFIYRSLG-----QF 288





DR WPI; 2003-029926/02.  
DR N-PSDB; ACA35056.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 59110; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1038 AA;

Query Match 3.2%; Score 85; DB 6; Length 1038;  
Best Local Similarity 18.8%; Pred. No. 5.2e+02;  
Matches 111; Conservative 88; Mismatches 189; Indels 202; Gaps 32;  
QY 4 KLGRMAASLLAVLLLLERGMFSSPS-----PPPALLEKVFQYIDLHQ 46  
DB 535 RTGRM-MMIIYAALCLALFAGLSTLPSSFLPDEDQGYFMSSIQLPSDATMQRTLKVDTFE 593  
QY 47 DEFVQ-----TLKEWVAIESDSVQVPFRFRQELFRMMA 79  
DB 594 EEIAHRQAVESNIMILGFGSGGQNSAMFTTLKDWKQRKGTAAQE-----640  
QY 80 VAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCFYGHLDVQPAD 139  
DB 641 -EADHIQ---SOMANV-----PDAVTMSLLPPAISDMGT-----670  
QY 140 RGDGWLTPYVLTEVDGKLYG--RGATD-----NKGPLAWINAVSAFRALEQDLPVNI 191  
DB 671 -SSGF---TYYLQDRGKGQYQALKKAADDELIVQANHNPFLADV-----709  
QY 192 KFIIEGMEEAGSVALLELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMV 251  
DB 710 --YIDGLGEGTSLSLH--VDREKAEAM-GVSFDEINQTSIVAAGSNVNDYTNNGRVQQV 764  
QY 252 EVKCRDQDFHSGTFGGILHEPMADLVAL-----LGS�VDSSGHILVPGIYDEVVPLTEEE 306  
DB 765 IVQA-DAPYRM-----QP-EQLLALSVMKRLGOMPLPSAFVILSW---NVAPQQLIR 811  
QY 307 INTYKAIHLDEEYRNSSRVEKFLEFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIP 366

DB 812 YQGYPAIRITGSSAQGKS--SGTAMAAMDNLAKHL--PPGFAGEWAGSSLOEKESASQLP 867  
QY 367 GRVICK-----FSIRLVPHMNV--SAVEKQVTRHLEDVFSKRNSSNK 406  
DB 868 GLIVLSVLVVFVWVLAALYESWIPFAVMLVPLGLLGAVLAVSVTNMTNDVFFK-----921  
QY 407 MVVSMTLGLHPWIANIDDTQYLAAKRAIRTV-FGTEPDMIRDG-----STIPIAKM-FQE 459  
DB 922 -----VGLITLIG-----LSAKNAILLIEFARQ--LMKEGKSLLIDATLTAAKRLRP 966  
QY 460 IVHKSVV-----LIPL----GAVDDGEHSQNEKINRWNVIEGTKLFAPAFEL 501  
DB 967 ILMTSLAFTLGVVPLMLASGASDSTQHAIGTGV-FGGMISCT-LLAIFV 1014

RESULT 1178  
ADS22844  
ID ADS22844 standard; protein; 1126 AA.  
XX  
AC ADS22844;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #11877.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR WPI; 2004-061375/06.  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 11877; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification





Db 404 ASQXMERVLRFRIRGVKTNIPFLANVVHRPFRQTGDSTNFI-----DTTPELF 453

QY 396 DVFSKRNSSNK---MVVSMTLGLHPWIANIDDTQYLAAK 431

Dh 454 EFPKERNRGNKALRFISDVTVNAYPGVGNVEKPRLLKPK 492

RESULT 1180  
AAY71557  
ID AAY71557 standard; protein; 1162 AA.

DT 02-NOV-2000 (first entry)

XX DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
central nervous system; neoplastic disease; antiproliferative; glioma;  
antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
structural plasticity; screening; mutant; mutagen.

OS *Rattus* sp.

PN WO200031235-A2.

02-JUN-2000.

05-NOV-1999; 99WO-US026160.

PR 06-NOV-1998; . 98US-0107446P.

PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.

PI Schwab ME, Chen MS;

DR WPI; 2000-400052/34.

xx Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 py of the central nervous system and inducing regeneration of neurons.  
 yy

Example: Page: 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a truncated form of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant Nogo-A. Nogo-A is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred



OS XX Rattus sp. Location/Qualifiers  
FT FH Key  
FT Inhibitory-site 1. .171  
FT FT /note= "Inhibits NIH 3T3 fibroblast spreading"  
FT Modified-site 30  
FT FT /note= "Casein kinase II site"  
FT Region 31. .58  
FT FT /note= "Acidic region"  
FT Region 31. .57  
FT FT /note= "Region specifically described in claim 16"  
FT Region 172. .259  
FT FT /note= "This region is not essential for inhibitory  
FT activity"  
FT Modified-site 233  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 242. .244  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 291  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 295  
FT FT /note= "Protein kinase C (PKC) site"  
FT Misc-difference 404  
FT FT /note= "Encoded by TTG"  
FT Modified-site 436  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 468. .470  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 484  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 488  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 502  
FT FT /note= "Casein kinase II site"  
FT Inhibitory-site 542. .722  
FT Modified-site 576  
FT FT /note= "Casein kinase II site"  
FT Peptide 623. .640  
FT FT /note= "used as immunogen to generate antibody AS 472"  
FT Modified-site 626  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 694. .696  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 715  
FT FT /note= "Casein kinase II site"  
FT Peptide 762. .1163  
FT FT /note= "used as immunogen to generate antibody AS Bruna"  
FT Modified-site 784  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 821  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 850  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 855  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 863  
FT FT /note= "Casein kinase II site"  
FT Modified-site 868  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 893  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 912. .914  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 925. .927  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 954  
FT FT /note= "PKC and casein kinase II sites"  
FT Modified-site 956  
FT FT /note= "PKC and casein kinase II sites"  
FT Region 975. .1162  
FT FT /note= "This region is not essential for inhibitory  
FT activity"  
FT Region 976. .1163

FT FT /note= "C-terminal common region found in Nogo A, B and C  
FT isoforms"  
FT 988. .1023  
FT FT /label= Transmembrane domain  
FT FT /note= "C-terminal hydrophobic region specifically  
FT described in claim 16"  
FT Modified-site 1024  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 1071. .1073  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 1073  
FT FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 1089  
FT FT /note= "Protein kinase C (PKC) site"  
FT Domain 1090. .1125  
FT FT /label= Transmembrane domain  
FT FT /note= "C-terminal hydrophobic region specifically  
FT described in claim 16"  
FT Modified-site 1141. .1143  
FT FT /note= "Asn is N-glycosylated"  
FT Modified-site 1143  
FT FT /note= "Protein kinase C (PKC) site"  
XX  
PN WO200031235-A2.  
XX  
PD 02-JUN-2000.  
XX  
XX  
PF 05-NOV-1999; 99WO-US026160.  
XX  
PR 06-NOV-1998; 98US-0107446P.  
XX  
PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX  
DR WPI; 2000-400052/34.  
DR N-PSDB; AAD01173.  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Claim 3; Fig 2A; 122pp; English.  
XX  
CC The present sequence is a rat Nogo A protein which is a potent neural  
CC cell growth inhibitor and is free of all central nervous system (CNS)  
CC myelin material with which it is natively associated. The protein was  
CC derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated  
CC from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18  
CC cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins  
CC and fragments displaying neurite growth inhibitory activity are used in  
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,  
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: The present sequence  
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown  
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence  
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However, the specification does not include sequences for  
CC these SEQ ID numbers  
XX  
SQ Sequence 1163 AA;

Query Match 3.2%; Score 85; DB 3; Length 1163;  
Best Local Similarity 20.0%; Pred. No. 6.3e+02;  
Matches 121; Conservative 68; Mismatches 210; Indels 206; Gaps 29;

QY 26 SSPSPPPALLEKVFQYI-----DLHQDEFVQTLKEWVAIE----- 60  
Db 16 SPPRPPPAF---KYQFVTEPEDEDEDEDEDEDEDELEELERKPAAGLSAAAVPP 72

QY 61 -----SDSVQPVPR-----FRQELF-RMMAVAADTLQRLGARVASVDMG 98  
Db 73 AAAAPLLDFSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVL----- 126

QY 99 PQQLPDGQSLPI-----PPV---ILAEIGSDPTKGTVCFCYGHLDVQPADRGDWL----- 145  
Db 127 PSKLPEDDEPARPPPPAGASPLAEPAAPPS-----TPAAPKRGSGSVDETLEF 177

QY 146 -----TDPYV-----LTEVDGKLYGRGATDNKG-----PVLAWINAVSAFRA 182  
Db 178 ALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSTVS-FK- 235

QY 183 LEQDLPVNFKFI--IEG-MEEAGSVALEELVEKEKORF-----FSGVDYIVISDNLWI 232  
Db 236 -EHYGLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRLDAEFSELEY----- 285

QY 233 SQRKPAITYTRGNSYFMV----EVKCRDQDFHSGTGGILHEPMAADLVALLGSLVDSS 287  
Db 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQE-----SPVGKE 338

QY 288 GHILVP----GIYDE----VVPLTEE-----EI-NTY----- 310  
Db 339 DRVVSPEKTMDFNEMQMSVAVPVREEYADFKPFEQAWVEVKDTYEGSRDVLAAANVESK 398

QY 311 ---KAIHLDLEEYR----NSSRVEKFLFDTKKEILMHLWR-----Y 344  
Db 399 VDRKCIEDSLQKSLGKDSGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTF 458

QY 345 PLSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLPHMNVSAVEKQVTRHLEDVFSKRNS 404  
Db 459 PLEDHTSENKTKDEKKIERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSK--VT 516

QY 405 NKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRGDSTIPIAKMFQEIHK 464  
Db 517 EAAVSNMPEGLTPDLVQEAACESLNEATGTKIAYETKVDLVQTSSEAI-----QESLYPT 570

QY 465 VVLIP 469  
Db 571 AQLCP 575

RESULT 1182  
ADJ80176  
ID ADJ80176 standard; protein; 1274 AA.  
XX AC ADJ80176;  
XX DT 06-MAY-2004 (first entry)  
XX DE Novel human nucleic acid-associated protein #52.  
XX KW cyostatic; antiarteriosclerotic; cerebroprotective; antiparkinsonian;  
KW anticonvulsant; anti-HIV; antiallergic; antibacterial; virucide;  
KW gene therapy; nucleic acid-associated protein; cancer; atherosclerosis;  
KW stroke; parkinson's disease; epilepsy; Cushing's syndrome; AIDS; allergy;  
KW microarray element; protein-protein interaction; drug-target interaction;  
KW gene expression; chromosomal mapping; diagnosis.  
XX OS Homo sapiens.  
XX PN WO2003038052-A2.  
XX PD 08-MAY-2003.  
XX

PF 29-OCT-2002; 2002WO-US034846.  
XX 29-OCT-2001; 2001US-0348442P.  
PR 01-NOV-2001; 2001US-0335544P.  
PR 05-NOV-2001; 2001US-0337535P.  
PR 09-NOV-2001; 2001US-0344650P.  
PR 15-NOV-2001; 2001US-0334762P.  
XX (INCY-) INCYTE GENOMICS INC.  
PA Becha SD, Borowsky ML, Burford N, Chawla NK, Elliott VS;  
PI Emerling BM, Forsythe IJ, Gietzen KJ, Gorvad AE, Griffin JA;  
PI Hafalia AJA, Ison CH, Lal PG, Lee EA, Lee S, Lee SY, Marquis JP;  
PI Ramkumar J, Sprague WW, Swarnakar A, Tang YT, Warren BA, Yang J;  
PI Yue H, Zebarjadian Y;  
XX WPI; 2003-430514/40.  
DR N-PSDB; ADJ80234.  
XX PT New human nucleic acid-associated protein (NAAP) and polynucleotide,  
PT useful for diagnosing, treating, and preventing disorders associated with  
PT aberrant expression of NAAP, e.g. cancer, AIDS, stroke or infection.  
XX PS Claim 1; SEQ ID NO 52; 443pp; English.  
XX CC The invention relates to novel human nucleic acid-associated proteins and  
CC genes encoding them, sequences that have at least 90-99 % identity to the  
CC sequences; or biologically active or immunogenic fragments of these. The  
CC polypeptides and polynucleotides are useful in diagnosing, treating and  
CC preventing disorders associated with aberrant expression of NAAP, such as  
CC cell proliferative (e.g. cancer or atherosclerosis), neurological (e.g.  
CC stroke, Parkinson's disease or epilepsy), developmental (e.g. Cushing's  
CC syndrome), autoimmune/inflammatory (e.g. AIDS or allergies), or  
CC infections. These may also be used as elements on a microarray which may  
CC monitor or measure protein-protein interactions, drug-target  
CC interactions, and gene expression profiles. The polynucleotide may also  
CC be used in chromosomal mapping and in various diagnostic assays. These  
CC are also useful in assessing the effects of exogenous compounds on the  
CC expression of nucleic acids and amino acid sequences of NAAP, in  
CC facilitating drug discovery process, and in investigating the  
CC pathogenesis of diseases or medical conditions. This sequence corresponds  
CC to one of the proteins of the inventions.  
XX SQ Sequence 1274 AA;

Query Match 3.2%; Score 85; DB 7; Length 1274;  
Best Local Similarity 20.6%; Pred. No. 7.2e+02;  
Matches 92; Conservative 72; Mismatches 165; Indels 118; Gaps 22;

QY 29 SPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMMAVAADTLQRL 88  
Db 54 SPPPSLCRFM-----ATSLMSELQKDSIQLEDSESKVVKM---LLRLLEDKNGEVQNL 105

QY 89 GARVASVDMGP--QQLPDGQSLPIPPVILAEIGSDPTK-----GTVCFYGHLDVQP 137  
Db 106 AVKC----LGPLVVKVKEYQVETIVDTLCTNMRSDEQLRDIAGIGLKTVL----SELPP 157

QY 138 ADRGDGWLTDYPVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKF--II 195  
Db 158 AATGSGLATN--VCRKITGQL-----TSAI-AQQEDVAVQLEALDIL 196

QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVIS--DNLWISQRKPAITYGTRG-----NS 247  
Db 197 SDMLSRLGVPL-----GAFHASLLHCLLPQSSPRLAVRKRAV--GALGHAAACST 246

QY 248 YFMVEVKCRDQDFHSGTGGILHEPMAADLVALLGSLVDSSGHILVPGIY-DEVVPLTEEE 306  
Db 247 DLFVELADHLLDRLPGPRVPTSPTAIRTLIQCLGSGVGRQAGHRL--GAHLDRLVPLVEDF 304

QY 307 INTYKAIHLDLEEYRNS--SRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTV 364  
Db 305 CN-----LDDDELRESCLQAFEAFLRKCPCMGPHVFNVTSLCQ----- 344









RESULT 1187	Matches 39; Conservative 28; Mismatches 58; Indels 40; Gaps 6;
ADS21405	
ID ADS21405 standard; protein; 1390 AA.	
XX	
AC ADS21405;	
XX	
DT 02-DEC-2004 (first entry)	
XX	
DE Bacterial polypeptide #10438.	
XX	
KW Recombinant DNA construct; transformed plant; improved plant property;	
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;	
KW pathogen tolerance; pest tolerance; plant disease resistance;	
KW cell cycle pathway modification; plant growth regulator;	
KW homologous recombination; seed oil yield; protein yield; carbohydrate;	
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;	
KW bacterial polypeptide.	
XX	
OS Bacteria.	
XX	
PN US2003233675-A1.	
XX	
PD 18-DEC-2003.	
XX	
PF 20-FEB-2003; 2003US-00369493.	
XX	
PR 21-FEB-2002; 2002US-0360039P.	
XX	
PA (CAOY/) CAO Y.	
PA (HINK/) HINKLE G J.	
PA (SLAT/) SLATER S C.	
PA (CHEN/) CHEN X.	
PA (GOLD/) GOLDMAN B S.	
XX	
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;	
XX	
DR WPI; 2004-061375/06.	
XX	
PT New recombinant DNA construct comprising a promoter positioned to provide	
PT for expression of a polynucleotide encoding a polypeptide from a	
PT microbial source, useful for producing plants with improved properties.	
XX	
PS Claim 1; SEQ ID NO 10438; 122pp; English.	
XX	
CC The invention relates to a recombinant DNA construct comprising a	
CC promoter functional in a plant cell, where the promoter is positioned to	
CC provide for expression of a polynucleotide encoding a polypeptide from a	
CC microbial source. The invention also relates to a transformed plant	
CC comprising the recombinant DNA construct and a method of producing a	
CC transformed plant having an improved property. The plant is a crop plant	
CC such as maize or soybean. The method of producing a transformed plant	
CC having an improved property comprises transforming a plant with the	
CC recombinant DNA construct and growing the transformed plant, where the	
CC polynucleotide or polypeptide is useful for improving plant properties.	
CC The recombinant DNA construct is useful for producing plants with	
CC improved plant properties, e.g. improved cold, heat or drought tolerance,	
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,	
CC increased resistance to plant disease, better growth rate by modification	
CC of the cell cycle pathway with plant growth regulators, increased rate of	
CC homologous recombination, modified seed oil or protein yield and/or	
CC content, improved yield by modification of carbohydrate, nitrogen or	
CC phosphorus use and/or uptake, by modification of photosynthesis or by	
CC providing improved plant growth and development under at least one stress	
CC condition, improved lignin production or improved galactomannan	
CC production. This sequence represents a bacterial polypeptide used in the	
CC scope of the invention. Note: The sequence data for this patent did not	
CC form part of the printed specification but was obtained in electronic	
CC format from USPTO at seqdata.uspto.gov/sequence.html.	
XX	
SQ Sequence 1390 AA;	
Query Match 3.2%; Score 85; DB 8; Length 1390;	
Best Local Similarity 23.6%; Pred. No. 8.2e+02;	

QY	305	EEINTYKAIHLDLEEYRNSSRVEKFLFDTKBEILMHLWRYPSLSIHGIEGAFDEP-----	359
Db	1043	EEGVTYRE-----ESDEQTHREKVIIVDTKDKT-----KNPAIIVNHKKG---EPKGYSI	1089
QY	360	-----GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVS	410
Db	1090	PVGAHLAVEDGDQVKPGQVLVKIPRSVGKTRDITGGLPRTV---ELFEARNPSNPAVVS	1145
QY	411	MTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAK	455
Db	1146	EIDGI-----VTYGAIKRGNREIFIESKDGVKKRYMVPLSK	1181
RESULT 1188			
ADR10227			
ID	ADR10227	standard; protein; 1433 AA.	
XX			
AC	ADR10227;		
XX			
DT	04-NOV-2004	(first entry)	
XX			
DE	Human protein useful for treating neurological disease Seq 3733.		
XX			
KW	human; oligo-capping method; diagnostic marker; gene therapy;		
KW	osteoporosis; neurological disease; Alzheimer's disease;		
KW	Parkinson's disease; dementia; short memory; cancer;		
KW	sense or motor function; emotional reaction; fear response; panic;		
KW	osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;		
KW	tranquilliser.		
XX			
OS	Homo sapiens.		
XX			
PN	EP1447413-A2.		
XX			
PD	18-AUG-2004.		
XX			
PF	12-FEB-2004; 2004EP-00003145.		
XX			
PR	14-FEB-2003; 2003JP-00102207.		
PR	09-MAY-2003; 2003JP-00131452.		
XX			
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.		
XX			
PI	Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;		
PI	Wakamatsu A, Ishii S, Nagai K, Irie R;		
XX			
DR	WPI; 2004-583265/57.		
DR	N-PSDB; ADR08271.		
XX			
PT	New 1995 cDNA, useful for treating osteoporosis, neurological diseases,		
PT	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.		
XX			
PS	Claim 1; SEQ ID NO 3733; 2686pp; English.		
XX			
CC	This invention relates to novel, isolated full length human cDNA		
CC	molecules and the encoded proteins thereof. Specifically, it refers to		
CC	cDNA clones obtained by an oligo-capping method, where none of these		
CC	clones are identical to any known human mRNAs. The present invention		
CC	describes an immunoassay to identify agonists and antagonists, as well as		
CC	antibodies, antisense molecules and siRNAs that can all be used to bind		
CC	to and modulate expression of the cDNA molecules. As such, these		
CC	molecules are useful for diagnostic markers or therapeutic targets for		
CC	the various diseases or morbid states. In particular, they are useful in		
CC	gene therapy for treating osteoporosis, neurological disease, Alzheimer's		
CC	disease, Parkinson's disease, dementia, short memory and various cancers,		
CC	as well as for maintaining equilibrium of sense or motor function, and		
CC	for treating emotional reaction, fear response and panic. Accordingly,		
CC	they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,		
CC	cytostatic and tranquilliser activities. This polypeptide is a protein		
CC	encoded by a full length human cDNA sequence of the invention. NOTE: This		
CC	sequence is not given in the sequence listing of the specification but		







Best Local Similarity 19.1%; Pred. No. 8.9e+02;  
Matches 117; Conservative 85; Mismatches 221; Indels 190; Gaps 31;  
Qy 28 P S P P P A L L E K V F Q Y I D L H Q D E F V Q T L K E W V A I E S D S V Q P V P R F R Q E L F R M----- 77  
Db 385 P S S P A V Q V K V-----L E E P P A L S K I K L Y A K E E Q I D D- P I L N K K I F K V D D G E L L V L V A 438  
Qy 78 -----M A V A A D T L Q R L G A R V A- S V D M G P Q Q L P D G Q S L P P P V I L A E L G S D P-----T K 124  
Db 439 K S S G K T K V H I A T D L N Q P I T L H W A L S K S R G E W M V P S S I L P G S I I L D K A A E T P F S A S S S D 498  
Qy 125 G T V C F Y G H L D V Q P A D-----R G D G W L-----T D P Y V L T E V D G K L Y G R G A T D N K G P 169  
Db 499 G L T S K V Q S L D I V I E D G N F V G M P F V L L S G E K W I K N Q G S D F Y V D F S A A S K L A L K A A G D S G T 558  
Qy 170 V L A W I N A V S A F R A L E Q D L P V N I K F-----I I E G M E E A G S-----V A L E E L----- 209  
Db 559 A K S L L D K I A D M E S E A Q S F M H- R F N I A A D L I E D A T S A G E L G F T G I L V W M R F M A T R Q L I W N 617  
Qy 210 -----V E K E K O R-----F F S G V D Y-----I V I S-----D N L W I 232  
Db 618 K N Y N V K P R E I S K A Q D R L T D L L Q N A F T S H P Q Y R E I L R M I M S T V G R G E G D V G Q R I R D E I L V 677  
Qy 233 S Q R K P A I T Y G T R G N S Y F M V E V K R C D Q D F H S G T F G G I L H E P M A D L V A L L G S L V D S S G H I L V 292  
Db 678 I Q R K N D C K G G-----W M E E--W H Q K L H N N T-----S P D D V V I C Q A L I D I Y K S D F D 720  
Qy 293 P G I Y D E V V---P L T E E E I N T Y- K A I H L D L E E Y R N S S R V E K F L F D T K E E I L M H L W R Y P S L- 347  
Db 721 L G V Y W K T L N E N G I T K E R L L S Y D R A I H S E-----P N F R G D Q K N G L L R D L G H Y M R T L 770  
Qy 348 -S I H G---I E G A F D E- P G T K T V I P G R V I G K F S I R L V P-----H M N V S A V E- K Q 389  
Db 771 K A V H S G A D L E S A I A N C M G Y K T E G E G F M V G---V Q I N P V S G L P S G F Q G L L H F V L D H V E D K N 827  
Qy 390 V T R H L E D V F S K R N S S N K M V S M T L G L H P W I---A N I D D T Q Y L A A K R A I R T V F G T E P D M I R 446  
Db 828 V E T L L E G L L E A R E E L R P L L L K P N N R L K D L L F L D I A L D S T V R T A V E R G Y E E L N N A N P E K I- 886  
Qy 447 D G S T I P I A K M F Q E I V H K S V V L I P L G A V D D G E-----H S Q N E K I N R W N Y I E G T 493  
Db 887 -----M Y F I S L V L E N L A L-----S V D D N E D L V Y C L K G W N Q A L S M S N G G D N H W----- 928  
Qy 494 K L F A A F F L E M A Q L 506  
Db 929 A L F A K A V L D R I R L 941

RESULT 1192  
ABR82880  
ID ABR82880 standard; protein; 1464 AA.

XX  
AC ABR82880;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE S. tuberosum R1 protein.  
XX  
KW R1 protein; transgenic; fodder plant; starch; potato.  
XX  
OS Solanum tuberosum.  
XX  
PN WO2003072791-A2.  
XX  
PD 04-SEP-2003.  
XX  
PF 20-FEB-2003; 2003WO-EP001763.  
XX  
PR 26-FEB-2002; 2002DE-01008133.  
XX  
PA (FARB ) BAYER CROPS SCIENCE GMBH.  
XX  
PI Froberg C, Leube M, Ruempler I;

XX  
DR WPI; 2003-721779/68.  
DR N-PSDB; ACF36477.  
XX  
PT Generating a transgenic fodder plant with an increased leaf starch  
PT content in comparison to corresponding wild-type plants comprises  
PT genetically modifying a cell of a fodder plant by introducing a foreign  
PT nucleic acid molecule.  
XX  
PS Disclosure; Page 60-65; 73pp; English.  
XX

Query Match 3.2%; Score 85; DB 7; Length 1464;  
Best Local Similarity 19.1%; Pred. No. 8.9e+02;  
Matches 117; Conservative 85; Mismatches 221; Indels 190; Gaps 31;

Qy 28 P S P P P A L L E K V F Q Y I D L H Q D E F V Q T L K E W V A I E S D S V Q P V P R F R Q E L F R M----- 77  
Db 385 P S S P A V Q V K V-----L E E P P A L S K I K L Y A K E E Q I D D- P I L N K K I F K V D D G E L L V L V A 438  
Qy 78 -----M A V A A D T L Q R L G A R V A- S V D M G P Q Q L P D G Q S L P P P V I L A E L G S D P-----T K 124  
Db 439 K S S G K T K V H I A T D L N Q P I T L H W A L S K S R G E W M V P S S I L P G S I I L D K A A E T P F S A S S S D 498  
Qy 125 G T V C F Y G H L D V Q P A D-----R G D G W L-----T D P Y V L T E V D G K L Y G R G A T D N K G P 169  
Db 499 G L T S K V Q S L D I V I E D G N F V G M P F V L L S G E K W I K N Q G S D F Y V D F S A A S K L A L K A A G D S G T 558  
Qy 170 V L A W I N A V S A F R A L E Q D L P V N I K F-----I I E G M E E A G S-----V A L E E L----- 209  
Db 559 A K S L L D K I A D M E S E A Q S F M H- R F N I A A D L I E D A T S A G E L G F T G I L V W M R F M A T R Q L I W N 617  
Qy 210 -----V E K E K O R-----F F S G V D Y-----I V I S-----D N L W I 232  
Db 618 K N Y N V K P R E I S K A Q D R L T D L L Q N A F T S H P Q Y R E I L R M I M S T V G R G E G D V G Q R I R D E I L V 677  
Qy 233 S Q R K P A I T Y G T R G N S Y F M V E V K R C D Q D F H S G T F G G I L H E P M A D L V A L L G S L V D S S G H I L V 292  
Db 678 I Q R K N D C K G G-----W M E E--W H Q K L H N N T-----S P D D V V I C Q A L I D I Y K S D F D 720  
Qy 293 P G I Y D E V V---P L T E E E I N T Y- K A I H L D L E E Y R N S S R V E K F L F D T K E E I L M H L W R Y P S L- 347  
Db 721 L G V Y W K T L N E N G I T K E R L L S Y D R A I H S E-----P N F R G D Q K N G L L R D L G H Y M R T L 770  
Qy 348 -S I H G---I E G A F D E- P G T K T V I P G R V I G K F S I R L V P-----H M N V S A V E- K Q 389  
Db 771 K A V H S G A D L E S A I A N C M G Y K T E G E G F M V G---V Q I N P V S G L P S G F Q G L L H F V L D H V E D K N 827  
Qy 390 V T R H L E D V F S K R N S S N K M V S M T L G L H P W I---A N I D D T Q Y L A A K R A I R T V F G T E P D M I R 446  
Db 828 V E T L L E G L L E A R E E L R P L L L K P N N R L K D L L F L D I A L D S T V R T A V E R G Y E E L N N A N P E K I- 886  
Qy 447 D G S T I P I A K M F Q E I V H K S V V L I P L G A V D D G E-----H S Q N E K I N R W N Y I E G T 493  
Db 887 -----M Y F I S L V L E N L A L-----S V D D N E D L V Y C L K G W N Q A L S M S N G G D N H W----- 928  
Qy 494 K L F A A F F L E M A Q L 506  
Db 929 A L F A K A V L D R I R L 941

RESULT 1193













XX claim 18; segid 261; 310pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 10

CC contiguous nucleotides of any of the 233 polynucleotide sequences given

CC in the specification, or its complement. The nucleic acids encode cancer-

CC associated proteins. Also included are an expression vector comprising

CC the isolated nucleic acid cited above, a host cell comprising the above

CC recombinant nucleic acid or expression vector, a microarray for detecting

CC a cancer-associated (CA) nucleic acid comprising at least one probe

CC comprising at least 10 contiguous nucleotides of any of the above-

CC mentioned nucleotide sequences, an isolated polypeptide (encoded within

CC an open reading frame of a CA sequence selected from any of the 95

CC polynucleotide sequences as mentioned in the specification, or its

CC complement), an isolated antibody, (or its antigen binding fragment) that

CC binds to the above polypeptide, a hybridoma that produces the above

CC monoclonal antibody, a pharmaceutical composition comprising the above

CC antibody and a pharmaceutical excipient, a kit for detecting cancer

CC cells (comprising the antibody cited above, methods for diagnosing cancer

CC or for detecting the presence or absence of cancer cells in an

CC individual, a method for inhibiting growth of cancer cells in an

CC individual, a method for delivering a therapeutic agent to cancer cells

CC in an individual, an electronic library comprising the above

CC polynucleotide or polypeptide (or their fragments), methods of screening

CC for anticancer activity or for a bioactive agent capable of modulating

CC the activity of a CA protein (CAP), methods for detecting cancer

CC associated with expression of a polypeptide in a test cell sample, a

CC method for treating cancers and a method for inhibiting the expression of

CC CA gene in a cell. The composition and methods are useful for detecting,

CC diagnosing, preventing and treating cancers, especially lymphoma and

CC leukaemia. These may also be used in screening for agents that modulate

CC cancer. The present sequence is a human CAP protein sequence. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 2102 AA;

Query Match 3.2%; Score 85; DB 8; Length 2102;

Best Local Similarity 18.6%; Pred. No. 1.6e+03;

Matches 90; Conservative 71; Mismatches 177; Indels 146; Gaps 23;

QY 26 SSPSPPPALLEKFQYIDLHQDEFVQTLKEWVA-----IESD-----SVQPVPRF 70

DB 1486 SPSPSP-----HEEFIDWWSKFFASIGEREKCGSYLEKDFDTLKVYDTQLE 1532

QY 71 ROELFRMMAVAADTLQRLGARVASVDMGPQ-----QLPDGQSLPIPPVILAE 118

DB 1533 NVEAFEGSLDFCNTFKLYRGKTOEETDPSVIGFKGLFKIYLPEDPAIPMPPRQFHQL 1592

QY 119 GSD-PTKGTVCFY--GHLDVQPADRGDGLTDPYVLTVEVDGKLYGRGANDKNG----- 168

DB 1593 AAQGPQECLEVRIVYRAFGLOPKD--PNGKCDPIKISI-GK---KSVDQDNYPCTLE 1646

QY 169 PVLAWINAVSAFRALEQDLPVNI--KFIIIEGMEEAGSVALE--ELVEKEKDRFFSGVDY 223

DB 1647 PVFGKMFELTCTLPLEKDLKITLYDYDLLSKDEKIGETVVDLENRLLSKFGARCGLPQTY 1706

QY 224 IVISDNLWISQRK-----AITYGT-----RGNSYFMVEVKC-RDQDFHSG 263

DB 1707 CVSGPNQWRDLRPSQLLHLFCQQHRVKAPVYRTDRVMFQDKKEYSIEIEAGRIPNPHLG 1766

QY 264 TFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHLDLEEYRNS 323

DB 1767 -----PVEERLAL-----HVLQ---QQGLVPEHVESRPLYSPLQPDIEQGKLQ 1806

QY 324 SRVEKF-----LFDTKEEILMHLWRYPISLSIHG----- 351

DB 1807 MWVDLFPKALGRPGPPPNITPRRARRFFLRCCIWNTRDVIL-----DDLSTGEKMSDI 1860

QY 352 -IEG---AFDEPGTKTIPGRVI---GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 404

DB 1861 YVKGWIGFEEHKQKTDVHYSRLSGEGNFWRFPPFDYLPAPAEQVCTIAKKDAFWRLDKT 1920

QY 405 NKQV 408

DB 1921 ESKI 1924

RESULT 1199

ABB67210

ID ABB67210 standard; protein; 3263 AA.

XX

AC ABB67210;

XX

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 28422.

XX

KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

KW

XX Drosophila melanogaster.

OS

XX WO200171042-A2.

PN

PD 27-SEP-2001.

XX

XX 23-MAR-2001; 2001WO-US009231.

PF

XX 23-MAR-2000; 2000US-0191637P.

PR

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE ) PE CORP NY.

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

DR WPI; 2001-656860/75.

DR

DR N-PSDB; ABL11313.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

PT

PT

PS Disclosure; SEQ ID NO 28422; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 3263 AA;

Query Match 3.2%; Score 85; DB 4; Length 3263;

Best Local Similarity 20.3%; Pred. No. 3.1e+03;

Matches 88; Conservative 64; Mismatches 175; Indels 106; Gaps 18;

QY 47 DEFVQTLKEWVAIESDSVQPVPRFQELFRMMAVAADTLQRLGARVASVDMGPQLPDGQ 106

DB 2861 EEAIEDLKLKAV-SQEVQSDILFSHEITEEQHQALETIEKLTSAIEDTVQQKLLSQE 2919

QY 107 SLPIPPVILAE-LGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGRGATD 165

DB 2920 ELIIAEVLPSETVGRDVT-----DVRP-----PGETISPLTP 2952

QY 166 NKGPVLAWINAVSAFRALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIV 225

DB 2953 NMSLCITECPEDSIGEMQQAAKERMETPSMSVTESKAVGGQEL-----EVLENVDHM- 3005

QY 226 ISDNLWISQRKPAITYGTRGNSYFMV---EVKCRDQDFHSGTFGGILHEPMA----- 274









Masignani V, Tettelin H, Fraser C;  
 WPI; 2003-040579/03.  
 N-PSDB; ABX05911.  
 New proteins and nucleic acid molecules from *Streptococcus pneumoniae*,  
 useful as medicaments for treating or preventing a disease or infection  
 due to *Streptococcus bacteria*, such as pneumonia, sepsis, otitis media or  
 ear infection.  
 Claim 1; SEQ ID NO 398; 56pp; English.  
 The invention relates to a protein comprising or having at least 50%  
 identity to any of the 2469 amino acid sequences, identified in the  
 specification (available on a computer readable format), or its fragment,  
 expressed from 2469 of 2489 identified DNA coding regions from the  
*Streptococcus pneumoniae* type 4 strain genomic sequence appearing as  
 AB56454. Also included are an antibody which binds one of the proteins,  
 treating a patient by administering the protein, DNA or antibody (in a  
 composition), a kit comprising first and second primers, which are the  
 nucleic acid cited above or fragments between nucleotides 8-100 of a  
 sequence not defined in the specification, for amplifying a target  
 sequence contained within a *Streptococcus nucleic acid* sequence, where  
 the first primer is substantially complementary to the target sequence  
 and the second primer is substantially complementary to the complement of  
 the target sequence, and where the parts of the primers having  
 substantial complementarity define the termini of the target sequence to  
 be amplified, assay comprising contacting a test compound with the  
 protein, and determining whether the test compound binds to the protein  
 and a *Streptococcus pneumoniae bacterium*, where one or more genes  
 encoding the proteins has been rendered inactive. The proteins, nucleic  
 acid molecules, antibody and compositions are useful as medicaments for  
 treating or preventing a disease or infection due to *Streptococcus*  
*bacteria*, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis  
 media or ear infection. They are also useful in developing vaccines,  
 diagnostics and antibiotics. The methods are useful for identifying  
 immunodominant proteins. The present sequence is one of the 2469 proteins  
 expressed by the identified coding regions from the genomic sequence.  
 Note: The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to  
 standardise OS field)  
 Sequence 332 AA;  
 Query Match 3.2%; Score 84.5; DB 6; Length 332;  
 Best Local Similarity 20.7%; Pred. No. 1e+02;  
 Matches 56; Conservative 45; Mismatches 86; Indels 83; Gaps 14  
 80 VAADTLQRL--GARVASVDMGP-QQLPDGQSLLPPIPVILAEGLSDPTKGTVCFYGHLDVQ 136  
 121 VAANIKEAKDGKIKALPEELNPVEEVSAAAPVAQTAIPE-----GTVIGDGKLKIN 173  
 137 PADRGDWLTDPPVLTVEVDGK-LYGRGATDNKGPVLAWINAVSAFRAL-----EQDLP 188  
 174 -----LARLDTRLHGGQVAT-----AWTPDSKANRIIVASDNVAKDDL 212  
 189 VN-IKFTIEGMEEAGSVALEELVEKEKORFFSGVDYVIVISDNLWISQKPAITYGTRGNS 247  
 213 KELIKQAAPGNVKANVVPQKLEISKDPFRGETHALILFET----- 254  
 248 YFMVEVKCRDOPHSGTFFGGILHEPMADLVALLGSLVSSGHILVPGIYDEVVPLTEEEI 307  
 255 -----PQDALRAIEGGV---PIKTL--NVGSMASHSTGKTLV---NTVLSMDKEDV 296  
 308 NTYK-----ATHLDLEEYRNSSRVEKFLFD 332  
 297 ATFEKMRDLGVDFVRKVPNDK--KDLFD 324  
 RESULT 1206  
 ABP81542

ID		ABP81542 standard; protein; 332 AA.
XX	AC	ABP81542;
XX	DT	04-MAR-2003 (first entry)
XX	DE	Streptococcus pneumoniae polypeptide SEQ ID NO 620.
XX	KW	Streptococcus pneumoniae; infection; otitis media; antibacterial; diagnosis; gene therapy.
XX	OS	Streptococcus pneumoniae.
XX	PX	WO200283855-A2.
XX	PD	24-OCT-2002.
XX	PF	12-APR-2002; 2002WO-US011524.
XX	PR	16-APR-2001; 2001US-0283948P.
XX	PP	18-APR-2001; 2001US-0284443P.
XX	PA	(AMCY ) AMERICAN CYANAMID CO.
XX	ZJ	Zagursky RJ, Masi AW, Green BA, Chakravarti DN, Russell DP, Wooters JL;
DR	WI	WPI; 2003-093010/08.
DR	N-	N-PSDB; ABZ42390.
CC		New Streptococcus pneumoniae polynucleotides, useful for treating or preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae.
PS	CN	Claim 42; Page 861-862; 1091pp; English.
CC		The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABP81299-ABP81674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy
SQ		Sequence 332 AA;
		Query Match            3.2%; Score 84.5; DB 6; Length 332;
		Best Local Similarity 20.7%; Pred. No. 1e+02;
	Matches	56; Conservative 45; Mismatches 86; Indels 83; Gaps 14
QY	80	VAAADTLQLRL--GARVASVDMGP-QQLPDGQSLLPIPVPVLIAELGSDPTKGTVCFYCHLDVQ 136
Dd	121	VAANIIEAKDGIKALPEELNPVEEVASAAAAFVAQTAIPE-----GTVIGDGKLKIN 173
QY	137	PADRGDGLTDPYYLTLEVDCK-LYGRGATDNKGFPVLAWINAVSAFRAL-----EQDLPL 188
Dd	174	-----LARDTRLHGQVAT-----AWTSPSKANRIIVASDNVAKDDL R 212
QY	189	VNI-KFIIEGMEEAGSVALHELVKEKDRFFSGVDYIVISDNLWLISQRKPITYGTRGNS 247
Dd	213	KELIKQAAPGNVKANVVPIQKLIETSKDFRGETHALILFET----- 254
QY	248	YFMVEVKCRDQDFHSGTFGGIIHPMADLVALLGS�VSSSHILLPGIYDEVVPLTEEEEI 307
Dd	255	-----PQDALRAIEGV---PIKTL--NVGSMASHSTGKTLY----NTVLMDKD V 296
QY	308	NTYK-----AIHLDDLEYRNSSRVKF LFD 332
Dd	297	AFFEKKRD LGVFEDVRKVNDISK--KDLFD 324











PR	26-JUL-1999;	99US-0145276P.
PR	27-JUL-1999;	99US-0145913P.
PR	27-JUL-1999;	99US-0145918P.
PR	27-JUL-1999;	99US-0145919P.
PR	28-JUL-1999;	99US-0145951P.
PR	02-AUG-1999;	99US-0146386P.
PR	02-AUG-1999;	99US-0146388P.
PR	02-AUG-1999;	99US-0146389P.
PR	03-AUG-1999;	99US-0147038P.
PR	04-AUG-1999;	99US-0147204P.
PR	04-AUG-1999;	99US-0147302P.
PR	05-AUG-1999;	99US-0147192P.
PR	05-AUG-1999;	99US-0147260P.
PR	06-AUG-1999;	99US-0147303P.
PR	06-AUG-1999;	99US-0147416P.
PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
PR	10-AUG-1999;	99US-0148171P.
PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
PR	16-AUG-1999;	99US-0149368P.
PR	17-AUG-1999;	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.
PR	20-AUG-1999;	99US-0149723P.
PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149902P.
PR	23-AUG-1999;	99US-0149930P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 3.2%; Score 84.5; DB 3; Length 336;		
Best Local Similarity 22.4%; Pred. No. 1e+02; Mismatches 35; Indels 65; Gaps 14;		
Matches 54; Conservative 54; Mismatches 87; Indels 65; Gaps 14;		
QY	38	VFOYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDM 97
Db	111	IFIYYQL--DNYIQNHRRYVKRS-----QQLLHGLEY-----SHTSSCE- 149
QY	98	GPQQLPDGQSLPIPP--VILAELGSDPTKGTVCFYGHLDVQPADRGD-GWLT----- 147
Db	150	-PEESSNG--LPIVPCGLIAWSMFND-----TFTFSRERTKLNVRNNIAWKSDREHKFGK 202
QY	148	-PYVLTEVDGKLYRGATDNKGPV-----LAWINAVS--AFRAL---EQDLPVNIKFI 194
Db	203	NVYPINFQNTLIGGAKLDPKIPLSDQEDFIVWMRAAALLSFRKLYGRIEEDL----- 255
QY	195	IEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKRP--AITYGTRGNSYFMVE 252
Db	256	-----EPGKVVVEVNLMMNNYNTYSFSGQKKLILSTSNWLGGRNDFLGITYLVVGGSSSIVIS 310
QY	253	V 253
Db	311	I 311
RESULT 1212		
AAG39350		
ID	AAG39350	standard; protein; 342 AA.
XX		
AC	AAG39350;	
XX		
DT	18-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 48674.
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130891P.
PR	28-APR-1999;	99US-0131449P.

PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
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XX						
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PD	06-SEP-2000.					
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Query Match 3.2%; Score 84.5; DB 3; Length 343;

Best Local Similarity 22.4%; Pred. No. 1e+02; Mismatches 87; Indels 65; Gaps 14;  
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Db 157 -PEESSNG--LPIVPCGLIAWSMFND----TFTFSRERTKLNVSNNIAWKSDDREHKFGK 209

QY 148 -PYVLTEVDGKLYGRGATDNKGPV-----LAWINAVS--AFRAL-----EQDLPVNIKFI 194

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Db 318 I 318

RESULT 1214

ADN47805

ID ADN47805 standard; protein; 396 AA.

XX AC ADN47805;

XX DT 01-JUL-2004 (first entry)

XX DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1683.

XX KW gene disruption; gene targeting; marker gene; transformation;  
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;  
KW gene structure; gene function; enzyme activity; medicine;  
KW forensic science; food; drug inspection; molecular biology; immunology.

OS Thermococcus kodakaraensis.

XX PN WO2004022736-A1.

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PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
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DR WPI; 2001-137957/14.  
DR N-PSDB; AAF72149.  
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PT Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway  
PT proteins, useful for producing fine chemicals in microorganisms,  
PT including organic acids, nonproteinogenic amino acids, and purine and  
PT pyrimidine bases.  
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PS Claim 20; Page 1255; 1737pp; English.  
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CC AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic  
CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP  
CC nucleic acids are useful for the production of fine chemicals in  
CC microorganisms, including organic acids, nonproteinogenic amino acids,  
CC purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated  
CC and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,  
CC vitamins, cofactors, polyketides and enzymes  
XX  
SQ Sequence 434 AA;

Query Match 3.2%; Score 84.5; DB 4; Length 434;  
Best Local Similarity 19.8%; Pred. No. 1.5e+02;

Matches 79; Conservative 49; Mismatches 137; Indels 135; Gaps 18;  
QY 25 FSSPPPPALLEKVF--QYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAA 82  
Db 31 FGSVGGQARFIEKAHGSTLIDVDGNEYVDLVCSWGPMMLGHAHP----- 74  
QY 83 DTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEGLSDPTKGTV----- 127  
Db 75 -----AVVEAVQKAVVDGLSFGAPTIGEVEVLAQDIVKRTSVEEVRLVNSCTEATM 124  
QY 128 -----CFYGHLDVQPADRGDWLTPPYVLTEVDGKLYGRGATDNK 167  
Db 125 SAVRLARGYTORSKILKFECCYHGHVDALLASAGSGVAT--FALPDSFG-ITGAQTSDT- 180  
QY 168 GPKLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGS----- 203  
Db 181 --IVVPYNDIEAVRNAFAEYVPEIACII--AEAAGNNGTVAPKDNFNDKLLAIAHADGA 236  
QY 204 -VALEELVE--KEKDRFFSGVDYI---VISDNLWISQKPAITYGTRGNSYFMVEVKCRD 257  
Db 237 LLILDVMTGFRTSYRGWFGVDKVAADLVTFGKVVSGGLPAAAFG--GKAEIMNMLAPQG 294  
QY 258 QDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDDL 317  
Db 295 PVYQAGTLSG--NPVA-VAAGRASL-----KLADESL--YTTIN--- 328  
QY 318 EEYRNSSRVEKFLFD--TKBEILMHLWRYPs-LSIHGIEG 354  
Db 329 ---ANADRLHGLISDALTHEGVAHHIQRASNMLSIRFAEG 365  
RESULT 1218  
AAG90238  
ID AAG90238 standard; protein; 437 AA.  
XX  
AC AAG90238;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE C glutamicum protein fragment SEQ ID NO: 3992.  
XX  
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
KW organic acid synthesis.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN EP1108790-A2.  
XX  
PD 20-JUN-2001.  
XX  
PF 18-DEC-2000; 2000EP-00127688.  
XX  
PR 16-DEC-1999; 99JP-00377484.  
PR 07-APR-2000; 2000JP-00159162.  
PR 03-AUG-2000; 2000JP-00280988.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX  
DR WPI; 2001-376931/40.  
DR N-PSDB; AAH65457.  
XX  
PT Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analyzing  
PT expression profile or pattern of a gene and identifying homologous gene.  
XX  
PS Claim 17; SEQ ID NO 3992; 246pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and analysing  
CC the expression profile or expression pattern of a gene derived from  
CC Coryneform bacterium, and identifying a homologue of a gene derived from  
CC coryneform bacterium. Coryneform bacteria are useful for producing amino  
CC acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a protein described in the  
CC exemplification of the invention. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the European Patent Office  
XX  
SQ Sequence 437 AA;

Query Match 3.2%; Score 84.5; DB 4; Length 437;  
Best Local Similarity 19.8%; Pred. No. 1.5e+02;  
Matches 79; Conservative 49; Mismatches 137; Indels 135; Gaps 18;  
QY 25 FSSPSPPPALLEKF--QYIDLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMAVAA 82  
Db 34 FGSVGGQARFIEKAHGSTLIDVDGNEYVDLVCSWGPMMLGHAHP----- 77  
QY 83 DTLQRLGARVASVDMGPQLPDGQSLPIPPVILAEIGSDPTKGTV----- 127  
Db 78 -----AVVEAVQKAVVDGLSFGAPTIGEVELAQDIVKRTSVEEVRLVNSGTEATM 127  
QY 128 -----CFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNK 167  
Db 128 SAVRLARGYTQRSKILKFEGCYHGHVDALLASAGSGVAT--FALPDSPG-ITGAQTSDT- 183  
QY 168 GPVLAWINAVSAFRALEQDLPVNIKFIIEGMEERAGS----- 203  
Db 184 --IVVPYNDIEAVRNAFAEYPGEIACII--AEAAGNMGTVAPKDNFNDKLLAIAHADGA 239  
QY 204 -VALEELVE--KEKDRFFSGVDYI---VISDNLWISQKPAITYGTRGNSYFMVEVKCRD 257  
Db 240 LLILDEVMTGFRTSYRGWFGVDKVAADLVTFGKVSSGCLPAAAFG--GKAEIMMWLAPQG 297  
QY 258 QDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLHDL 317  
Db 298 PVYQAGTLSG---NPVA-VAAGRASL-----KLADES---YTTIN--- 331  
QY 318 BEYRNSSRVEKFLFD--TKBEILMHLWRYPs-LSIHGIEG 354  
Db 332 ---ANADRLHGLISDALTHEGVAHHIQRASNMMLSIKFAEG 368

RESULT 1219  
ADB09765  
ID ADB09765 standard; protein; 442 AA.  
XX  
AC ADB09765;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Alloiooccus otitis antigenic protein SEQ ID NO:3858.  
XX  
KW Alloiooccus otitis; antigenic protein; immunogenic; immunisation;  
KW gene therapy; Gram-positive bacterium; infection.  
XX  
OS Alloiooccus otitis.  
XX  
PN WO2003048304-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 25-NOV-2002; 2002WO-US036123.  
XX  
PR 29-NOV-2001; 2001US-0333777P.  
PR 18-NOV-2002; 2002US-0426742P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
XX  
PI Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;  
XX

DR WPI; 2003-505284/47.  
DR N-PSDB; ADB09768.  
XX  
PT New Alloiooccus otitis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.  
XX  
PS Claim 33; SEQ ID NO 3858; 1019pp; English.  
XX

CC The present invention describes an isolated polynucleotide (I) of  
CC Alloiooccus otitis genomic DNA, which encodes an antigenic protein.  
CC Alloiooccus otitis is a Gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its  
CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloiooccus otitis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloiooccus  
CC otitis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloiooccus  
CC otitis. The present sequence represents an Alloiooccus otitis  
CC antigen protein from the present invention.  
XX

SQ Sequence 442 AA;  
Query Match 3.2%; Score 84.5; DB 6; Length 442;  
Best Local Similarity 19.9%; Pred. No. 1.6e+02;  
Matches 57; Conservative 45; Mismatches 84; Indels 101; Gaps 15;

QY 143 GWLTDPPYVLTEVDGKLYGRG-----ATDN-KGPVLAWINAVSAFRALEQDLPVNIK- 192  
Db 22 GWLNDP-----NGAVYFKGTYHVYHQYVPDNPKGATHWGHKTSKDLVHFKEPVLSP 75  
QY 193 ---FIIEGMEERAGSVALEELV-----EKEKDRFFSGVD---YIVISDNLWISQR 235  
Db 76 GKCFDKDGVYSGGAMKLGDIHFFYTGNVKKEGDYDLYNGRDQNVVHVSSDGYSIDQR 135  
QY 236 KPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMA-----DLVALLGSLVDSSGH 289  
Db 136 HVVIPH-----EDFPPG-FTNHIRDPKVFOHGNLFYMLGGRKLDNTGA 178  
QY 290 ILVPGIYDEVVPLTEEEINTYKAHLDLLEEYRNSSRVEKFLFDTKKEILMHLWRYPsL-- 347  
Db 179 ILL-----FESEDLHDWDYKGN-----LLEGNEQ-QGYMWEAPDLVE 214  
QY 348 -----SIHGIEGAFDEPGTKTIVPGRVIGKF---SIRLVP 379  
Db 215 FGDQAVLLFSPQIRANHNSFLNPHS----AGYLVGRMDWDSLQFIP 257

RESULT 1220  
AAW13081  
ID AAW13081 standard; protein; 453 AA.  
XX  
AC AAW13081;  
XX  
DT 08-MAY-1997 (first entry)  
XX  
DE Pseudomonas aeruginosa exoenzyme S.  
XX









QY 132 -----HLDVQPADRGDGL-----TDPYVLTEVDGKLYGRGA----- 163  
Db 76 ARTDEDLFRKGEHLEILNDTQGDWWLARSKKTRSEGIPSNYVAKLSIEAEPWYFKI 135  
QY 164 --TDNKGPPVLAWINAVSAF-----RALEQDLPVNIK-----FIIEGMEEAAGSV----- 204  
Db 136 KRTEAKKLLLPENEHGAFLIRDSERHNDYSLSVRDGDTVKHVIRQLDEGGFFIARRT 195  
QY 205 ---ALBELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYG---TRGNSYFMVEVKCRDQ 258  
Db 196 TERTLQELVE-----HYSKSDGLCVNLCKPCVQIEKPVTEGLSH-----RTRDQ 240  
QY 259 -----DFHSGTFGGILHEPMADLVALLSGLVDSSGHILVPGIYDEVVPLTEES 306  
Db 241 WEIDRTSLKFVRKLGSGQFGDVWE-----GLWNNTPVA--- 274  
QY 307 INTYKAIHLDLEEYRNSRRVEKFLFDTKEEILMHLWRYPSLSIHGEGAFDEPGTKVIP 366  
Db 275 IKTLKSGTMDPKDFLAEQIMKKLRHTK--LIQLYAVCTV-----EEP----- 315  
QY 367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSK-RNSSNKMVVSMTLGLHPWIANIDDT 425  
Db 316 -----IYIITEL---MKHGSLLLEYLQAIAGKGRSLKMOTLIDMAAQIAGMAYLESQ 364  
QY 426 QYLAAKRAIRTVFGTEPDMRDGSTITPIA 454  
Db 365 NYIHRDLARNV-----LVGDGNIVKIA 387

RESULT 1226  
ABO14652  
ID ABO14652 standard; protein; 531 AA.  
XX ABO14652;  
XX  
DT 25-AUG-2003 (first entry)  
XX Novel human protein #25.  
DE  
XX Human; NOV; gene therapy; endocrine related disease; diabetes;  
KW metabolism-related disease; obesity; central nervous system disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
KW stroke; infection.  
OS Homo sapiens.  
XX  
PN WO2003023002-A2.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028539.  
XX  
PR 07-SEP-2001; 2001US-0318120P.  
PR 07-SEP-2001; 2001US-0318130P.  
PR 10-SEP-2001; 2001US-0318430P.  
PR 17-SEP-2001; 2001US-0322636P.  
PR 17-SEP-2001; 2001US-0322781P.  
PR 17-SEP-2001; 2001US-0322816P.  
PR 17-SEP-2001; 2001US-0322817P.  
PR 19-SEP-2001; 2001US-0323519P.  
PR 20-SEP-2001; 2001US-0323631P.  
PR 20-SEP-2001; 2001US-0323636P.  
PR 25-SEP-2001; 2001US-0324969P.  
PR 25-SEP-2001; 2001US-0325091P.  
PR 26-SEP-2001; 2001US-0324990P.  
PR 17-APR-2002; 2002US-0373212P.

PR  
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SQ

Query Match 3.2%; Score 84.5; DB 6; Length 531;  
Best Local Similarity 20.9%; Pred. No. 2.1e+02;  
Matches 77; Conservative 45; Mismatches 118; Indels 129; Gaps 19;  
QY 21 ERGMFSSPPPALLEKVFQYIDLHQDEFVQTLK-----EWAIESDSVQVPFRQEQE 73  
Db 106 ERGL-----PTPRTEAVFRNLGL-QSPFLSWLPDNSDAELEEVSVENGVSVP-PPFKQS 157  
QY 74 LFRMMAVAADTLQRLGARVASVDMGPPQQLPDQSLLPIPPVILAEGLSDPTKGTVCIFYGHL 133  
Db 158 P-RIRRKGNQAHQRPQTR-AEGESDSQDMGMDAHKSP-----NMGNPMDGDCVYENL 208  
QY 134 DVQ-----PADRGDGWLTDPYVLTVEVDCKLYGRGATDNKGPVLAWINAVSAFRALE 184  
Db 209 AFQKEEDLEKKREASESTGTNSSAAHNEELSKALKGEGGTDSD-----HMR 254  
QY 185 QDLPVNIKFIIEGMEE-----AGSVALEELVEKEKORFFSGVD-----YIV 225  
Db 255 HEASLAIRSPCPGLEEDMEAYVLRPALPGTNMWCYLTRDK---HGVDKGLFLYYLYLE 310  
QY 226 ISDNLWIS-----QRKPAITYGRGNSYFMVEVK---CRDQD----- 259  
Db 311 TSDSLQSRLLAGKRRRSKT-----SNYLISLDPTHLSRDGDNFVGKVRNSNVFSTKFTI 364  
QY 260 FHSQT-----FGGILHEPMADLVALLSGLVDSSGHILVPGIYDE---- 298  
Db 365 FDNGVNPDRHLTRNTARIRQELGAVCYEP-----NVLYGLGPRKMTVLPGTNSQNQRI 419  
QY 299 -VVPLTEEE 306  
| | | | |

06-SEP-2002; 2002US-00236177.  
(CURA-) CURAGEN CORP.  
Spytek KA, Patturajan M, Goiman L, Li L, Anderson DW, Zhong M;  
Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;  
Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;  
Lepley DM, Edinger SR, Burgess CE;  
WPI; 2003-313242/30.  
N-PSDB; ACD19345.  
New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
and polynucleotides, useful in gene therapy, e.g. for treating or  
preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
stroke or infections.  
Claim 1; Page 137; 586pp; English.

The invention describes a new isolated polypeptide (NOVX). The NOVX  
polypeptide, nucleic acid and antibody are useful as therapeutics,  
particularly in the manufacture of a medicament for treating a syndrome  
associated with a human disease, which includes a pathology associated  
with NOVX polypeptide. The DNA encoding the protein is useful in gene  
therapy for treating the disease or condition. In particular, the NOVX  
polypeptide or polynucleotide is useful for treating endocrine/  
metabolism-related diseases (e.g. obesity or diabetes), central nervous  
system disorders (e.g. Alzheimer's disease, Parkinson's disease,  
epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune  
and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,  
asthma, inflammatory bowel disease, rheumatoid arthritis or  
osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,  
prostate or brain cancers, or melanoma), liver diseases (e.g. liver  
cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),  
haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).  
These are also useful in developing powerful assay system for functional  
analysis of various human disorders, as well as in diagnostic  
applications, and for monitoring the effects of drugs during clinical  
trials. This is the amino acid sequence of a novel human NOV protein





CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 571 AA;

Query Match 3.2%; Score 84.5; DB 6; Length 571;  
Best Local Similarity 21.5%; Pred. No. 2.3e+02;  
Matches 98; Conservative 66; Mismatches 172; Indels 119; Gaps 22;

QY 50 VQTLEWVAIESDSVQVPRFRQELFRMMAVAADTLQLGARVAS--VDMGPQLPDGQS 107  
Db 8 LSTLKETPA-DAEIVSHQMLRAGMIRKLASGLYDWMPTGVRVLRKIEKIVREEMDNAGS 66  
QY 108 LPI--PPVILAEAGSDPTKGTGFCYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATD 165  
Db 67 LEISMPVVQPADLWQE--SGRWEYGPPELLRFTDRGE----RPFVL---GPTHEEVVTD 116  
QY 166 NKGPVLAWINAVSAFRALEQDL-PVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYI 224  
Db 117 -----IVRNEITSYKQLPLNLQIOTKFRDEVRPRFGVRSREFIMKDAYSEH----- 164  
QY 225 VISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLV 284  
Db 165 -----ISQESLQETYDRMQAYSNIFTRI-----GLDFRP---VLADTGSIG 203  
QY 285 DSSGH---ILVPGIYDEVVPLTEEEINTYKAHLDLEEY-----RNSRVEKFLFDTK 335  
Db 204 GSASHEFQVLADSGEDDIVFSTASYD---AANIELAEAVMPATPRSPATEELRLVDT-- 257  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLE 395  
Db 258 -----PNAKTI-----AELVEQFNL-PIEXTVKTLLI- 282  
QY 396 DVFSKRNSNMVSMTLGLHPWIANIDDTQYLAAGR---AIRTVEGTEPDMIR----- 446  
Db 283 -VHATEESGHKLVALVRGDH-----ELNEIKAEKCSIVASPLVFATEEIRQAVNAG 334  
QY 447 DGSTIPIAKMFQEIIVKSVVLIP---LGAVDDGEH 478  
Db 335 PCSLGPINLPLPIIIDRAVSVMSDFGAGANIDGKH 369

RESULT 1229  
ABU41576  
ID ABU41576 standard; protein; 575 AA.  
XX  
AC ABU41576;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #27103.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Pseudomonas syringae.  
XX  
PN WO200277183-A2.  
XX

PD 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002WO-US0009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA45446.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 69500; 1766pp; English.  
XX

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 575 AA;

Query Match 3.2%; Score 84.5; DB 6; Length 575;  
Best Local Similarity 19.8%; Pred. No. 2.3e+02;  
Matches 81; Conservative 60; Mismatches 116; Indels 153; Gaps 24;  
QY 148 PYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRA-----LEQDLPVNI--KFIE 196  
Db 158 PAIKLAEDGFVLGGQDVD---MLS--SATDVFKADMADSGSIFLDKCKPMQVQKLVQK 211  
QY 197 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQR-----KPAIT-----YG 242  
Db 212 DLAR---TLKEVSEKSGDGFYKG-----WVAKALVDSOQAGKGIITQADLDHYK 257  
QY 243 TRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYD--EVW 300  
Db 258 TRE----LAPVECDYRGYH-----VVSAPPSSGGVVICQILNILEGY 296

QY 301 PLTEEEINTYKAIHLDLLEEYRNSRVEK--FLFDTKEEILMHLWRYPSLSIHGIEGAFD- 357  
Db 297 PMKELGRSAQGMHYQIEAMRH-AYVDRNSYLGD-----PDFVKNPVEHLLDV 343  
QY 358 -----EP---GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSCRNS 403  
Db 344 KYAAKLREAIEPQKAGDSNKIKPG-----VAPH-----EGSNTTHYSIVDKWNA 388  
QY 404 SNKMVVSMTLGLHPW-----IANIDDTQYLAAKRAIRTVFGT---EPDMIRDG 448  
Db 389 -----VSVTYTLNNWFGAGVMASKTGVIIN-DEMDDFTVKGVGNMYGLVQGEANAIPG 442  
QY 449 STIPIAKMFQEIIVHK-----SVVLIPLCAVDDGEHSQ 480  
Db 443 KT-PLSSMSPTIVTKDGKTMVMVVGTPGGSRIITATLLTMLNVIDYGMNIQ 491  
RESULT 1230  
ADF06299  
ID ADF06299 standard; protein; 575 AA.  
XX  
AC ADF06299;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Bacterial polypeptide #2412.  
XX  
KW Proteus mirabilis infection; bacterial infection; antibacterial;  
KW immunostimulant.  
XX  
OS Proteus mirabilis.  
XX  
PN US6605709-B1.  
XX  
PD 12-AUG-2003.  
XX  
PF 05-APR-2000; 2000US-00543681.  
XX  
PR 09-APR-1999; 99US-0128706P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton GL;  
XX  
DR WPI; 2003-895291/82.  
DR N-PSDB; ADF02127.  
XX  
PT New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.  
XX  
PS Disclosure; SEQ ID NO 6584; 870pp; English.  
XX  
CC The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis, a  
CC method for evaluating a compound for the ability to bind a P. mirabilis  
CC polypeptide and a method for screening test compounds for anti-bacterial  
CC activity. The polypeptides and polynucleotides are useful as molecular  
CC targets for diagnosing, preventing and treating pathological conditions  
CC resulting from bacterial infection, as reagents for diagnosis of  
CC bacterial diseases, as components of antibacterial vaccines, as targets  
CC for antibacterial drugs or as bio-control agents for plants. This  
CC sequence represents a Proteus mirabilis polypeptide of the invention.  
XX  
SQ Sequence 575 AA;

Query Match 3.2%; Score 84.5; DB 7; Length 575;  
Best Local Similarity 21.5%; Pred. No. 2.3e+02;  
Matches 98; Conservative 66; Mismatches 172; Indels 119; Gaps 22;

QY 50 VQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVAS--VDMGPQQLPDGQS 107  
Db 12 LSTLKETPA-DAEIVSHQLMLRAGMIRKLASGLYDWMPTGVRVLRKIEKIVREEMDNAGS 70  
QY 108 LPI--PPVILAEGLSDPTKGTVCFCYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATD 165  
Db 71 LEISMPVVQPADLWQE--SGRWEQYGPPELLRFTDRGE---RPFVL---GPTHEEVVTD 120  
QY 166 NKGVPVLAWINAVSAFRALEQDL-PVNIKFIIEGMEAEAGSVALEELVEKEKDRFFSGVDYI 224  
Db 121 -----IVRNEITSYKQLPLNLQIQTKFRDEVPRFGVMRSREFIMKDAYSFH----- 168  
QY 225 VISDNLWISORKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLV 284  
Db 169 -----ISOESLQETVDRMYQAYSNIFTRI-----GLDFRP---VLADTGSIG 207  
QY 285 DSSGH---ILVPGIYDEVVPLTEEEINTYKAIHLDLLEHY-----RNSSRVEKFLFDTKE 335  
Db 208 GSASHEFQVLADSGEDDIVFSTADY---AANIELAEAVMPATPRSPATEELRLVDT-- 261  
QY 336 EILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLE 395  
Db 262 -----PNAKTI-----AELVEQFNL-PIEKTVKTLI- 286  
QY 396 DVFSKRNSNKMVSMVMTLGLHPWIANIDDTQYLAAKR-----AIRTVFGTEPDMIR 446  
Db 287 -VHATEESGHKLVALLVRGDH-----ELNEIKAEKCSIVASPLVFATEEIRQAVNAG 338  
QY 447 DGSTIPIAKMFQEIIVHKSVVILIP---LGAVDDGEH 478  
Db 339 PGSLGPIINLPLPIIIDRAVSVMSDFGAGANIDGKH 373

RESULT 1231  
AAW27300

ID AAW27300 standard; protein; 586 AA.  
XX  
AC AAW27300;  
XX  
DT 22-APR-1998 (first entry)  
XX  
DE Bacillus sp. alpha-glucosidase.  
XX  
KW Bacillus sp; alpha-glucosidase; trehalose; variant; disaccharide;  
KW reduced affinity; purity.  
XX  
OS Bacillus sp.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 273 /note= "Modified at this position to any amino acid,  
FT preferably to Pro"  
XX  
PN JP09234081-A.  
XX  
PD 09-SEP-1997.  
XX  
PF 04-MAR-1996; 96JP-00084388.  
XX  
PR 04-MAR-1996; 96JP-00084388.  
XX (SUNR ) SUNTORY LTD.  
XX  
DR WPI; 1997-497322/46.  
DR N-PSDB; AAT91329.  
XX  
PT Modified alpha-glucosidase has Gly residue at position 273 replaced - to  
PT give enzyme with reduced affinity for trehalose, but not other  
PT di:saccharide(s), useful for producing high purity trehalose.  
XX  
PS Claim 2; Page 7-11; 15pp; Japanese.  
XX





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XX WPI; 2003-492172/46.
DR N-PSDB; ACA62946.
XX
XX New koji malt-derived glutaminase protein and gene useful in food
PT processing industry, especially in the manufacture of soy sauce or
PT seasonings.
XX
XX Claim 1; Page 7-9; 1lpp; English.
PS
XX
XX The present invention relates to the isolation of a koji malt-derived
CC glutaminase from Aspergillus sojae, and the polynucleotide sequence
CC encoding it. The glutaminase protein (or a sequence having a deletion,
CC substitution or addition of one or several amino acids), and the
CC polynucleotide sequence encoding it are useful in the food processing
CC industry, especially in the manufacture of soy sauce and seasonings. The
CC present sequence represents A. sojae glutaminase
XX
SQ Sequence 643 AA;

Query Match          3.2%; Score 84.5; DB 6; Length 643;
Best Local Similarity 18.6%; Pred. No. 2.8e+02;
Matches 82; Conservative 55; Mismatches 133; Indels 171; Gaps 16;

QY 1 MDPKLGMAASLLA---VLLLLRGMFSSPPPPALLEK-----VFQY 41
Db 104 IDSQLSNYASILKSSGTDVLLVDSEVHTASSDSTITAQLTKELPSGPYFVSLYTGVEFRA 163
QY 42 IDLHQDEFVQTLKEWVAIESDSVQVPRFRQE-----A 73
Db 164 YRLYPDDNLAFIQAGISDEKGGVLPDPAVTENAMTKDVAVPSRLYYTPTAEKPLAGRLG 223
QY 74 -----LFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPP 112
Db 224 VKDIYHVKLGKTSGSRSYYYLYGTQNTAPSIQRL-----LDLG-----A 264
QY 113 VILAEIGS-----DPTKGTVCFYCHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATD 165
Db 265 VFVGKTGTQVFANGDRPTADWVDFHCFPN-----QRGEGYQAP-----SGSSS 307
QY 166 NKGPVLA---WIN-AVSAFRALEQDLPVNIKFIIEGMEEGSVALEELVEKEKDRFFSGV 221
Db 308 GSGVAIAAYDWLDLAVGSDTGGSMRSPAAVQGIYGNRPSTGAISLDHVLPLSPALDTAGV 367
QY 222 DYIVISDNLW-----IS-ORKPAITYGTRGNS 247
Db 368 --FARSASLWSHTVQAWYPHQLQHNFTSFPRQLLLAGGGWDGKGISPEAHQSLTFTTRGLE 425
QY 248 YFM-----VEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVP 301
Db 426 AFLGNTHTNVDSQRWLDTHSPTTPSL--BEMLNLTATLTSVDQFNHLAVPLFAD---- 479
QY 302 LTEEEINTYKAIHLDLEEYRN 322
Db 480 -----YKAVHGRGQPFIN 492

RESULT 1234
ABU25261
ID ABU25261 standard; protein; 739 AA.
XX
AC ABU25261;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #10788.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Clostridium difficile.
XX
PN WO200277183-A2.
XX
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PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA29131.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 53185; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 739 AA;

Query Match          3.2%; Score 84.5; DB 6; Length 739;
Best Local Similarity 19.6%; Pred. No. 3.4e+02;
Matches 104; Conservative 96; Mismatches 182; Indels 149; Gaps 28;

QY 48 EFVQTLKEWV-----AIESDSVQPV-PRFRQELFRMMAVAADTLQRLGARVAS--VD- 96
Db 45 ESIEVEGKWNHKKIYGTQFEVNSFMFVTPSSLEGY--VYLSSGMTHGIGEKMAKRIIDK 102
QY 97 MGPPQLPDGQSLPIPPVILAEIGSDPTKGTVCFY-----GHLDVQPADRGDGLWLTDPYV 150
Db 103 FGVDLTLEVIQNSPEKQLQEVGEGIGSKVKQIVKSYEEDRELNRNIILQSPFG---ITPNYC 159
QY 151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEGSVALEELV 210
Db 160 L-----KIYKYKS-----SAIEVINKPNPYQLAEDIRGI--GFKVADSIASKIGI 202
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Db 327 ---NRLIQAGRSKHLLEVSEAYIATGVEDYLSLIQAKRAIEGKLERIKPYENALDV 383  
QY 171 LAW-----INAVSAFRALEQDLVP-NIKF-----IIEGMEEGAGSVALBELVEKE 213  
Db 384 LAHFIVGLLIEYQKLVNHEPYRMAKETYPYRNKWEHYLEVINVLEDAGIIRBEGILKL 443  
QY 214 KDRFF-----SGVDYIVIS-----DNLWISQRKPAITYGTRGNSYFMVE 252  
Db 444 GRRAPKYFDNLSTIPDEVSQKVDIGSGKVGIRLDENFVMDLEEGMEFIMHGRSWLVLE 503  
QY 253 -----VKCRDQDFHSGTFGG-----ILHEPM----- 273  
Db 504 IDGENLIQVRESENIEGAIPSWEGELIPVPEVAREVGRRLRRTLLYDPRKAPDLIKGVE 563  
QY 274 ---ADVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRN---SSRVE 327  
Db 564 FNGEELELALNSLKQNT---LIPSDRDIIITVLPDITV---IIHSDLGKNVNEGISRIL 616  
QY 328 KFLFDTKKEILMHLWRYPYSLSIHG-----IEGAFDEPGTKTIVIPGRVIGKFSIRLV 378  
Db 617 GFLYSKYGRVFTAKSQAHSIHAPFKMNPNEVKEILLKDYDTKTII-SKTIRDSTVYRW 675  
QY 379 PHMNVS---AVEKQV-TRHLEDVFSKRNSSNMVSMVLG--LHPW--IANIDDTQYLA 429  
Db 676 KMINVAKRMGALSRRARIRNVQKLF-----EGTIEVETLNEVFHDKVDVQKVEEVLKLI 730  
QY 430 AKRAIRTVFG---TEPDMI-RDGSTI-----PIAKMF-QEIVHKSVVLIPLG 471  
Db 731 AKGEIR-ITGRILNEPEIDKEHGTISMFEFVMSLHHTDEEIVELFKQIRIMSSIVMCTN 789  
QY 472 AVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 790 CGFSWETKVGVRVNRVRELECPKCGS---IMLAPLH 822

RESULT 1238  
ADN20063  
ID ADN20063 standard; protein; 1014 AA.  
AC ADN20063;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #2716.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
XX US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
XX 20-FEB-2003; 2003US-00369493.  
PF  
XX 21-FEB-2002; 2002US-0360039P.  
XX  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
DR  
XX

PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 2716; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 1014 AA;

Query Match 3.2%; Score 84.5; DB 8; Length 1014;  
Best Local Similarity 19.0%; Pred. No. 5.6e+02;  
Matches 91; Conservative 57; Mismatches 139; Indels 191; Gaps 21;  
QY 26 SSPSPPPALLEKVFQYIDLHQ--DEFVQTLKEWVAIESDSVQVPRFRQELFRMMVAAD 83  
Db 119 TKFPSPPELLARVKTHLELKQTRDNLHHTLLEQA-----RTAEALAC 160  
QY 84 TLQRLGARVASVDMGPPQLPDGQ-----SLPIPPVILAEIGSDPTKGTVCVF 129  
Db 161 TSTRLGILVQNMQAG-VLMTDAQGTVVNVNPEFARLNLGFPADLL--LGKNLTA----- 212  
QY 130 YGHLDVQPADRGDGLWTDYPVLTEVDGKL-YGRGATDNKGPVLAWINAVSAFRALEQDLF 188  
Db 213 -----IAPRINGLISHGQGVTHN-----FLAIESPEP 239  
QY 189 VNIKFIIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVI-----SDNLW-----ISQRKPA 238  
Db 240 L-----LKVELALEDGRRFFER-DYVPIMLGDSQGHFWLYRDISQRKQV 282  
QY 239 ITYGTRGNSYFM-----VEVKCRDQDFHSGTGGILHEPMDLV 277  
Db 283 EM--IQQSLEMERMRQQLAEQNQELVAATTAEEAANRSKSEFLATMSHEIRTPMNAII 340  
QY 278 ALLGSLVD-----SSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEY-- 320  
Db 341 GMTGLLLDLDLTQOKYFAQTIRNSGETLLTLINDIL-----DFSKEIAGKLDLEVYFF 394  
QY 321 -----RNSRVEKFLFDTKKEILMHLWRYPYSLSIHGIEGAFDEPGT 361  
Db 395 DLGQCLEEALDVVVP SARQKSLTLIRRLFTPIPPNLQGDVTRLRLQILVNLLSNA-----V 449  
QY 362 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLED-----VFSKRNSS 404  
Db 450 KFTAGQV--KTVVEVVDH-DAAKGEYQICFAVQDTGIGIAPNQOQALFQAFSQGNSS 504  
RESULT 1239  
ABM83554  
ID ABM83554 standard; protein; 1198 AA.





CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 1207 AA;

Query Match 3.2%; Score 84.5; DB 8; Length 1207;  
Best Local Similarity 21.5%; Pred. No. 7.4e+02;  
Matches 114; Conservative 69; Mismatches 180; Indels 167; Gaps 29;

QY 34 LLEKV-----FQYIDLHQDEFVQTLKEWVAIESDSVQVPV-RF----- 70  
Db 505 LLEKIPEDAATVVLVGCVPFLEQPAAAFVR-LNEAVLLESVLEVPVPRFLFVMLGPSH 563  
QY 71 -----RQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVI 114  
Db 564 TSTDYHELGRSIATLMSDKLFHEAAYQADRDQLLSAIS-----EFLDG-SIVIPP-- 613  
QY 115 LAEL-GSDPTKGTVCFYGHLDVQPADRGD-----GWLTDPPYVLTEVDGKLYGRGATD 165  
Db 614 -SEVEGRDLLRSVAAFQRELLRKRREOTKVEMTTRGGYTAPG--KELSLELGGSEATP 670  
QY 166 NKG PVLAWINAVSAFRALEQDL-----PVNIKFIIEGMEEGSV-----ALEELVE-- 211  
Db 671 EDDPLL--RTGSVFGGLVRDVRRRYPHYPSDLRDALHSQCVAAVLFYFAALSPAITFG 727  
QY 212 ---KEKDRFFSGVDYIVISDNLW-----ISQRKPAITYGTRG-----NSYFMVEVKCRD 257  
Db 728 GLLGEKTEGLMGVSELIVSTAVLGVLFSLGAPQLLVVGFSGPLLVFEEAFFKF---CRA 784  
QY 258 QDFHSGT---FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAIH 314  
Db 785 QDLEYLTGRVWVGLW-----LVVFVLALVAEGSFLV---RYISPFTQEIF---AFL 830  
QY 315 LDLEEYRNSRVEKFLFDTKBEILMHLWRYPSSLTHGIEGAFDEPGTKTIVPGRVIGKFS 374  
Db 831 ISL-----IFIYETFYKLYKVFTFHEPLLPFPYEPGALE-----GSLD 867  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVMSMTLGLHP-----WIANIDDTQYLA 429  
Db 868 AGLEP--NGSALPP-----TEGPPSPRNQPNNTALLSLMLGTFFIAFFLRKFRNSRFLG 920  
QY 430 AK-RAIRTVFGTEPDMIRDCGSTIPIAKMFQEIYVHKS-----VLIPLG 471  
Db 921 GKARRIIGDFG-----IPISILVMVLVDYSITDITYTQKLTVP TG 959

RESULT 1241  
ABM83552

ID ABM83552 standard; protein; 1225 AA.

XX

AC ABM83552;

XX 18-NOV-2004 (first entry)

DT Human diagnostic and therapeutic pprotein SEQ ID NO:3801.

DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

XX

PN

XX WO2004023973-A2.

PD 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN42204.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 1225 AA;

Query Match 3.2%; Score 84.5; DB 8; Length 1225;  
Best Local Similarity 21.5%; Pred. No. 7.5e+02;  
Matches 114; Conservative 69; Mismatches 180; Indels 167; Gaps 29;

QY 34 LLEKV-----FQYIDLHQDEFVQTLKEWVAIESDSVQVPV-RF----- 70

Db 532 LLEKIPEDAATVVLVGCVPFLEQPAAAFVR-LNEAVLLESVLEVPVPRFLFVMLGPSH 590

QY 71 -----RQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVI 114

Db 591 TSTDYHELGRSIATLMSDKLFHEAAYQADRDQLLSAIS-----EFLDG-SIVIPP-- 640

QY 115 LAEL-GSDPTKGTVCFYGHLDVQPADRGD-----GWLTDPPYVLTEVDGKLYGRGATD 165

Db 641 -SEVEGRDLLRSVAAFQRELLRKRREOTKVEMTTRGGYTAPG--KELSLELGGSEATP 697

QY 166 NKG PVLAWINAVSAFRALEQDL-----PVNIKFIIEGMEEGSV-----ALEELVE-- 211

Db 698 EDDPLL--RTGSVFGGLVRDVRRRYPHYPSDLRDALHSQCVAAVLFYFAALSPAITFG 754

QY 212 ---KEKDRFFSGVDYIVISDNLW-----ISQRKPAITYGTRG-----NSYFMVEVKCRD 257

Db 755 GLLGEKTEGLMGVSELIVSTAVLGVLFSLGAPQLLVVGFSGPLLVFEEAFFKF---CRA 811

Qy 258 QDFHSGT---FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIH 314  
Db 812 QDLEYLTGRVWVGLW-----LVVFVLALVAEGSFLV-----RYISPFTQEIF-----AFL 857  
Qy 315 LDLEEYRNSRVEKFLDFTKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 858 ISL-----IFIYETFYKLYKVFTTEHPLLPFFYPPEGALB-----GSLD 894  
Qy 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHP-----WIANIDDTQYLA 429  
Db 895 AGLEP--NGSALPP-----TEGPPSPRNQPNNTALLSLILMLGTFFFIAFFLRKFRNSRFLG 947  
Qy 430 AK-RAIRTVFGTEPDMIRDSGTIPAKMFQEIYVHKS-----VLIPLG 471  
Db 948 GKARRIIGDFG-----IPISILVMVLVDYSITDTYTKLTVPPTG 986

RESULT 1242  
ABM83551  
ID ABM83551 standard; protein; 1234 AA.  
XX  
AC ABM83551;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3800.  
XX  
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX  
OS Homo sapiens.  
XX  
PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
XX  
PR 12-SEP-2002; 2002US-0410259P.  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;  
XX  
DR WPI; 2004-329368/30.  
DR N-PSDB; ACN42203.

XX  
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
XX  
SQ Sequence 1234 AA;  
Query Match 3.2%; Score 84.5; DB 8; Length 1234;  
Best Local Similarity 21.5%; Pred. No. 7.6e+02;  
Matches 114; Conservative 69; Mismatches 180; Indels 167; Gaps 29;  
Qy 34 LLEKV-----FOYIDLHQDEFVQTLKWEVAIESDSVQVPV-RF----- 70  
Db 532 LLEKIPEDAEATVVLVGCVPFLEQPAAFVR-LNEAVLLESVLEVPVVRFLFVMLGSPH 590  
Qy 71 -----RQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVI 114  
Db 591 TSTDYHELGRSIATLMSDKLFHEAAYQADDRQDLLSAIS-----EFLDG-SIVIPP-- 640  
Qy 115 LAEL-GSDPTKGTVCFYGHLDVQPADRGD-----GWLTPPYVLTEVDGKLYGRGATD 165  
Db 641 -SEVEGRDLLRSVAAFQRELLRKRREERQTKVEMTRGGYTAPG--KELSLELGGSEATP 697  
Qy 166 NKGPVLAWINAVSAFRALEQDL-----PVNIKFIEGMEEAGSV-----ALEELVE-- 211  
Db 698 EDDPLL--RTGSVFGGLVRDVRRRYPHYPSDLRDALHSQCVAALFIYFAALSPAITFG 754  
Qy 212 ---KEKDRFFSGVDYIVISDNLW-----ISQRKPAITYGTRG-----NSYFMVEVKCRD 257  
Db 755 GLLGEKTEGLMGVSELIVSTAVLGVLFSLGGAQPLLVVFGSGPLLVFEEAFFKF---CRA 811  
Qy 258 QDFHSGT---FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIH 314  
Db 812 QDLEYLTGRVWVGLW-----LVVFVLALVAEGSFLV-----RYISPFTQEIF---AFL 857  
Qy 315 LDLEEYRNSRVEKFLDFTKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 858 ISL-----IFIYETFYKLYKVFTTEHPLLPFFYPPEGALB-----GSLD 894  
Qy 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHP-----WIANIDDTQYLA 429  
Db 895 AGLEP--NGSALPP-----TEGPPSPRNQPNNTALLSLILMLGTFFFIAFFLRKFRNSRFLG 947  
Qy 430 AK-RAIRTVFGTEPDMIRDSGTIPAKMFQEIYVHKS-----VLIPLG 471  
Db 948 GKARRIIGDFG-----IPISILVMVLVDYSITDTYTKLTVPPTG 986  
RESULT 1243  
ADJ70768  
ID ADJ70768 standard; protein; 1259 AA.  
XX  
AC ADJ70768;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human heat mitochondrial protein as a therapeutic target SeqID2574.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003087768-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX  
DR WPI; 2003-845369/78.  
XX  
XX Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX  
PS Claim 1; SEQ ID NO 2574; 180pp; English.  
XX  
CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytosstatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 1259 AA;  
  
Query Match 3.2%; Score 84.5; DB 7; Length 1259;  
Best Local Similarity 21.5%; Pred. No. 7.9e+02;  
Matches 114; Conservative 69; Mismatches 180; Indels 167; Gaps 29;  
  
QY 34 LLEKV-----FQYIDLHQDEFVQTLKEWVAIESDSVQVP-RF----- 70  
Db 532 LLEKIPEDAEATVVLGCVPFLEQPAAFVR-LNEAVLLESVLEVPVPRFLFVMLGPSH 590  
QY 71 -----RQELFRMMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVI 114  
Db 591 TSTDYHELGRSIATLMSDKLFHEAAQQADDRQDLLSAIS-----EFLDG-SIVIPP-- 640  
  
QY 115 LAEL-GSDPTKGTVCYGHLDVQPADRGD-----GWLTDYVLTVEVDGKLYGRGATD 165  
Db 641 -SEVEGRDLLRSVAAFQRELLRKRREEQTKVMTTRGGYTAPG--KELSLELGGSEATP 697  
  
QY 166 NKGPVLAWINAVSAFRALEQDL-----PVNIKFIIEGMEEGAGSV-----ALEELVE-- 211  
Db 698 EDDPLL--RTGSVFGGLVRDVRRRYPHPYPSDLRDLALHSQCVAALFIYPAALSPAITFG 754  
  
QY 212 ---KEKDRFFSGVDYIVISDNLW-----ISQRKPAITYGTRG-----NSYFMVEVKCRD 257  
Db 755 GLLGKTEGLMGVSELIVSTAVLGVLFSLLGAQLLVVGFSGPLLVFEEAFFKF---CRA 811  
  
QY 258 QDFHSGT---FGGILHEPMADLVALLGSLVDSSSHILVPGIYDEVVPLTEEEINTYKAIH 314  
Db 812 QDLEYLTGRVWVGLW-----LVVFLVALVAEGSFLV---RYISPTQEIPF---AFL 857  
  
QY 315 LDLEEYRNSRVEKFLDFTKEEILMHLWRYPSPSLSIHGIEGAFDEPGTKTIPGRVIGKFS 374  
Db 858 ISL-----IFYETFYKLYKVFTTEHPLLPFPYPPGEGALE-----GSLD 894  
  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHP-----WIANIDDTQYLA 429  
Db 895 AGLEP--NGSALPP-----TEGPPSPRNQPNNTALLSLMLGTFFIAFLRKRFRNSRFLG. 947

QY 430 AK-RAIRTVFGTEPDMIRDGSTIPIAKMFQEIYHKS-----VLIPLG 471  
Db 948 GKARRIIGDFG-----IPISILVMVLVDYSITDTYTKLTVPTG 986  
  
RESULT 1244  
ABO62323  
ID ABO62323 standard; protein; 1259 AA.  
XX  
AC ABO62323;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Klebsiella pneumoniae polypeptide seqid 8840.  
XX  
KW Recombinant expression vector; transcription regulatory element;  
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.  
XX  
OS Klebsiella pneumoniae.  
XX  
PN US6610836-B1.  
XX  
PD 26-AUG-2003.  
XX  
PF 27-JAN-2000; 2000US-00489039.  
PR 29-JAN-1999; 99US-0117747P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton GL, Osborne M;  
XX  
DR WPI; 2003-895346/82.  
DR N-PSDB; ACH95874.  
XX  
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
PS Disclosure; SEQ ID NO 8840; 932pp; English.  
XX  
CC The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention  
XX  
SQ Sequence 1259 AA;  
  
Query Match 3.2%; Score 84.5; DB 7; Length 1259;  
Best Local Similarity 20.6%; Pred. No. 7.9e+02;  
Matches 93; Conservative 55; Mismatches 150; Indels 153; Gaps 21;  
  
QY 67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEGLSDPTKGT 126  
Db 235 IQAFRGEQLRLTGDTDITVYNLLKVSII-----DQG-----MKLDALDIDSDQ GK 280  
  
QY 127 VCFYGHLDVQPADRGD GW-----LTDYVLTVEVDGKLYG-----RGATDNKGPV 170  
Db 281 VSASGSAQLQ-----DNWPVDITLAGTLNVDPMKGEKVQLKVGGEVRLTKVGVDSLGPV 335  
  
QY 171 LAWINAVSAFRALEQDLPVNIKFIIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNL 230  
Db 336 VATLRADA--QLAEAGLPLNM-----ELKSKQLAWPFSGEKQFQADD-- 375  
  
QY 231 WISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSSH 290  
Db 376 -----VQLK-----FSG-----KMTDYALAFSTAV--KGQS 399  
  
QY 291 LVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSRVE-KFLFDFTKEEILMHLWRYP SLSI 349



Db 400 LPSAKIDLNAKGNERQINLDKLTVNALE-----GKTELKALLDWQQAII---SWR-GELTL 450  
Qy 350 HGIEGAPDEPGTKTVIPGRVIGKFSI-----RLVPHMNVSAVEKQVTRHLEDVFSKRNS 403  
Db 451 DGINTAKEVPDWPCKLNGRIKTOGSLYGGSWQMSVPELKITGNVKQ----- 496  
Qy 404 SNKMVVSMTL-----GLHPWIA-----NID---DTQYLAAKRAI 434  
Db 497 -NKVDVAGSLQGNLSYLQWKIPGLHLALGPNASADIKGELGVKDLNLDATIDAPHL--DNAL 553  
Qy 435 RTVFGTEPDMIRDSGTIPIAKMFQEIHKSV 465  
Db 554 PGLGGTAKGLVKVRGTVDAPQLLADITARAL 584

RESULT 1245  
ABB48622  
ID ABB48622 standard; protein; 1444 AA.

XX ABB48622;

XX 05-FEB-2002 (first entry)

DE Listeria monocytogenes protein #1326.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;  
KW vitamin B12; bacterial infection; disease.

XX Listeria monocytogenes.

XX WO200177335-A2.

PD 18-OCT-2001.

XX 11-APR-2001; 2001WO-FR001118.

PR 11-APR-2000; 2000FR-00004629.

XX (INSP ) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Psihi H, Dehoux P;  
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;  
PI Daniels J, Goebel W, Krefte J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;  
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;

XX WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related  
PT polypeptides.

PS Claim 6; SEQ ID NO 1327; 192pp; French.

XX The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present invention is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccines compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1444 AA;

Query Match 3.2%; Score 84.5; DB 5; Length 1444;  
Best Local Similarity 18.2%; Pred. No. 9.7e+02;  
Matches 96; Conservative 94; Mismatches 181; Indels 157; Gaps 29;

Qy 35 LEKVQYIDLHQDEFVQTL-----KEWVAIESDSVQPVPR-FRQELFRMMAVAADTLQR 87  
Db 21 LQDVTTYEEFTKAKIEKLVADKKNTW-----QFHLHVPQIFPAALFHMMDVG---MKR 72

Qy 88 LGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFFYGLHDVQPADRGDWLTD 147  
Db 73 AFSQIAETEM--QIVPENQTI-----NETLIQDYWNLIVEPIGK-----QS 111

Qy 148 PYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL---PVNIKF---IIEGMEEA 201  
Db 112 PMI-----GKLLMEQKPTFKEPHFIEV-----AVHNDMEEATIOQRFQTKIIESYGKA 159

Qy 202 G-----SVALEELVEKEKDRF--FSGV-----DYIVISDNLWISQKPAITYGTRGNSY--- 248  
Db 160 GPPRLAMKMMLDQSETDEYKAFQAQAKQEEDQKKAABAVQVMQXRAEQSGGGGAAPLT 219

Qy 249 --FMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTE-E 305  
Db 220 GPFQIGYKIKDD-----EEVKRLGDIYDEERRITVQGL-----IFATEIR 259

Qy 306 EINTYKA-IHLDLEEYRNSRVEKFLFDTKEEILMH-----LWRYPSLSIHGIEGAFDEP 359  
Db 260 ELRSGRSLLOFKITDYTSSMIKMFSDNEDAAMFQNLKKGWV---VKVRG----- 307

Qy 360 GTKTVIPGRVIGKFSIRLVPHMNV-----SAVEKQVTRHLEDVFSKRNSNKM--- 407  
Db 308 ----SVQNDTFVRDLIMMAQDVNEIAGVKRLDTAEKRAELHLHSPMSQMDATSSVDSLIF 363

Qy 408 -----VVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTIPIAKMFQ 458  
Db 364 KQAADWGHKAIAIT--DHSVAQSFPPEAYGAGQKYGLKVIFGIEANLIDDG--VPIAYNDQ 419

Qy 459 EIVHKSVVLIPLGAVDGDGHSQNEKINRWNYIEGTKLEAAF--FLEMA 504  
Db 420 HI-----ALEDATYCVFD-----VETTGLSAVYDTIIELA 449

RESULT 1246  
ABU33053

ID ABU33053 standard; protein; 1444 AA.

XX AC ABU33053;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #18580.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Listeria monocytogenes.

PN WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US0009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.  
PA (ELIT-) ELITRA PHARM INC.



QY 92 VASVDMGPOQLPDGQSLPIPPVILAEIGSDPTKGTVCFYGHL---DV-----QPAD 139  
Db 153 VAEVELGKKFLKSCNR-----CLSGEDNTLYATNDFGHLLSVDVACFALKPQWQPTS 205  
QY 140 RGDGWLTPVVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGME 199  
Db 206 ESDS-----VTEMEKMPRSHGLTYHKSGLIW-NSTTAYYVKKAGVFKLEWEFEG-- 255  
QY 200 EAGSVALEELVEKEKDRFFSG-----VDYIVISDNLWISQR-----KPAIT 240  
Db 256 -----RLNEVV-----RFLSNNNGEITYAERRRPGHIDQVVVDRNGTVSLEAVVPTGKPVIT 305  
QY 241 YG-----TRGNSYFMVEV-----KCRDQDFH---SGTFGG-- 267  
Db 306 FRVVOGLKDECVVLHDEGVAMMDLAKGNTLCEVSVPGATAMCNHRSLALVVVGTLDASI 365  
QY 268 -ILHEPMDLVALGSL-----VDSSGHILVPGIY 296  
Db 366 VLIHFERASLPHVLCDLKMETAAVVVGIEFNDSWVVFQDMKVLHVQVDNRPHKLTH--Y 423  
QY 297 DEVVP--LTJEEINTYKA-----IHLDLLEYRNSRVEKELFDTKEEILMHLWRYP 345  
Db 424 FEMNPPELSQVFIHTFLLADGPRLMVFENRDHSMKRPFGFATELWLYNWGDKRLHRRREYI 483  
QY 346 SLSIHGI-----EGAFDEPGTKTVIPGRVIGKFSIRLVP 379  
Db 484 LPKQYGFQCPVPVGRWALIEIVATEYNTLNFQDFALNEKDELOQWIASTKSGHFSYILGA 543  
QY 380 HMNVSAVEKQVTRHLED-----VFSKRNSNK---MVVS-MTLGLH-PWIANIDD--- 424  
Db 544 GM-----TKHLVTSWLGILVHFQKHAKKPFMICRFLNLGMQTEYILRVKECFN 594  
QY 425 TOY---LAAKRAIRTV-FGTEPDMIRDGSTIP-----IAKMFQIIVHKSVVLIPLGAVD 474  
Db 595 SKYLIILLANKSMRVMLPSLADFVRBNVALPLPTEEGIPCFVBEQIIHKVDMFVPLSQ-- 652  
QY 475 DGEHSQNEKINRWNYIEGTLKF 496  
Db 653 --RQEVKEEYTRADLAKREKLF 672

RESULT 1248  
AAE18271  
ID AAE18271 standard; protein; 1812 AA.  
XX  
AC AAE18271;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Protein encoded by Bugula neritina PKS cluster from clone 3A.  
XX  
KW Polyketide; bryopyran ring; byrostatin; breast cancer; anticancer;  
KW antifungal; antimicrobial; immunomodulatory; polyketide synthase; enzyme;  
KW PKS.  
XX  
OS Bugula neritina.  
XX  
PN WO200111024-A2.  
XX  
PD 15-FEB-2001.  
XX  
PF 04-AUG-2000; 2000WO-US021326.  
XX  
PR 04-AUG-1999; 99US-0147283P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Haygood M, Davidson SK, Allen SW, Hildebrand M;  
XX  
DR WPI; 2002-154285/20.  
DR N-PSDB; AAD28999.  
XX  
PT Composition comprising a polypeptide isolated from marine organism, which

PT catalyzes at least one step in synthesis of polyketide/bryopyran ring,  
PT useful for producing polyketide or bryopyran ring containing  
PT compositions.  
XX  
PS Claim 65; Fig 14B; 233pp; English.  
XX  
CC The invention relates to compositions comprising nucleic acid molecules  
CC encoding a polypeptide which catalyzes at least one step in synthesis of  
CC polyketides including bryopyran ring, such as byrostatin. These novel  
CC sequences are derived from marine organisms. Compositions containing  
CC sequences of the invention are useful for producing base structure,  
CC bryopyran rings that can form the basis of combinatorial chemistry to  
CC form a wide variety of compounds which can be screened for bioactivities  
CC including anticancer activity. The cloned genes and linked genes involved  
CC in byrostatin synthesis can be used to screen environmental samples for  
CC polyketide synthase (PKS) genes. They are also used for combinatorial  
CC creation of novel polyketide/byrostatin analogues that may exhibit  
CC improved anti-cancer properties. Compositions of the invention are useful  
CC for producing byrostatin and its analogues which are useful for treating  
CC breast cancer and as anticancer, antifungal antimicrobial and  
CC immunomodulatory compounds. They are useful for producing novel  
CC polyketides such as bryopyran rings including byrostatin. The present  
CC sequence is a protein encoded by Bugula neritina PKS cluster from clone  
CC 3A  
XX  
SQ Sequence 1812 AA;  
Query Match 3.2%; Score 84.5; DB 5; Length 1812;  
Best Local Similarity 21.1%; Pred. No. 1.4e+03;  
Matches 70; Conservative 44; Mismatches 110; Indels 107; Gaps 15;  
QY 8 MAASLLAVLLLLLGERGMFSSPPALLEKFQYID---LHQDEFVQT-----LKEWV 57  
Db 1366 LAANGLLIILNEFSQKSVFSS-----VIFGLIDGWLASEDTGLRIPGSPGLYPKQWQ 1416  
QY 58 AIESDS-----VQVPFRFRQELFRMMVAADTLQRLGARVAS--VDMGPQQLPD----- 104  
Db 1417 AVLEASGFGDVEFFPLHDARELGQQIILATNAHANVASDLATSVIDHAPKRLPSAEVSMDE 1476  
QY 105 -----GQSLPI-----PPVILAEIGSDPTKG----- 125  
Db 1477 RVSHDAMMKASVKQLLVEQLSQSLKLDMNEIHPDESFADYGVDSITGASFIQQLNDTLTL 1536  
QY 126 ---TVCFYGHLDVQP-----ADRGDG---WLTDPPVLTB-----VDGKLYGRGATDNKG 168  
Db 1537 TLKTVCLFDHSSVNRLLTAYLLSDYGDDIAQWLATAPALVDHPQSVSVQVLPERSPASTQA 1596  
QY 169 PVLAWINAVSAFRALEQDLPVNIKFI-IEGMEEAGSVALBELVEKEKDRFFSGVDYIVIS 227  
Db 1597 KPLP-----SVPPSLSMESPQQESIAIIGM--SGRFAASENLEAFWQQLAQGVDLV--- 1646  
QY 228 DNLWISQRKPAITYGTRGNSYFMVEVKCRDQ 258  
Db 1647 -----EPASRWGPQAEITYGSLKDMQDQ 1669  
RESULT 1249  
ADN96825  
ID ADN96825 standard; protein; 1812 AA.  
XX  
AC ADN96825;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Bugula neritina polyketide synthase cluster protein (clone 3A) SeqID 38.  
KW degenerate; polyketide; bryopyran ring; byrostatin; polyketide synthase;  
KW PKS; toxic; cytostatic; immunomodulatory; protein therapy; cancer;  
KW metastatis.  
XX  
OS Bugula neritina.  
XX  
PN WO2003099219-A2.



XX PD 04-DEC-2003.  
XX PF 20-MAY-2003; 2003WO-US016299.  
XX PR 20-MAY-2002; 2002US-0382181P.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PA (HAYG/) HAYGOOD M.  
XX PA (HILD/) HILDEBRAND M.  
XX PA (ANDE/) ANDERSON C.  
XX PA (WAGG/) WAGGONER L E.  
XX PA (SHER/) SHERMAN D H.  
XX PA (LIUH/) LIU H.  
XX PI Haygood M, Hildebrand M, Anderson C, Waggoner LE, Sherman DH;  
XX PI Liu H;  
XX DR WPI; 2004-053143/05.  
XX DR N-PSDB; ADN96816.  
XX PT New compositions comprising a polyketide synthase or nucleic acid  
XX PT encoding the polyketetic synthase, useful in biosynthesizing polyketides,  
XX PT bryopyran rings and bryostatins having anti-cancer or antimetastatic  
XX PT activity.  
XX PS Example 4; SEQ ID NO 38; 342pp; English.  
XX CC This invention relates to a novel composition that comprises at least one  
XX CC polypeptide that catalyses the one step synthesis of a polyketide or  
XX CC bryopyran ring. Specifically, it refers to nucleic acid molecules derived  
XX CC from marine organisms that encode enzymes that catalyse the synthesis of  
XX CC bioactive compounds such as polyketides and bryostatins that are based on  
XX CC the bryopyran ring structure. The present invention describes methods for  
XX CC the use of polyketide synthases (PKSs) to generate toxic polyketides that  
XX CC exhibit cytostatic and immunomodulatory activities, such that they can be  
XX CC used for protein therapy in the treatment of cancer and metastasis. This  
XX CC polypeptide is a Bugula neritina PKS protein sequence (also given in fig  
XX CC 14b) of the invention.  
XX SQ Sequence 1812 AA;  
Query Match 3.2%; Score 84.5; DB 8; Length 1812;  
Best Local Similarity 21.1%; Pred. No. 1.4e+03;  
Matches 70; Conservative 44; Mismatches 110; Indels 107; Gaps 15;  
QY 8 MAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYID---LHQDEFVQT-----LKEWV 57  
Db 1366 LAANGLLIILNEFSQKSVFSS-----VIFGLIDGWALSEDTLRIPGSPGLYPKQWQ 1416  
QY 58 AIESDS----VQPVPRFRQELFRMMVAADTLQRLGARVAS--VDMGPQQLPD----- 104  
Db 1417 AVLEASGFGDVEFPLHDARELGQQIILATNAHANVASDLATSVIDHAPKRLPSAEVSMDE 1476  
QY 105 -----GQSLPI-----PPVILAEELGSDPTKG----- 125  
Db 1477 RVSHDAMMKASVKQLLVEQLSLSKLDMNEIHPDESADYGVDSTITGASFIOQLNDTLTL 1536  
QY 126 ---TVCFYGHLDVQP-----ADRGDG---WLTDPYVLTE-----VDGKLYGRGATDNKG 168  
Db 1537 TLKTVCLFDHSSVNRLTFAYLLSDYGDIDIAQWLATAPALVDHPQSVSVQLPERSPASTQA 1596  
QY 169 PVLAWINAVSAFRALEQDLFPVNIKFI-IEGMEEAGSVALEELVEKEKDRFFSGVDYIVIS 227  
Db 1597 KP LP-----SVPPSLSMESVQQESIAIIGM--SGRFAASENLEAFWQQLAQGVDLV--- 1646  
QY 228 DNLWISQRKPAITYGTRGNSYFMVEVKCRDQ 258  
Db 1647 -----EPASRWGPQAEITYGSLKMDMQ 1669  
RESULT 1250  
ADJ70511

ID XX ADJ70511 standard; protein; 2021 AA.  
AC XX ADJ70511;  
DT XX 06-MAY-2004 (first entry)  
XX DE Human heat mitochondrial protein as a therapeutic target SeqID2317.  
XX KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX OS Homo sapiens.  
XX PN WO2003087768-A2.  
XX PD 23-OCT-2003.  
XX PF 04-APR-2003; 2003WO-US010870.  
XX PR 12-APR-2002; 2002US-0372843P.  
XX PR 17-JUN-2002; 2002US-0389987P.  
XX PR 20-SEP-2002; 2002US-0412418P.  
XX PA (MITO-) MITOKOR.  
XX PA (BUCK-) BUCK INST AGE RES.  
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX DR WPI; 2003-845369/78.  
XX PT Identifying a mitochondrial target for drug screening assays and for  
XX PT treating diseases associated with altered mitochondrial function,  
XX PT comprises detecting a modified polypeptide in a sample and correlating  
XX PT with the disease.  
PS Claim 1; SEQ ID NO 2317; 180pp; English.  
XX CC This invention relates to novel mitochondrial targets that can be used  
XX CC for therapeutic intervention in treating a disease associated with  
XX CC altered mitochondrial function. Specifically, it refers to a method for  
XX CC identifying proteins of the human heart mitochondrial proteome that are  
XX CC useful for drug screening assays, as well as therapeutic targets. The  
XX CC present invention describes a method for identifying such proteins that  
XX CC can be used in the treatment of various diseases associated with altered  
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,  
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
XX CC compositions have neuroprotective, nootropic, antidiabetic,  
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
XX CC cytotatic activities. This polypeptide sequence is a human heart  
XX CC mitochondrial protein of the invention.  
XX SQ Sequence 2021 AA;  
Query Match 3.2%; Score 84.5; DB 7; Length 2021;  
Best Local Similarity 22.8%; Pred. No. 1.6e+03;  
Matches 66; Conservative 39; Mismatches 105; Indels 79; Gaps 15;  
QY 268 ILHEPMADLVALLGSLVDSS-----GHILVPGIYDEWVPLTEEEINT----YKAHLD 316  
Db 28 VRNEANVDLASVDSITDPKPRLRDFGHLFRKTVADSNAPVQEKALDALIAFLRAADSD 87  
QY 317 LEEY-----RNS-----SRVEKFLFDTKKEILMHLWR--- 343  
Db 88 AGRYAKEVCDALXCLTGRKNTVDKAQAFLLWVELEAVDVF-LDTMEKAIKNKVAKAV 146







KW immune; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003072827-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 31-OCT-2002; 2002WO-US035433.  
XX  
PR 31-OCT-2001; 2001US-0336220P.  
XX  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX  
PI Hirsch R, Thornton SL;  
XX  
XX WPI; 2003-712740/67.  
DR GENBANK; NP\_003913.  
XX  
PT Diagnosing and analyzing autoimmune disease using gene expression  
PT profiles and microarray technology, useful for diagnosing and treating  
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
PT gout.  
XX  
PS Disclosure; Page; 56pp; English.  
XX  
CC The invention relates to a novel method for diagnosing and analysing  
CC autoimmune disease or arthritides. The method comprises obtaining a  
CC patient sample containing mRNA, analysing gene expression using the mRNA  
CC that results in a gene expression signature of the mRNA, and using that  
CC gene expression signature to diagnose or analyse the autoimmune disease  
CC or arthritides in the patient, where gene expression of at least 60% of  
CC the genes correlates with that of the gene signature. The invention  
CC further comprises: a treatment of rheumatoid arthritis; identification of  
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with collagen-  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritides, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This sequence represents a  
CC protein sequence relating to the genes used in the analysis and treatment  
CC of autoimmune diseases or arthritides. Note: This sequence is not shown  
CC in the specification. It has been supplied in an electronic format from  
CC WIPO.  
XX  
SQ Sequence 4861 AA;  
  
Query Match 3.2%; Score 84.5; DB 7; Length 4861;  
Best Local Similarity 19.9%; Pred. No. 6.4e+03;  
Matches 79; Conservative 57; Mismatches 150; Indels 111; Gaps 18;  
  
QY 152 TEVDGKLYGRGAT----DNKG----PVLAWI-NAVSAPRALEQDLPV---NIKFIIEGME 199  
Db 4463 TMVQGNYPQITVKRISTRGRKCKPIFVQIARQVVKLNASDLRLPSRAWKVLVGEAD 4522  
  
QY 200 EAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQD 259  
Db 4523 DAGGVFDDTITEMCQELETGIVDLLIPSN-----ATAEVGNRDRFLFNPSACLDEH 4575  
  
QY 260 FHSGTGGILHEPMADLVALLGSLVDSSGHI--LVPGIYDEV--VPLTEEEINTYKAIH 314  
Db 4576 LMQFKFLGI-----LMGVAIRTKKPLDLHLAPLVWKQLCCVPLTLE----- 4616  
  
QY 315 LDLEEYRNSRVEKFLDFTKEEILMLWRYPSLSIHGIEGAFDEPGTKTVIP----- 366

Db 4617 -DLEE-----VDLLYVQTLSIL-----HIEDSGITEESFHEMIPLDSFVGQS 4658  
QY 367 --GRVI-----GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Db 4659 ADGKMWPIIPGNSIPLTFNSRKEYVERAIEYRLHEM-----DRQVAAVREGM-SWIV 4710  
QY 421 NIDDTQYLAAKRAIRTVFCTPEPDMIRDGSTIPIAKMFQEIIVHKSVWLIPLGAVDD----- 475  
Db 4711 PVPLLSLLTAKQLEQMWCG-----MPEISVEVLKK---VVRVREVDQHQQLV 4754  
QY 476 -----GEHSQNEKINRWNYIEGTKLFAAFFLEMAQ 505  
Db 4755 QWFVHTLEEFSENEERVLEFMRVSGRSRLPANTADISQ 4791  
  
RESULT 1255  
ABB65885  
ID ABB65885 standard; protein; 4899 AA.  
XX  
AC ABB65885;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 24447.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
DR N-PSDB; ABL09988.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 24447; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 4899 AA;  
  
Query Match 3.2%; Score 84.5; DB 4; Length 4899;  
Best Local Similarity 19.5%; Pred. No. 6.5e+03;  
Matches 54; Conservative 45; Mismatches 99; Indels 79; Gaps 12;  
  
QY 270 HEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAI----- 313  
Db 3494 HSPFAAVDALTGGM--SGGANILP-----PLSAGPLSAFQSLTGSLSMSGSLSSSALP 3544



QY 261 HSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEY 320  
Db 157 NPP-----KEPMKD-----DITGE-----PLIRSDDNKALKIRLQAY 190  
QY 321 RNSRVEKFLDFTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 191 H-----TQTTPLIEYRK-----RGIHSAIDASQTPDVVFASILAAFS 228  
RESULT 1258  
ADJ69026  
ID ADJ69026 standard; protein; 232 AA.  
XX AC ADJ69026;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human heat mitochondrial protein as a therapeutic target SeqID832.  
XX KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX OS Homo sapiens.  
XX PN WO2003087768-A2.  
XX PD 23-OCT-2003.  
XX PF 04-APR-2003; 2003WO-US010870.  
XX PR 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX DR WPI; 2003-845369/78.  
XX PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX PS Claim 1; SEQ ID NO 832; 180pp; English.  
XX CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX SQ Sequence 232 AA;

Query Match

3.2%; Score 84; DB 7; Length 232;

Best Local Similarity 22.8%; Pred. No. 64;  
Matches 67; Conservative 40; Mismatches 105; Indels 82; Gaps 15;  
QY 94 SVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGT-----VCFYGHLDVQPADRGDG 143  
Db 4 SVPAAEPEYPKG-----IRAVLLGPPGAG--KGTQAPRLAENFCVCHLATGDMLRAMVASG 57  
QY 144 WLTDYPYLVTEVDGKLYGRGATDNKGPVLAWINAVSAF-RALEQDLPVNKFIEGNEEAG 202  
Db 58 -----SELGKKL-----KATMDAGKLVSDVMVVELIEKNLETPLCNK-GFLDGFPTV 105  
QY 203 SVA--LEELVEKEKDRFFSGVDYIVISDNLWISQKPKPAITYGTRGNSYFMVEVKCRDQDF 260  
Db 106 RQAEMLDDLMEKRKEKLDVIEF-SIPDSLLIRITGRLIHPKSGRSY-----HEEF 156  
QY 261 HSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEY 320  
Db 157 NPP-----KEPMKD-----DITGE-----PLIRSDDNKALKIRLQAY 190  
QY 321 RNSRVEKFLDFTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 191 H-----TQTTPLIEYRK-----RGIHSAIDASQTPDVVFASILAAFS 228  
RESULT 1259  
ADP56377  
ID ADP56377 standard; protein; 232 AA.  
XX AC ADP56377;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human PRO protein sequence SEQ ID NO:2353.  
XX KW human; PRO; immune related disease; inflammatory immune response;  
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;  
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;  
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
KW virucide; gene therapy.  
XX OS Homo sapiens.  
XX PN WO2004039956-A2.  
XX PD 13-MAY-2004.  
XX PF 28-OCT-2003; 2003WO-US034381.  
XX PR 29-OCT-2002; 2002US-0422472P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
PI Wood WI, Wu TD;  
XX DR WPI; 2004-376182/35.  
DR N-PSDB; ADP56376.  
XX New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
PT and treating an immune related disease, e.g. systemic lupus  
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
PT stimulating an immune response.  
XX PS Claim 1; SEQ ID NO 2353; 3009pp; English.  
XX CC The present invention describes an isolated PRO nucleic acid (I). Also  
CC described: (1) a vector comprising (I); (2) a host cell comprising the  
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
CC antibody which specifically binds to a polypeptide of (4); (7) a





XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
KW Borrelia cepacia.  
XX WO200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA23552.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 47606; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 319 AA;

Query Match  
Best Local Similarity 3.2%; Score 84; DB 6; Length 319;  
Matches 58; Conservative 23; Mismatches 96; Indels 98; Gaps 10;

QY 81 AADTL-----QRLGARVASVDMGPOQLPDGQSLPIPPPVILAEIGSDPTKGTVCFYGHLDV 135  
Db 70 ASDWLALQWKQLACAR---ADITVEQVAH-TGFPQKSVILTRGSDPAAGTVLGGHLD- 124

QY 136 QPADRGDGLTDPYVLTVEVDGKLYGR-----GATDNKGPVLAWINAVSAFPALEQDL 187  
Db 125 -----STVGRTTENTRSPGADDDASGIASLTEALRVLLANNYRP 163  
QY 188 PVNIKFIEGMEEGSVALEELVEK-----EKDRFFSGVDYIV 225  
Db 164 KRTIKFVGAAEEAGLLGSKAIKQFRTQNAVVGVLQDMTNYKGPDKDIYLI-TDVTN 222  
QY 226 ISDNLWISQRK----PAITYGTRGNSY-----FMVEVKCRDQDF----- 260  
Db 223 AAQNTYVKNLAATYLPDLAVGTSCGYACSDHASWNAQGYPASFPFEADQNDSPYIHTVN 282  
QY 261 -----HSGTFGGILHEPMADLVALLGSLV 284  
Db 283 DTLENSDRQANHALKFKLALAYAVDLGGLAGATV 317  
RESULT 1262  
ABU20860  
ID ABU20860 standard; protein; 339 AA.  
XX AC ABU20860;  
XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #6387.  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX KW Bacteroides fragilis.  
XX OS WO200277183-A2.  
XX PN 03-OCT-2002.  
XX PD 21-MAR-2002; 2002WO-US009107.  
XX PF 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA24730.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 48784; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 319 AA;



CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 339 AA;

Query Match 3.2%; Score 84; DB 6; Length 339;  
Best Local Similarity 19.3%; Pred. No. 1.1e+02;  
Matches 50; Conservative 42; Mismatches 77; Indels 90; Gaps 11;  
QY 66 PVPFRQELFRMMAVAADTLQRLGARVASVDMGFPQQLP---DQSLPIPPVIL---AELG 119  
Db 94 PTERFKEAILKV-----VKLNERFIPPYESGASLYIRPLLIGTSAQVG 136  
QY 120 SDPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 137 VHPADEYMFVVFVTPVGPYFKG-GFSTNPYVII---REYDRAAPHGTGIYKVGNYAAS 191  
QY 180 FRALEQ--DLPVNIKFIIEGME-----EAGSVALEELVEKEKDRFFSGVDYIVISDNLWI 232  
Db 192 LRANKKAHDLGYSCFYLDAKEKKYIDECAGAA-----NFFG-----IKDNTYI 234  
QY 233 SQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILV 292  
Db 235 TPKSTSI-----LPSITNKSMLQLAEDMGMKVERR----- 264  
QY 293 PGIYDEVVPLTEEEINTYK 311  
Db 265 -----PVPEEELSTFE 275

RESULT 1263  
ABG91583  
ID ABG91583 standard; protein; 363 AA.  
XX  
AC ABG91583;  
XX  
DT 18-NOV-2002 (first entry)  
XX  
DE Purine/pyrimidine triphosphate type nucleotidyltransferase #168.  
XX  
KW Nucleotidyltransferase; enzyme; active site engineering;  
KW alpha-D-glucopyranosyl phosphate thymidyltransferase; Ep;  
KW substrate specificity; nucleotide sugar;  
KW glycosylated bioactive natural product.

XX Schizosaccharomyces pombe.  
XX  
PN WO200248331-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 13-DEC-2001; 2001WO-US047953.  
XX  
PR 13-DEC-2000; 2000US-0254927P.  
XX  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX  
PI Thorson JS, Nikilov DB;  
XX  
DR WPI; 2002-608282/65.

XX Nucleotidyltransferase mutated at one or more amino acids, useful in  
PT the synthesis of nucleotide sugars.  
XX  
PS Claim 3; Page; 182pp; English.  
XX  
CC The invention relates to a Nucleotidyltransferase mutated at one or  
CC more amino acids selected from V173, G147, W224, N112, G175, D111, E162,  
CC T201, I200, E199, R195, L89T, L109, Y146 or Y177 (with reference to  
CC the *Salmonella enterica* rmlA-encoded alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase, Ep, enzyme appearing as ABG91798). The mutations  
CC alter the substrate specificity of the enzymes. The mutants and methods  
CC involving them are used in the synthesis of nucleotide sugars for  
CC altering nucleotidyltransferase substrate specificity. The  
CC nucleotidyltransferase exhibits different substrate specificity for  
CC GTP, CTP, TTP, UTP and ATP than a non-mutated nucleotidyltransferase.  
CC The mutant may also exhibit a high degree of sequence identity to  
CC *Salmonella enterica* LT2 alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase (Ep) and can convert a wide variety of phosphates.  
CC The mutants can be exploited in the biosynthesis of glycosylated  
CC bioactive natural products of pharmacological use. The present sequence  
CC is a nucleotidyltransferase exhibiting a high degree of sequence  
CC identity to *Salmonella enterica* LT2 alpha-D-glucopyranosyl phosphate  
CC thymidyltransferase (Ep). Note: The present sequence is not displayed  
CC in the specification but was obtained from Genbank  
XX  
SQ Sequence 363 AA;

Query Match 3.2%; Score 84; DB 5; Length 363;  
Best Local Similarity 20.4%; Pred. No. 1.3e+02;  
Matches 76; Conservative 62; Mismatches 128; Indels 106; Gaps 22;  
QY 148 PYVLTEVDGKLYGRGATDNKGPVLAWIN-----AVSAFRALEQDLPVNIKFIIEG--MEE 200  
Db 32 PMILHQVEA-LAAAGVTD---IVLAVNYRPEIMVEALKKYEKYNVNITFSVENEPLGT 86  
QY 201 AGSVAL-EELVEKEKDRFFSGVDYIVISDNLWISQRKP---AITYGTRGNSYFMVEVKC 255  
Db 87 AGPLALARDILAKDHSPPF-----VLNSD---VICEYPPADLAAAFHKAHGAEGTIVVTKV 138  
QY 256 RDQDFHSGTGGILHEPMADL-----VALLGSLVDSSGHILVPGIYDEVVVP---LT 303  
Db 139 EE---PSKYGVVVHYHPNSESLIERFVEKPEVFEVSNRINGVLYILNPSVLDRIEPRPTSI 194  
QY 304 EEE-----INTYKAIHLGLEEY-RNSSRVEKFLFDT-----KEEILMHLWRYPSL 347  
Db 195 EKEVFPAMVNDKQLHSFDLEGYWMVDVGQPKDYLTGTCLYLSLRKHKPEIL----- 245  
QY 348 SIHGIEGADEPPTKTVI-----PGRVICKFSIRLVPHM-----NVSAVEKQVTRHLEDV 397  
Db 246 -----APASSNIIGNVLIDPSATIGK-NCKIGPNVVIGPNVTIGDGVRLQRCAIL 294  
QY 398 FSKRNSSNMVVSMTLG---LHPWTIANIDDTQYLAAKRAIRTVFGTEPDMIRDCGSTIPI 453  
Db 295 KSSRVRDHAWKSSIVGWNSTLGSW-SRLNENSVLG-----DDVVVNDEIYVNGGSILP- 347  
QY 454 AKMFQEIIVHKSV 465  
Db 348 -----HKSI 351

RESULT 1264  
AAW04270  
ID AAW04270 standard; protein; 397 AA.  
XX  
AC AAW04270;  
XX  
DT 16-OCT-2003 (revised)  
DT 15-DEC-1996 (first entry)  
XX  
DE B.t. alkaline protease.  
XX  
KW Alkaline protease; apr gene; neutral protease; npr gene;





QY 156 GKLYGRG-ATDNKGPVLAWINAV-----SAFRALEQDLPVNIKFIIEGMEEA 201  
Db 13 GLRYMRGRAADRFGRFVSWLSTIGITLGVMAVTVLTVSMNGFERELQNNILGL---MPQA 69  
QY 202 -----GSVALEELVEKEK-----DRFFSGVDYIVISDNLWI--SQRKPAI 239  
Db 70 ILSAKQGSVNPQQLPEREAKLNGVTRVAPITGDDVVLQSARSVAVGMLGIDPAQNPLT 129  
QY 240 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALLGSLVDSSG---HILVPGIY 296  
Db 130 PY-----LVNVK--QSDLOAGKYNVILGEQLA-----GQLGVNRGDKIRVMVPSA- 172  
QY 297 DEVVPLTE-----EEINTYKAIHLDLEEYRNSRRVEKFLDFTKEEILMHLWRYPSLSI 349  
Db 173 SQFTMGVRVPSQRLFTVIGTFAA-----NSEVDGYQMLTNIDDAASRLMRYPLGNI 222  
QY 350 HGIEGAFDEP-----GKTVTIPGR-----VIGKFS 374  
Db 223 TGWRLWLDKPLQVDTLSQOTLPPGTQWDWRERKGELOFQVRMEKNMMGLLSLIVAVAA 282  
QY 375 IRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 283 FNITSLGMVMVEKQ-----GEVAILQTOGLTP-----RQI 313  
QY 435 RTVP---GTEPDMI-----RDGSTIPIAKMFQEIYVHKS 465  
Db 314 MAVFMVQGSAGIVGALLGAVLGALLASQLNMLPIIGAFLDGAALPVA-----IEPLQV 368  
QY 466 VLIPLGAV 473  
Db 369 IVIALVAM 376

RESULT 1266  
ADN27166  
ID ADN27166 standard; protein; 420 AA.  
XX  
AC ADN27166;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #9819.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 9819; 122pp; English.  
PS  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 420 AA;

Query Match 3.2%; Score 84; DB 8; Length 420;  
Best Local Similarity 20.5%; Pred. No. 1.6e+02;  
Matches 86; Conservative 59; Mismatches 164; Indels 110; Gaps 18;  
QY 147 DPYVLT--EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLP--VNIKFIIEGMEEA 201  
Db 2 DRYVITGKQQLLEGRLNRSGAKNSSLPLLAASLLVSGKTTL-LDIPHLADISNMIEVLEYL 60  
QY 202 GSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFH 261  
Db 61 GA-----HVEDQKEAL-----LVDSADLARWEVDEGLMRQMRASNLIPLIARNGVR 109  
QY 262 SGTFGG--ILHEPMADLVALLGSL-----VDSSGHI 290  
Db 110 ISKPGGCAIGSRPMDQHIKGLQELGVKVKKHGYIEAWADQLQAKIYLDLPSVGTATENL 169  
QY 291 LVPGIYDEVVPLTEEBEINTYKAIH---LDLEEYRN--SSRVEKFLDFTKEEILMHLWRY 344  
Db 170 MMAAV-----LAKGTTTIYNAAREPEIIDLQNFNLKMGAKVRGAGMDV----- 212  
QY 345 PLSIHGIEGAFDEPGTKTVIPGRV-IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS 403  
Db 213 --LRIEGVSKLY--PVEHTVIPDRIEAGTHMVAAMVTQGDIEISNVIPEHLEPVTAKLLQ 268  
QY 404 SNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVF-----GTEPDM-----IRD 447  
Db 269 AGAEII---LG-----DDTIRVKGKRRIKGVCKTMRPHPGFPTDMQPFMALLSMAE 317  
QY 448 GSTIPIAKMFQEIYVHKSIVLPLGAVDDGSHSQNEKINRWNYIEGTKLEFAAFFLEMAQL 506  
Db 318 GTSIITETIFENRFQHVDELRRMGA-----QITVEGRTAIRGVKSLEGAFVEATDL 369  
RESULT 1267  
AAB41647  
ID AAB41647 standard; protein; 424 AA.  
XX  
AC AAB41647;  
XX  
DT 08-FEB-2001 (first entry)  
XX

DE Human ORFX ORF1411 polypeptide sequence SEQ ID NO:2822.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; KW hypotensive; dermatological; immunosuppressive; antiinflammatory; KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid; KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension; KW neurodegenerative disorder; osteoarthritis; graft vs host disease; KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; KW cholesterol ester storage; systemic lupus erythematosus; infection; KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma; KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; KW bone damage; cartilage damage; antiinflammatory disease; coagulation; KW thrombosis; contraceptive.

XX Homo sapiens.

OS WO200058473-A2.

PN

XX

XX 05-OCT-2000.

PD

XX 31-MAR-2000; 2000WO-US008621.

PF

XX 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX

PA (CURA-) CURAGEN CORP.

XX

XX Shimkets RA, Leach M;

PI WPI; 2000-602362/57.

DR N-PSDB; AAC75856.

DR

XX Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

PT

PT Claim 11; Page 2058-2059; 5507pp; English.

PS

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC dermatological; immunosuppressive; antiinflammatory; antibacterial; CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX

SQ Sequence 424 AA;

Query Match 3.2%; Score 84; DB 3; Length 424;

Best Local Similarity 20.6%; Pred. No. 1.6e+02;

Matches 49; Conservative 38; Mismatches 81; Indels 70; Gaps 13;

QY 225 VISDNLWISQRKPAIT-----YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLV 277

DB 142 VVKDVAWV--KKDSLCLXECFY---GSDYSLMGVCEKREKQSEPTLLXRGHAGSVDSI 196

QY 278 ALLGSLVDSSGHILVPGIYDEV-----VPLTEEEINTYKAHLDLEEYRNSR----- 325

DB 197 A-----VDGSGTKFCGSDWKMLKIWSTVPTDEED-----EMEESTNRPRKKQKTE 242

QY 326 -----VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPG 367

DB 243 QLGLTRTPIVTLSGHMEAVSSVLWSDAEEICSAWDH-TIRVWDVESG----SLKSTLTG 297

QY 368 RVIGKFSIRLVPHMNVSAVEKQVTRHLE--DVFSKRNSSNMVWSMTLGLHP-WIANI 422

DB 298 NKV--FNCISYSPLCKRLASGSTRHRLWDPRTKDGS----LVSLSLTSGTWVTSV 349

RESULT 1268

ADQ26344

ID ADQ26344 standard; protein; 436 AA.

XX

AC ADQ26344;

XX

DT 23-SEP-2004 (first entry)

XX

DE Chromobacterium violaceum CV34644 involved in haemolysin synthesis.

XX

KW Haemolysin; anticoagulant; CV34644.

XX

OS Chromobacterium violaceum.

XX

PN WO2004056960-A2.

XX

PD 08-JUL-2004.

XX

PF 16-DEC-2003; 2003WO-BR000207.

XX

PR 19-DEC-2002; 2002BR-00007239.

XX

PA (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.

XX

PI De Vasconcelos ATR, Simpson AJG, Abreu HNS, De Almeida DF; Almeida FC, De Almeida R, Antonio RV, Araripe JR, De Araujo MFF; PI Bogo RM, Bonatto SL, Brigido MDM, De Brito CFA, Brochi M, Burity HA; PI Camargo A, Carraro D, Carvalho CMB, Cascardo JCDM, Cavada BS; PI Chueire LMDO, Da Cunha MH, Fantinatti F, Farias IP, Felipe MSS; PI Ferrari LP, Ferro JA, Franco GR, De Freitas NSA, Furlan LR; PI Gattapaglia D, Gazinelli RT, Gomes JAA, Goncalves PR, Grangeiro TB; PI Grisard EC, Guimaraes CT, Hanna ES, Jardim SN, Laurino JP, Lima LFA; PI De Lyra MDCCP, Madeira HMF, Maranhao AQ, Manfio GP, Martins WS; PI De Medeiros SRB, Meissner RDV, Moreira MA, Do Nascimento FF; PI Nicolas MF, De Oliveira JG, Oliveira SC, Paixao RFC, Parra J; PI Pasa TBC, Pedrosa FDO, Pena SDJP, Pereira JO, Pereira M, Pinto LSRC; PI Pinto LDS, Porto JIR, Potrich DP, Ramalho CE, Reis AMM; PI Rondinelli E, Sampaio AH, Dos Santos FR, Schneider MPC, Silva DW; PI Silva R, Soares CMDA, De Souza EM, De Souza KRL, Souza RC; PI Steindel M, Teixeira SMR, Trevillato PB, Urmenyi TP, Wassen R; PI Azevedo V, Bartoletti LA, Batista JDS, Filho AS, Zaha A; PI Andrade EDM, Gonzaga L, Dos Santos EBP, Soares RDBA, Bataus LAM; PI Cardoso DDFDP, Parente JA, Rigo LU, Steffens MBR;

XX WPI; 2004-500292/47.

DR

XX New gene-coding polynucleotides of the chromosome of Chromobacterium violaceum, useful for therapeutic, diagnostic or pharmacological applications, in control processes for environmental parameters or in enzyme synthesis.

PT

PT

PT

XX

PS Claim 4; SEQ ID NO 17; 31pp; English.

XX

CC The present sequence is that of the protein encoded by the CV34644 gene of Chromobacterium violaceum strain ATCC 12472 (NCIB 9131, NCTC 9757, JCM 1249, DSM 30191, IAM 12470, LMG 1267). The invention relates to 29 polynucleotides that have been identified by sequencing the genome of this strain, to the polypeptides ADQ26328-ADQ26356 encoded by these polynucleotides, and to the uses of the polynucleotides and polypeptides



CC for therapeutic, diagnostic, medicinal, pharmacological and  
CC pharmacognostic applications, in control processes for environmental  
CC parameters, and in enzyme synthetic processes. The CV34644 gene is  
CC involved in haemolytic activity. The gene and the encoded polypeptide can  
CC be used in the production of haemolysins for pharmaceutical use as  
CC anticoagulants.  
XX  
SQ Sequence 436 AA;

Query Match 3.2%; Score 84; DB 8; Length 436;  
Best Local Similarity 20.5%; Pred. No. 1.7e+02;  
Matches 81; Conservative 45; Mismatches 113; Indels 156; Gaps 21;  
QY 5 LGRMAASLLAVL-----LLLLRGMFSSPPPALLEKVFQYI----- 42  
Db 115 LGELVPKRLALLNPERVAMALARPMLLSRA--SAP-----LVQVFSRVTGILLRVLGA 166  
QY 43 -----DLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVD 96  
Db 167 KKSDEPSITEDE-IRTLMEQGADEG---VFDRAEQEL-----VENIFRLDNRKASAV 214  
QY 97 MGPPQLPDGQSLPIPPPVILAEELGSDPTKGTVCFYGH-LDVQPADRGDGLTDPYV----- 150  
Db 215 MTPRK-----DVVILDLEDGPERNRELLLGHFPFHPVCRGD---TDQVIGMLNA 261  
QY 151 LTEVDGKLYGRG-----ATDNKGPVLAWIN 175  
Db 262 KTLDDRLLRGEALDFAAELSPPLYVPSTCSLMQLEQFKQARSHSALVVDEYGELEGLVS 321  
QY 176 AVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQR 235  
Db 322 INNVMFAIVGDLPA-----IDGEE-----DEIVQRE-----DGSWLVDG 355  
QY 236 KPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSGGHILVPGI 295  
Db 356 MVSL---DRFREFFELEAPL-----PGEAGGNIH-----TLAGVMVLYQLGR--VPSV 397  
QY 296 YDEVVPLTEEEINTYKAHLDLLEEYRNSSRVEKFL 330  
Db 398 TDRF-----EWNGFSFEVVDMDR-----TRVDKIL 422

RESULT 1269  
AAU35231  
ID AAU35231 standard; protein; 472 AA.  
XX  
AC AAU35231;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Enterococcus faecalis cellular proliferation protein #518.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Enterococcus faecalis.  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US009180.  
XX  
PR 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS53090.  
XX  
PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 10824; 511pp; English.  
XX  
CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 472 AA;

Query Match 3.2%; Score 84; DB 4; Length 472;  
Best Local Similarity 20.9%; Pred. No. 1.9e+02;  
Matches 62; Conservative 48; Mismatches 94; Indels 92; Gaps 16;  
QY 271 EPMADLVALLGS-----LVDSSGHILVPGIYDEVVP--LTEEE 306  
Db 139 EPTKGKIAVVGSGPSGLTVAGDLAKLGYEVIIFEALHEAGGLTYGIPEFRLPKKIVKQE 198  
QY 307 INTYKAHLDLLEEYRNSSRVEKFLFDTKEEILM-----HLWRYPSLSIHGI 352  
Db 199 IASIEALGVITIE--TNVVVGKTI--TMEIIMSEFDACYLSVGAGAPNFMGIPGTSINGV 253  
QY 353 EGA-----FDEPGTK----TVIPGRVIGKFSIRLVPHMNVSAVEKQVT 391  
Db 254 YSSSEFLTRINLMHSYEFPEYDTPIKRAKNQVVVIGGNNVAMDAAARSAKRLGAENVNIVYR 313  
QY 392 RHLEDVFSKRNSNKNQVVSMTLGL-HPWTIAN----IDDTQ-YLAAKRAIRTVFGTEPDMI 445  
Db 314 RSLEELPARIEEYHH---SLEEGINYWLTNPFIAYLDDQQGNLAGVECIKMVLG-EPDV- 368  
QY 446 RDGSTIPIAKMFQEIHKSVVLIPLGAVDD--GEHSQNE-----KINRWNYIE 491  
Db 369 -SGRRRP-----EPVPDSTFTIPADAVIEAIGQEANRVLLSTYPEIELNQWGYIQ 417

RESULT 1270  
AA51648  
ID AA51648 standard; protein; 482 AA.  
XX  
AC AA51648;  
XX  
DT 06-AUG-2003 (revised)  
DT 01-JUN-2000 (first entry)  
XX  
DE Methanobacter sp. MTH1405 protein fragment.  
XX  
KW Thermostable; template-dependent elongation; staple protein;  
KW elongation protein; amplification; reverse transcription.  
XX  
OS Methanothermobacter sp.  
XX











CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX  
SQ Sequence 565 AA;

Query Match 3.2%; Score 84; DB 8; Length 565;  
Best Local Similarity 21.1%; Pred. No. 2.5e+02;  
Matches 70; Conservative 36; Mismatches 129; Indels 96; Gaps 14;  
QY 4 KLGMAASULLAVLLLLERGMFSSPPPALKEKFQYIDLHODEFVQTLKEWVAIESDS 63  
Db 61 QIGDTEAIFDAQLLFLE-----DPVLEAAHQRI---LDHYINAEAAWQAV-VDE 107  
QY 64 VQPVPFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE----- 117  
Db 108 VATSYRTLEDAYLQERV--EDVVDVQQRVLRLLAG--NAPANLHSEPAILVATDLTPSD 163  
QY 118 -----LGSDPKTKGVCFYGHLDVQ-----PADRGDGLWLTDPVLTVEVDGKLYGRGAT 164  
Db 164 TARLDPRMVLGICTTSGSATSHSAIARTLGIPAVLG---VDSQVLHLADGTLMALDGE 219  
QY 165 DNKGPVLAWINAVSAFRALEQDLPVNFKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYI 224  
Db 220 SGK----AWVEPES-----HILDLEAKREAWQTAQEE----- 248  
QY 225 VISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLV 284  
Db 249 -----ARATAHQPAITLDGRQSVF-----ANIGSI-----NDVQVAVASGA 285  
QY 285 DSSGHILVPGIYDE--VWPLTEEEINTYKAI 313  
Db 286 EGVGLLRTEFLYLDRTSAPTEEEQLEVYQAI 316

RESULT 1277  
ABU40392  
ID ABU40392 standard; protein; 582 AA.  
XX  
AC ABU40392;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #25919.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Pseudomonas putida.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA44262.

XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

XX  
PS Claim 25; SEQ ID NO 68316; 1766pp; English.

XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 582 AA;

Query Match 3.2%; Score 84; DB 6; Length 582;  
Best Local Similarity 22.1%; Pred. No. 2.6e+02;  
Matches 47; Conservative 33; Mismatches 67; Indels 66; Gaps 12;  
QY 275 DLVALLGSLVDSSG-HIL---VPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFL 330  
Db 119 EFIVLVRLTPEQGQHVLDLKVPGVY-----GLEEFRR----- 151  
QY 331 FDTKEEILMHLWRYPSLSIHGIEG---AFDE-----PGTKVIP---GRVIGKFSIRLVP 379  
Db 152 FYPAGDVTAHMVGFDTLDDHGREGVELAYEEWLAGVPGKRQVIKDRRGRLIKDIQVT--- 208  
QY 380 HMNVSA-----VEKQVTRHLEDVFSKRNSNKMVMSMTLGLHPWIANIDDTQYL 428  
Db 209 -KNAKAGKTLALSIDLRLQLATFELRNAIAEQDAKAGSLVIMDVKTGEVLAMVNQPTYN 267  
QY 429 AAKRAIRTVFGTEP-----DMIRDGSTI-PIA 454  
Db 268 PNNR--RSMFPAAMRNRAIIDVPEPGSTVKPIS 298

RESULT 1278



ADJ49863  
ID ADJ49863 standard; protein; 586 AA.  
XX AC ADJ49863;  
XX DT 06-MAY-2004 (first entry)  
XX DE Oil-associated gene related protein #1363.  
XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.  
XX OS Unidentified.  
XX PN US2004025202-A1.  
XX PR 05-FEB-2004.  
XX PF 14-MAR-2003; 2003US-00389566.  
XX PR 15-MAR-2002; 2002US-0365301P.  
XX PR 26-JUN-2002; 2002US-0391786P.  
XX PR 26-JUN-2002; 2002US-0392018P.  
XX PA (LAUR/) LAURIE C C.  
XX PA (RAVA/) RAVANELLO M.  
XX PA (SAVA/) SAVAGE T.  
XX PA (LEDE/) LEDEAUX J R.  
XX PA (ROGE/) ROGERS J A.  
XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;  
XX WPI; 2004-142683/14.  
XX DR  
XX PT Novel recombinant DNA construct comprising a promoter functional in  
XX PT plants operably linked to an oil-associated gene for producing transgenic  
XX PT plant seed.  
XX PS Example 3; SEQ ID NO 1867; 22pp; English.  
XX CC The invention relates to a recombinant DNA construct comprising a  
XX CC promoter functional in plants operably linked to an oil-associated gene.  
XX CC The construct is useful for transgenic plant seed which has in its genome  
XX CC the construct, that is functional in the plant to transcribe the oil-  
XX CC associated gene. The transgenic plant seed grows into a plant having  
XX CC enhanced seed oil as compared to wild type. The construct is useful for  
XX CC producing hybrid maize seed. The transgenic plant seed is useful for  
XX CC producing vegetable oil. The present sequence represents the amino acid  
XX CC sequence of an oil-associated gene related protein.  
XX SQ Sequence 586 AA;  
Query Match 3.2%; Score 84; DB 8; Length 586;  
Best Local Similarity 34.4%; Pred. No. 2.7e+02;  
Matches 22; Conservative 16; Mismatches 16; Indels 10; Gaps 5;  
QY 48 EFVQTLKEWVAIESDSVQPV-PRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQ 106  
Db 432 EYVETLEDWF---KDNVDPFWPRYREDALRIL-IEDRLQOI-IKI-----MGEDVLPDDQ 482  
QY 107 SLPI 110  
Db 483 KLTV 486  
RESULT 1279  
ADA54987  
ID ADA54987 standard; protein; 594 AA.  
XX AC ADA54987;  
XX DT 20-NOV-2003 (first entry)  
XX DE Human protein, SEQ ID 2555.

XX KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
KW inflammatory disease; osteoporosis; neurological disease.  
XX OS Homo sapiens.  
XX PN EP1293569-A2.  
XX PD 19-MAR-2003.  
XX PF 21-MAR-2002; 2002EP-00006586.  
XX PR 14-SEP-2001; 2001JP-00328381.  
XX PR 24-JAN-2002; 2002US-0350435P.  
XX PA (HELI-) HELIX RES INST.  
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-395539/38.  
XX DR N-PSDB; ADA53348.  
XX PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
PT and/or membrane proteins, useful for developing medicines for diseases in  
PT which the gene is involved, or as target molecules for gene therapy.  
XX PS Claim 14; SEQ ID NO 2555; 205pp; English.  
XX CC The present invention relates to novel human secretory or membrane  
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
CC ADA54071). The coding sequences are useful in the gene therapy of  
CC diseases caused by abnormalities of the proteins, e.g. cancer,  
CC inflammatory diseases, osteoporosis or neurological disease.  
XX SQ Sequence 594 AA;  
Query Match 3.2%; Score 84; DB 6; Length 594;  
Best Local Similarity 18.2%; Pred. No. 2.7e+02;  
Matches 62; Conservative 52; Mismatches 107; Indels 120; Gaps 15;  
QY 248 YFMVEVKCR---DQDFHSGTGGILHEPM-----ADLVAL 279  
Db 256 FYYQDVKCREMYDKDIIMLQIGASLMDPNKFKLLLVQRYELAEAFNKTIKQDQLIKQ 315  
QY 280 LGS�VDSSGHILVPGIYDEVVP---LTEEINTYKAHLDLEEYRNSRVKFLFDTK- 334  
Db 316 YNTLIEEMLQVLIIYVGERYPGVGNVTKEEVTMREIIHLLCIEPMPHSAIAKNLPENEN 375  
QY 335 -----EEIL--MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 376 NETGLENVINKVATFKKPGVSGHGVYELKDES-----LKDFNMYF---YHYSKTQ 422  
QY 388 QVTRHLEDVFSKRNSSNK-----MVVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 423 HSKAEHMQK--KRRQENKDEALPPPPPPPEFCPAFSKVINL---LNCDIMMYI-----L 471  
QY 435 RTVF---GTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGHEHSON----- 481  
Db 472 RTVFERAIDTDSNLWTEG-----MLQMAFH-----ILALGLLEEKQQLQKAPEEVTFD 520  
QY 482 -----EKINRWNYIEGTKLFAPFFLEM 503  
Db 521 FYHKASRLGSSAMNIQMLLEKLGIPQLEGQKDMITWILQM 561  
RESULT 1280  
ABB91100  
ID ABB91100 standard; protein; 605 AA.  
XX









XX (GENO-) GENOME THERAPEUTICS CORP.  
PA Breton GL;  
PI  
XX WPI; 2003-895291/82.  
DR N-PSDB; ADF00288.  
DR  
XX New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.  
XX  
PS Disclosure; SEQ ID NO 4745; 870pp; English.  
XX  
CC The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis, a  
CC method for evaluating a compound for the ability to bind a P. mirabilis  
CC polypeptide and a method for screening test compounds for anti-bacterial  
CC activity. The polypeptides and polynucleotides are useful as molecular  
CC targets for diagnosing, preventing and treating pathological conditions  
CC resulting from bacterial infection, as reagents for diagnosis of  
CC bacterial diseases, as components of antibacterial vaccines, as targets  
CC for antibacterial drugs or as bio-control agents for plants. This  
CC sequence represents a Proteus mirabilis polypeptide of the invention.  
XX  
SQ Sequence 724 AA;

Query Match 3.2%; Score 84; DB 7; Length 724;  
Best Local Similarity 19.9%; Pred. No. 3.7e+02;  
Matches 96; Conservative 60; Mismatches 169; Indels 158; Gaps 23;

QY 11 SLLAVLLLLLLERGMFESSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRF 70  
Db 17 SIFAWRQIMLSKDPKSTPIDPASVL-----KDEAINQVKNRVQSKVNETLSTP-- 64  
QY 71 RQELFRMMAVAADTLQRLGARVASVDMGP-----QQLPDGQSLPIP-PVILAE LG 119  
Db 65 TQKVAGMASAAASLTQASASANRVTAHPLIHGGGFTGGQTFAENQALQAAHGALLDALG 124  
QY 120 SDP-----TKGT-----VCIFYGHLDVQP 137  
Db 125 MDSLEGLVFTCTIGGLPDDTFQVTEFNLTEGLSSLSISAVSALPFIDFQRHLGLAS 184  
QY 138 ADRGDGWL T---DPYVLTEVDGKLYG--RGATDNKGPVLAW---INAVSAFRALEQDL P 188  
Db 185 S-----LTVKRDGVLIRKVGILAGAVQNTDG---VKTWYHFDIRPEMWMVMTLNQDSR 235  
QY 189 VNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISO-RKPAITYGTR--- 244  
Db 236 I---FQHQSVPTILKTLTLLDEAHVKADCQFYR---EDLHPERLYTTQKRESAFDFWCR LAF 289  
QY 245 --GNSYFMVEVKCRDQDFHSGTFGGI--LHEPMADLVALLGSLVDSSGHILVPGIY---D 297  
Db 290 BEGINWFEEEQLFYSDEHMGMTAGIHLTYNPQADT-----DISDSTAMTWQYGEYLCVD 344  
QY 298 EVV-----PLTEEE-----INTYKAIHLD-----LEEYRNSSRV 326  
Db 345 ETIHKDNNFVRPSYPLSHENKVEQGQHSVFESYGRFQLDDEGRPLTVQRFELRNGSKV 404  
QY 327 EK-----FLFDTKEEILMHLWRYPSSLIHGIEGAFDEPG-----TKTV 364  
Db 405 GQATTNCFALMPGKIFTLTSLQHPHQPMNDRWQVTSVSHHGVSQPLADNSGGEGTQLSNSVSF 464  
QY 365 IPG 367  
Db 465 IPG 467

RESULT 1286  
AAW69761

ID AAW69761 standard; protein; 735 AA.  
XX  
AC AAW69761;  
XX  
DT 17-OCT-2003 (revised)  
DT 23-NOV-1998 (first entry)  
XX  
DE Acetobacter xylinum beta-glucosidase.  
XX  
KW Acetobacter xylinum; sucrofermentans; cellulose synthesis complex; bcSA;  
KW bcSB; bcSC; bcSD; CMCase; beta-glucosidase; enzyme; cellulose;  
KW microorganism.  
XX  
OS Gluconacetobacter xylinus.  
XX  
PN WO9839455-A1.  
XX  
PD 11-SEP-1998.  
XX  
PF 09-OCT-1997; 97WO-JP003633.  
XX  
PR 04-MAR-1997; 97JP-00063927.  
XX  
PA (BIOP-) BIO-POLYMER RES CO LTD.  
XX  
PI Tonouchi N, Tahara N, Hayashi T, Tsuchida T, Yano H, Yoshinaga F;  
XX  
DR WPI; 1998-495854/42.  
DR N-PSDB; AAV52831.  
XX  
PT Gene encoding Acetobacter xylinum cellulose synthetase complex -  
PT containing a group of genes including those for conventional and novel  
PT beta-glucocidases.  
XX  
PS Claim 8; Page 36-37; 50pp; Japanese.  
XX  
CC This represents the amino acid sequence of a Acetobacter xylinum  
CC subspecies sucrofermentans beta-glucosidase. The invention provides a  
CC gene encoding a Acetobacter xylinum subspecies sucrofermentans derived  
CC cellulose synthesis complex-produced protein. The gene sequence  
CC represents bcSA, bcSB, bcSC or bcSD, CMCase and a beta-glucosidase  
CC encoding gene. The novel gene and the enzyme participate in the synthesis  
CC of cellulose by microorganisms. Cells transformed with the genes may be  
CC used in the production of cellulose. (Updated on 17-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 735 AA;  
  
Query Match 3.2%; Score 84; DB 2; Length 735;  
Best Local Similarity 20.5%; Pred. No. 3.8e+02;  
Matches 113; Conservative 61; Mismatches 190; Indels 186; Gaps 29;  
  
QY 32 PALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQE-----LFRMMAVA 81  
Db 257 PYLLNKTLLKQ-DWHYPGFV--MSDWGATHSSARAALAGLDQESAGDHTDARPYFRTL-LA 312  
QY 82 ADT-----LQRLGARVAS-----VDMGPPQQLP----- 103  
Db 313 ADVKAGRVPEARINDMAERVVRALFAAGLVDPHPAQRGLDVVTDTLVAQKDEEGAVLLR 372  
QY 104 -DQOSLPPIPPVI-LAELGSDPTKGTVCIFYGHLDVQP----ADRGDG---WLTDPPYV---- 150  
Db 373 NQGNILPLSPTARIAVIGGHADAGVISGGSSQVDPIGGEAVKGPCKEWPQDPVYFPSS 432  
QY 151 -LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL PVNIKFIIEGMEEAGSVALEEL 209  
Db 433 PLKAMQAEAPGARITYDPGTSIA--SAVRAARAADVWVYATQFTFEGM-DAPSMHLDN 489  
QY 210 VEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD----- 257  
Db 490 AD-----ALITAVAAANPRTVVVMETGDPVLMFVNSSVAG 524  
QY 258 --QDFHSGTFCGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAIHL 315

Db	525	VLEAWFPGSGG-----PAIARLLFGKVAPSGHLTM-----TFPQAESQL-----AHP	567	Best Local Similarity 19.9%; Pred. No. 4e+02;	Matches 96; Conservative 60; Mismatches 169; Indels 158; Gaps 23;
QY	316	DLEEYRNSRRVEKFLFDTKKEILMHLWRYPSSLSIHGIEGA-----FDEPGTKTVIP----	366		
Db	568	DIAGV-TADNVFEMQFHTDQELVYD-----EGSDVGYRWFDNRNHFKPLYPFGY	614		
QY	367	GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQ	426		
Db	615	GLTYTFS---TDGLKVTERHGQVTA---TFNVHTGTR-----AGVDVPQ	654		
QY	427	YLA--KRAIRTVFGTEPDMIRDSGTIPAKMFQEI VHKSVVLP-LGAVDDGHSQNEK	483		
Db	655	VYVGLPDGGARRLAGWQRISLAPGESRQV-----SVQLEPRLLAHFDGKH-----	699		
QY	484	INRWNYIEGT	493		
Db	700	-DRWSVPSGT	708		
RESULT 1287					
ADNF05131	ID ADF05131 standard; protein; 754 AA.				
AC	ADNF05131;				
XX	12-FEB-2004 (first entry)				
DE	Bacterial polypeptide #1244.				
XX	Proteus mirabilis infection; bacterial infection; antibacterial;				
KW	immunostimulant.				
KW	Proteus mirabilis.				
OS	US6605709-B1.				
PN	12-AUG-2003.				
XX	05-APR-2000; 2000US-00543681.				
PF	09-APR-1999; 99US-0128706P.				
XX	(GENO-) GENOME THERAPEUTICS CORP.				
PA	Breton GL;				
XX	WPI; 2003-895291/82.				
DR	N-PSDB; ADF00959.				
XX	New Proteus mirabilis polypeptides and polynucleotides, useful as				
PT	reagents for diagnosis of bacterial disease, as components of				
PT	antibacterial vaccines, as targets for antibacterial drugs, or as				
PT	biocontrol agents for plants.				
XX	Disclosure; SEQ ID NO 5416; 870pp; English.				
PS	The invention relates to new Proteus mirabilis polypeptides and				
XX	polynucleotides. The invention also relates to antibodies against the				
CC	polypeptides, methods for producing the polypeptides, a method of				
CC	generating vaccines for immunising an individual against P. mirabilis, a				
CC	method for evaluating a compound for the ability to bind a P. mirabilis				
CC	polypeptide and a method for screening test compounds for anti-bacterial				
CC	activity. The polypeptides and polynucleotides are useful as molecular				
CC	targets for diagnosing, preventing and treating pathological conditions				
CC	resulting from bacterial infection, as reagents for diagnosis of				
CC	bacterial diseases, as components of antibacterial vaccines, as targets				
CC	for antibacterial drugs or as bio-control agents for plants. This				
CC	sequence represents a Proteus mirabilis polypeptide of the invention.				
XX	Sequence 754 AA;				
SQ	Query Match 3.2%; Score 84; DB 7; Length 754;				

QY	11	SLLAVLLLLLGERMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFR	70		
Db	17	SIFAWRQIMLSKDPKSTPIDPASVL-----KDEAINQVKNRVQSKVNETLSTP--	64		
QY	71	RQELFRMNAVAADTLQRLGARVASVDMGP-----QQLPDGQSLPI-PVILAEIG	119		
Db	65	TQKVAGMASAAAASLTQSASASANRVTAHPLIHGGGTGGQTTFAENQALQAAGALLDALG	124		
QY	120	SDP-----TKGT-----VCFYGHLDVQP	137		
Db	125	MDSLESLVFTCTIGGLPDDTFQVTEFNLTEGLSSLSISAVSALPFIDFQRLHGLAS	184		
QY	138	ADRGDGLWT---DPYVLTEVDGKLYG--RGATDNKGPVLAW---INAVSAFRALEQDLP	188		
Db	185	S-----LTVKRDGVLIRKVGILAGAVQGNIDG---VKTWYHFDIRPEMVMVMTLNQDSR	235		
QY	189	VNIKFIEGMEEGAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQ-RKPAITYGTR--	244		
Db	236	I---FQHQSVPITILKTLLEAHVKADCPYR---EDLHPERLYTTQKRESAFDFWCRLAF	289		
QY	245	--GNSYFMVEVKCRDQDFHSGTFFGGI--LHEPMADLVALLGSLVDSSGHILVPGIY---	297		
Db	290	EEGINFWFEEELFYSDHEHMGMTAGIHLTYNPQADT-----DISDSTAMTWQYGEYLCVD	344		
QY	298	EW-----PLTEEE-----INTYKAIHLD-----LEEYRNSSRV	326		
Db	345	ETIHKDNNFVRPSYPLSHENKVEQGGQSHSFESYGRFQLDDEGRPLTVRFEQLRNGSKV	404		
QY	327	EK-----FLFDTKEEILMHLWRYPSSLSIHGIEGAFDEPG-----TKTV	364		
Db	405	GQATTNCFALMPGKIPTLSQHPHQPMDRWQVIVSHHGVPQLADNSGGEGTQLSNSVSF	464		
QY	365	IPG 367			
Db	465	IPG 467			
RESULT 1288					
ADN20400	ID ADN20400 standard; protein; 793 AA.				
XX	AC ADN20400;				
XX	02-DEC-2004 (first entry)				
DE	Bacterial polypeptide #3053.				
XX	Recombinant DNA construct; transformed plant; improved plant property;				
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;				
KW	pathogen tolerance; pest tolerance; plant disease resistance;				
KW	cell cycle pathway modification; plant growth regulator;				
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;				
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;				
KW	bacterial polypeptide.				
XX	Bacteria.				
OS	US2003233675-A1.				
XX	18-DEC-2003.				
XX	20-FEB-2003; 2003US-00369493.				
XX	21-FEB-2002; 2002US-0360039P.				
PA	(CAOY/) CAO Y.				
PA	(HINK/) HINKLE G J.				
PA	(SLAT/) SLATER S C.				
PA	(CHEN/) CHEN X.				
PA	(GOLD/) GOLDMAN B S.				



XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 3053; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 793 AA;

Query Match 3.2%; Score 84; DB 8; Length 793;  
Best Local Similarity 18.5%; Pred. No. 4.3e+02;  
Matches 112; Conservative 93; Mismatches 191; Indels 210; Gaps 27;

QY 4 KIGRMAASLLAVLLLLRLGFMFSP---SPPALLEKVFQYID----- 43  
Db 211 ELSPLALKALAAALIKVYKVTMAEDNLKPPLLSIQRDYMLDSATVENLSLIPDRGKN 270  
QY 44 ----LHODEF---VQTLKEWVAIESDSVQVPRFRQELFRMMA-----VAADTLQRL 88  
Db 271 LFDVLNNTETPMGARLLKKWI-----LHPLVDRKQIEERLKAVERLVNDRVLSLEMRNL 324  
QY 89 GARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFYGHLVDVQ----- 137  
Db 325 LSNVRDVERIVSRVEYNRSVPRDLVALRET-----LEIIPKLNELVSTFGV 370  
QY 138 -----ADRGDGLTDPYVLTETVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDL 187  
Db 371 FKKLAFPEGLVDLLRKAIEDDPVSGPGKGVKRG-----FSSLEDEYRDL---- 416  
QY 188 PVNIKFIEGMEEGAGSVALLEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNS 247  
Db 417 -----LEHAAE-----RLKEFEKERER--TGQKLRVGYNQ-----VFG----- 449  
QY 248 YFMVEVKCRDQDFHSCTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEI 307  
Db 450 -YYIEVTKANLD-----KIPDDYERKQTL-----V 473  
QY 308 NTYKAHLDLEEYRNS-----SRVEKFLFDT-----KEEILMHL----- 341  
Db 474 NSERFITPELKEFETKIMAAKERIEELEKELFKSVCEEVKKHKEVLEISEDLAKIDALS 533  
QY 342 -WRYPSLSIHGIEGAFDEPGTKTVIPGR--VICKFISIRLVPHMNVSAVEKQVTRHLEDVF 398  
Db 534 TLAYDAIMYNTKPVFSEDRLE-IKGGRHPVVERFTQNFVENDIYMDNEKRFV-----VI 587

QY 399 SKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVF-----GTEPDMIRDGSTI 451  
Db 588 TGNMSGKSTFIROVGLISLMAQIG--SFVPAQKAILPVDFRIFTRMGARDDDLGRSTF 645  
QY 452 -----PIAKMFQEIHKSVVLIPLGAVDDGEHSONEKNRWNYIE-----GTK-LFAAPF 500  
Db 646 LVEMNEMALILLKSTNKSLLV--LDEVGRGTSTQDGVSIAWAISEELIKRGCKVLFATHF 703  
QY 501 LEMAOQL 506  
Db 704 TELTEL 709  
RESULT 1289  
ID ABU36359 standard; protein; 808 AA.  
XX ABU36359;  
AC  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #21886.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Mycoplasma pneumoniae.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA40229.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 64283; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent









PR 14-MAY-1998; 98US-0085598P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA Doucette-Stamm LA, Bush D;  
XX WPI; 2003-799836/75.  
DR N-PSDB; ADC93062.  
DR  
XX  
PT New isolated nucleic acid derived from Enterococcus faecium encoding an  
PT Enterococcus faecium polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.  
XX  
XX  
PS Example 1; SEQ ID NO 6343; 243pp; English.  
XX  
XX  
CC The invention relates to an isolated nucleic acid derived from  
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection), bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.  
XX  
SQ Sequence 823 AA;

Query Match 3.2%; Score 84; DB 7; Length 823;  
Best Local Similarity 20.2%; Pred. No. 4.5e+02;  
Matches 49; Conservative 40; Mismatches 71; Indels 82; Gaps 12;  
QY 194 IIEGMEERAGSVALEELVEKEKDRFFSGVDYIV-----ISDNLWISQRKPAITYGTRGN 246  
Db 7 LMENRQEQVQLTLEVM--GDRFGYSKYIIQERALPDIRDGLKPVQRRILFAMNKDGN 63  
QY 247 SYFWEVKCRDQDFHSG--TFGGIL--HEPMADLVALLGSLVDSSGHILVPGIYDEVVPL 302  
Db 64 TY-----DKGFRKSAKSVGNIMGNYPHGD-----SSIYEAMVRM 98  
QY 303 TEEETNTYKAHLDLEEYRNSRVE-----KFLFDTKKEILMHLW- 342  
Db 99 SQD-----WKLEVLIEHMGNGSMDGDPAAARYTEARLSKLSGEMLADIEKETVDLVWN 154  
QY 343 -----RYPSLSIHGIEGAFDEPGTKTVIPGRVIGKF---SIRLVPHMNVSAV 386  
Db 155 FDDTEKEPTVLPARYPNLLVNGSTGI--SAGYATEIPTHNLAEVIDGTIYMIDHPQAS-L 211  
QY 387 EK 388  
Db 212 EK 213  
RESULT 1293  
ADA54351  
ID ADA54351 standard; protein; 832 AA.  
XX  
AC ADA54351;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human protein, SEQ ID 1919.  
XX  
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;

KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
KW inflammatory disease; osteoporosis; neurological disease.  
XX Homo sapiens.  
XX EP1293569-A2.  
XX  
PD 19-MAR-2003.  
XX  
PF 21-MAR-2002; 2002EP-00006586.  
XX  
PR 14-SEP-2001; 2001JP-00328381.  
PR 24-JAN-2002; 2002US-0350435P.  
XX  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX  
DR WPI; 2003-395539/38.  
DR N-PSDB; ADA52712.  
XX  
PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
PT and/or membrane proteins, useful for developing medicines for diseases in  
PT which the gene is involved, or as target molecules for gene therapy.  
XX  
PS Claim 14; SEQ ID NO 1919; 205pp; English.  
XX  
CC The present invention relates to novel human secretory or membrane  
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
CC ADA54071). The coding sequences are useful in the gene therapy of  
CC diseases caused by abnormalities of the proteins, e.g. cancer,  
CC inflammatory diseases, osteoporosis or neurological disease.  
XX  
SQ Sequence 832 AA;

Query Match 3.2%; Score 84; DB 6; Length 832;  
Best Local Similarity 20.4%; Pred. No. 4.6e+02;  
Matches 114; Conservative 69; Mismatches 185; Indels 192; Gaps 31;  
QY 12 LLAVLALLLERGMFSSPPALL-----EKVQYIDLHQDEFVQTLKEWVAIESDSVQP 66  
Db 14 LLVLLWLLQVSIIDSVOQETDLDLTQTKETIYQPLRRSKRWVITLLEEDPGP 70  
QY 67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLG----SDP 122  
Db 71 FPKLIGELFNNM-----SYNMSLMYLISGPGVDEYP-----EIGLFSLEDH 111  
QY 123 TKGTVCFYGHLDVQPADRGDGLWTDPY-----VLTVEVDGKLYGRGATDNKGPVLWINAV 177  
Db 112 ENGR I--YVH---RPVDRE---MTPSFTVYFDVVERSTGKI----- 144  
QY 178 SAFRALEQDLVPNIKFIIEGMEERAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP 237  
Db 145 -----VDTSLIFNIR-ISDVNDHA-----PQFPEKE-----FNITVQENQS 179  
QY 238 AITYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVALL-----GSLVDS- 286  
Db 180 A-----GQPIFQMLAVDLDEE-----NTPNSQVLYFLISQTPLLKESGFRVDR 223  
QY 287 SGHILVPGIYD-EVVP-----LTEEEINTYKAHLDLEEYRN----- 322  
Db 224 SGEIRLSGCLDYETAPQFTLLIRARDCCGERSLSSTTTTHVDVQEGNNHRPAFTQENYKVQ 283  
QY 323 -----SSRVEKFLFDTKKEILMHLWRYPSLSIHG-IEGAFD--EPGKTIVIPGRVIGK 372  
Db 284 IPEGRASQGVRLRLVQDRDSPFTSAWRAKFNILHGNEEGHFDISTDPETNEGIL-NVIKP 342  
QY 373 FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMVLGL-----HP--WI 419  
Db 343 LDYETRPAQSLIIVVENEERLVFCERGLQPPRKAASATVSVQVTDANDPPAFHPQSF 402

QY 420 ANIDDTQYLAAKRAIRTVFET---EPD-----MIRD-----GSTIPIAKMFQ 458  
Db 403 VNKEE---GAPG--TLTGTFNAMDPDSQIRYELVHDPANWVSVDKNSGVVITVEPIDR 456  
QY 459 EIVH--KSVWLPLGAVDDG 476  
Db 457 ESPHVNSFYVIIHAVDVG 476  
RESULT 1294  
ABB65111  
ID ABB65111 standard; protein; 842 AA.  
XX  
AC ABB65111;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 22125.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
DR N-PSDB; ABL09214.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
PS Disclosure; SEQ ID NO 22125; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 842 AA;  
Query Match 3.2%; Score 84; DB 4; Length 842;  
Best Local Similarity 22.9%; Pred. No. 4.7e+02;  
Matches 93; Conservative 39; Mismatches 137; Indels 138; Gaps 22;  
QY 11 SLLAVLLLLLBERG-MFSSPSPPPALLEKVFQYIDLHQDEFVQ-TLKEWVAIESDSV---- 64  
Db 404 SALSIFPFLRRGDLRKEENTMGTSKNYQAPFWLTAEFLOVDVLKEHFKEEQLAVTELI 463  
QY 65 -----QPVPFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQS----- 107  
Db 464 VKSAQVGDAQAGFASEMHR-----ASFNLQRGTAPKGFVSIVKDHKPGQTGAVAHRSKLF 519  
QY 108 -----LP1PPVILAEALGSDPTKGTVCVPGHLDVQPADRGDGLWLTDPYVLTEVDGK 157

Db 520 KREILAYKEVLPRIQALLQSIGDQTKIAPTQY--TTESP-----EPFLILE-DMQ 567  
QY 158 LYG-----RGATDNKGPVLAWINAVSAFRA-----LEQD----- 186  
Db 568 LSGFENFERGRLLNLDYVLPRTIEKVAKLHACSALIAQDSPEVLEFFDEAPISRNPRDRDF 627  
QY 187 ---LPVNIKFIIIEGMEEGAGSVALEELVEKEKDRFF-----SGVDYIVIS 227  
Db 628 LTFFFPVNIRCVAE--EVAHWKGYEEITEK----MFNLAENVLQRALTMFESTGKDFRVFN 681  
QY 228 -DNLWISQRKPAITYGTRGNSYFMV--EVKCRDQ----DFHSGTGGILHEPMADL-VAL 279  
Db 682 LTDLWIN-----NLLFHINNETKEPDDVVVTLDFQLAYVG----SPTIDLNYFL 725  
QY 280 LGS�VDSSGHILVPGI---YDEVVPLTEEEIN-----TYKAIHLDL 317  
Db 726 YGSLNENVRKVHYKYIVREYQVRVLOQTLEKLNVOGHPTLKEIHIEL 772  
RESULT 1295  
ADI57186  
ID ADI57186 standard; protein; 879 AA.  
XX  
AC ADI57186;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human FAK protein SEQ ID NO:6.  
XX  
KW cell cycle arrest; CK2-specific siRNA molecule; short interfering RNA;  
KW CK2 inhibition; PIM1-specific siRNA molecule; PIM1 inhibition;  
KW Hbol-specific siRNA molecule; Hbol inhibition; cytostatic; gene therapy;  
KW cancer; proliferative disorder; human; FAK.  
XX  
OS Homo sapiens.  
XX  
PN WO2004007754-A2.  
XX  
PD 22-JAN-2004.  
XX  
PF 14-JUL-2003; 2003WO-US022164.  
XX  
PR 12-JUL-2002; 2002US-0395443P.  
XX  
PA (RIGE-) RIGEL PHARM INC.  
XX  
PI Hitoshi Y, Jenkins Y, Markovtsov V;  
XX  
DR WPI; 2004-122975/12.  
DR N-PSDB; ADI57185.  
XX  
PT Identifying a compound that modulates cell cycle arrest, useful for  
PT developing therapeutic reagents for treating cancer comprising contacting  
PT a cell comprising a target polypeptide with the compound.  
XX  
PS Claim 1; SEQ ID NO 6; 180pp; English.  
XX  
CC The present invention describes a method for identifying a compound (C)  
CC that modulates cell cycle arrest. The method comprises contacting a cell  
CC comprising a target polypeptide with the compound (C), where the target  
CC polypeptide encoded by the complement of a nucleic acid that hybridises  
CC under stringent conditions to a nucleic acid encoding a polypeptide  
CC having an amino acid sequence selected from 18 148-1408 amino acid  
CC sequences (SEQ ID NO: 2-36, even numbers only). Also described: (1)  
CC modulating cell cycle arrest in a subject; (2) a CK2-specific short  
CC interfering RNA (siRNA) molecule comprising the sequence: (I)  
CC AACATTGAATTAGATCCACGT, where the siRNA molecule is from 21-30 nucleotide  
CC base pairs in length; (3) inhibiting expression of a CK2 gene in a cell;  
CC (4) a PIM1-specific siRNA molecule comprising the sequence: (II)  
CC AAAACTCCGAGTGAACGTGTC, where the siRNA molecule is from 21-30 nucleotide  
CC base pairs in length; (5) inhibiting expression of a PIM1 gene in a cell;  
CC (6) an Hbol-specific siRNA molecule comprising the sequence: (III)





QY 262 SGT---FGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLE 318  
Db 546 INSPKQVSKILFEKLG-----IKPRGKTTKTGEYSTRIEVLLEEIANEHEIVPLIL- 595  
QY 319 EYRNSSRVKEFLFDTKEEILMHLWRYPSSLISIHGIEGAFDEPGT----- 361  
Db 596 EYRKIQKLKSTYIDTLPLKV-----NPKTGRIHASFHQTGTATGRLLSSDDPNLQNLPT 648  
QY 362 -----KTVIP-----GRVIGKFSIRLVPHMN-----VSAVEKQVTRHL----- 394  
Db 649 KSEEGKIRKAIVPQDDWIVSADYSQIELRILAHLSGDENLVKAFAEEGIDVHTLTASR 708  
QY 395 -----EDVFSKRNSSNMV-----VSMTLG-----LHPMIAN 421  
Db 709 IYNVKEEVMENRVRGMVNFISIYGVTPYGLSVRLGIPVKEAKMIISYFTLYPKVRS 768  
QY 422 IDDTQYLAAKRA--IRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHS 479  
Db 769 YIQQVVAEAKGKYVRTLFGRKD-----IP-----QLMARDKNTQS 805  
QY 480 QNEKINRWNYIEGKLFKFAAFFLEMAQL 506  
Db 806 EGERIAINTPIQGT---AADIKLANI 829

RESULT 1297  
AAU34107  
ID AAU34107 standard; protein; 917 AA.  
XX  
AC AAU34107;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Staphylococcus aureus cellular proliferation protein #383.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.  
PF  
XX 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
DR N-PSDB; AAS51966.  
XX

PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
PS Example 3; SEQ ID NO 5603; 511pp; English.  
XX  
CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 917 AA;

Query Match 3.2%; Score 84; DB 4; Length 917;  
Best Local Similarity 20.2%; Pred. No. 5.4e+02;  
Matches 107; Conservative 78; Mismatches 168; Indels 176; Gaps 34;  
QY 55 EWVAIESDSV--QPVPFRFQELFRMMAV-----AADTLQRLGARV---ASVDMGPOQL 102  
Db 450 EWV-ISRQVRVGVPLPVFAENGELIIMTKETVNHVADLFAEHGSIWFEREIDL----L 504  
QY 103 PDGQSLPIPPVILAEELGSDPTKGTVCFCYGHLDVQPADRGDGL-----TDPVYL 151  
Db 505 PEGFTHPGSP-----NGT--FTKETDIM-----DVWFDGSSSHRGVLETRPELS 546  
QY 152 TEVDGKLYGRGATDNKGPVLAWINA-----VSAPRALEQDLPVNIKFIIEG----- 197  
Db 547 FPAD--MYLEGSDQYRG---WFNSSITTSVATRGVSPYKFL-----LSHGFVMDGEGKK 595  
QY 198 -MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLMISQRKPAITYGTRGNSYFMVEVKCR 256  
Db 596 MSKSLGNVIVPDQVVVKQK-----GADIA---RLWVS-----STDYLAADVRI 634  
QY 257 DQDFHSGTGGILHEPMADLVALLGSLVD-----SSGHILVPGIY--DEVVPLTEEE 306  
Db 635 DEILKQTS--DVYRKIRNTLRFMLGNINDFNPDTSIPESELLEVDYRLNRLREFTAST 692  
QY 307 INTYKAI-HLDL-EEYRNSSRVE--KFLFDTKKEIL-----MHLWRYPSSLISIHGIEGAF 356  
Db 693 INNYENFDYLNIIYQEVQNFINVELSNFYLDYKGDIILYIEQRDSHIRRSMQTVLYQI--LV 750  
QY 357 DEPGTKTVIPGRV-----IGKFSIRLVPHMNVSAVEK-----QV 390  
Db 751 DM--TKLLAPILVHTAEVWSHTPHVKEESVHLADMPKVEVDQALLDKWRTFMNLRDDV 808  
QY 391 TRHLEDVFSKRNSNMVVSMTLGLHPWIANIDD--TQYLAAKRAIRTVFGTEP----D 443  
Db 809 NRALE-----TARNEKVIKGSLEAKVTIASNDKFNASEFLTSTFDALHQLFIVSQVKVVD 862  
QY 444 MIRDGSTIPIAKMFOEIVHKSVDLIPLGAVDDGEHSQNEKINR-WNYIE 491  
Db 863 KLDDQAT-----AYEHGDIVI-----EHADGEKCCRCWNYSE 894

RESULT 1298  
AAU36588  
ID AAU36588 standard; protein; 920 AA.  
XX  
AC AAU36588;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Staphylococcus aureus cellular proliferation protein #758.  
XX  
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.  
XX  
OS Staphylococcus aureus.  
XX  
PN WO200170955-A2.  
XX

PD 27-SEP-2001.  
XX 21-MAR-2001; 2001WO-US009180.  
PF 21-MAR-2000; 2000US-0191078P.  
XX 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX WPI; 2001-611495/70.  
DR N-PSDB; AAS54447.  
XX New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
PT  
XX Example 3; SEQ ID NO 12181; 511pp; English.  
XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 920 AA;  
SQ  
Query Match 3.2%; Score 84; DB 4; Length 920;  
Best Local Similarity 20.2%; Pred. No. 5.4e+02;  
Matches 107; Conservative 78; Mismatches 168; Indels 176; Gaps 34;  
QY 55 EWVAIESDSV--QPVPFRFRQELFRMMAV-----AADTLRLGARV-----ASVDMGPQQL 102  
Db 453 EWV-ISRQVWGVPPLPVFYAENGELIIMTKETVNVHVADLFAEHGNSIWFEREAILD-----L 507  
QY 103 PDGQSLPIPPVILAEELGSDPTKGTVCFYGHLDVQPADRGDGLW-----TDPYVL 151  
Db 508 PEGFTHPGSP-----NGT--FKETDIM-----DVWFDGSSSHRGVLETRPELS 549  
QY 152 TEVDGKLYGRGATDNKGPVLAWINA-----VSAFRALEQDLVPNIKFIIEG----- 197  
Db 550 FPAD--MYLEGSQYRG----WFNSSITTSVATRGVSPYKFL-----LSHGFVMDGEGKK 598  
QY 198 -MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 256  
Db 599 MSKSLGNVIVPDQVVKQK-----GADIA-----RLWVS-----STDYLDVVRIS 637  
QY 257 DQDFHSGTFGGILHEPMADLVALLGSLVD-----SSGHILVPGIY--DEVVPLTEEE 306  
Db 638 DEILKQTS--DVYRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDYLLNRLREFTAST 695  
QY 307 INTYKAI-HLDEL-EEYRNSSRVE--KFLFDTKKEIL-----MHLWRYPSLSIHGIEGAF 356  
Db 696 INNYENFDYLNLYQEVQNFINVELSNFYLDYGDKILYIEQRDSHRRSMQTVLYQI--LV 753

QY 357 DEPGTKTVIPGRV-----IGKFSIRLVPHMNVSAVEK-----QV 390  
Db 754 DM--TKLLAPILVHTABEWSHTPHVKEESVHLADMPKVVEVDQALLDKWRTFMNLRDDV 811  
QY 391 TRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDD---TQYLAAKRAIRTVFGTEP-----D 443  
Db 812 NRALE-----TARNEKVIKGSLEAKVTIASNDKFNASEFLTSFDALHQLFIVSQVKVVD 865  
QY 444 MIRDGSTIPIAKMFQEIHVHKSVVLIPLGAVDDGHSQNEKINR-WNYIE 491  
Db 866 KLDDQAT-----AYEHGDIVI-----EHADGEKCERCWNYS 897

RESULT 1299  
ADN21308  
ID ADN21308 standard; protein; 941 AA.  
XX  
AC ADN21308;  
XX

DT 02-DEC-2004 (first entry)  
XX Bacterial polypeptide #3961.  
XX

KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
XX 20-FEB-2003; 2003US-00369493.  
PF  
XX 21-FEB-2002; 2002US-0360039P.  
PR  
XX

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 3961; 122pp; English.  
XX

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of





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PD 15-FEB-1996.
XX
PF 30-MAY-1995; 95WO-JP001040.
XX
PR 29-JUL-1994; 94JP-00197780.
PR 01-DEC-1994; 94WO-JP002022.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
PI Ohta S, Usami S, Burnell NJ;
XX
DR WPI; 1996-129386/13.
DR N-PSDB; AAT12672.
XX
PT Recombinant cold-resistant pyruvate phosphate di.kinase - imparts
PT improved cold tolerance to transgenic plants which express the enzyme.
XX
PS Claim 1; Page 23-29; 70pp; Japanese.
XX
CC The sequences given in AAR90923-26 represent wild type pyruvate phosphate
CC dikinase (PPDK) enzymes from various organisms. These sequences were used
CC in the design of a novel protein having cold-resistant PPDK activity (see
CC also AAR90927). The cold-resistant PPDK is based primarily on the PPDK
CC sequence of F. brownii and comprises an addition, deletion or
CC substitution of one or more amino acids in the C-terminal portion, esp.
CC within the region residues 832-955. The cold-resistant PPDK may also be
CC based on the F. bidentis PPDK sequence having Pro at position 869 and/or
CC Leu at 885 and Val at 952. Plants, e.g. maize, transformed with DNA
CC encoding the cold-resistant PPDK, have improved cold resistance
XX
SQ Sequence 953 AA;
Query Match 3.2%; Score 84; DB 2; Length 953;
Best Local Similarity 20.1%; Pred. No. 5.7e+02;
Matches 97; Conservative 71; Mismatches 141; Indels 174; Gaps 28;
QY 29 SPPALLEKFQYIDLHQDEFVQTLKE-----WVAIESDSVQVPVFRFRQELFRM---MAV 80
Db 138 SLPPGLWDEISEGLDYVQKEMASASGLDPSKPLLLSVRSGAAISMPGMMDTVLNLGLNDEV 197
QY 81 AADTLQRLGARVA-----SVDMG-PQQLPDGQSLPIPPVILAEGLSDPTKGTV 127
Db 198 VAGLAGKSGARFAYDSYRRFLDMFGNVVMGIPHSLFDEK-----LEQMAE--KGI- 246
QY 128 CFYGH--DVQPADRGDGLWTDPY--VLTEVDGKLYGRGATDNKGPVLAWINAV----- 177
Db 247 ----HLDTDLTAADLKD--LVKEYKNVYVEAKGEKF---PTDPKKQLELAVNAVFDSWDS 297
QY 178 ---SAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQ 234
Db 298 PRANKYRSINQ-----ITGL-KGTAVNIQSMV----- 323
QY 235 RKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGIL--HEPMADLVALLGS-LVDSSGHIL 291
Db 324 -----FGNMGNT-----SGT--GVLFRNPSTGEKLYGEFLINAQGEDV 361
QY 292 VPGIYDEVVPLTEEEINT-----YKAHLDLLE---EYRNSSRVEKFLPDTKEEILM 339
Db 362 VAGI-----RTPEDLGTMETCMPDAYKELVENCEILEGHYKDMMDIE---FTVQEN--- 409
QY 340 HLWRYPSLSIHGIEGAFDEPGTKTIVPGRVIGKFSIRLVPHM-----NVSAVEKQVTR 392
Db 410 RLWMLQCRT-----GKRTKGAVRIADVDMVNEGLIDTRTAIKRVETQ 451
QY 393 HLEDV----FSKRNSNKNVVSMTLGLHP-----WIANIDDTQVLAAKRAIRTVEGT 440
Db 452 HLDQLLHPQFEDPSAYKSHVVATGLPASPGAAVQVCFSAEADAETWHAQGSAILVRTET 511
QY 441 EPD 443
Db 512 SPE 514
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RESULT 1302
ABG06406
ID ABG06406 standard; protein; 974 AA.
XX
AC ABG06406;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #6397.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
(HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS70593.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 36765; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 974 AA;
Query Match 3.2%; Score 84; DB 4; Length 974;
Best Local Similarity 21.4%; Pred. No. 5.9e+02;
Matches 82; Conservative 59; Mismatches 135; Indels 108; Gaps 26;
QY 45 HQDEFVQTLKEWVAIESDSVQVPVFRFRQELFRMMAVADTLQRLGAR-VASVDMGPQQLP 103
Db 563 HQKE--DSLRD-AAIPGSYRRPAPRMTR-----TGSQLAAREVTGSGAVPRQL- 608
QY 104 DQSLPIPPVILAEGLSDPTKGT-----VCFYGHLDVQPADRGDGLWTDTPYVLTEVD 155
Db 609 EGRR-----CQAGRANGGTSSDSSSSMAAIIYGVVE-----GGGTRSEVLLVSE-D 653
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication







Db 603 QGSDIATLKGVS SVKSVKTIPIFE-----SVDNVAVLKLP 640  
Qy 104 DGQSLPIPPVILAE-----LGSDPT-KGTVCFYGHLDVQPADRGDQ-WLTD----- 147  
Db 641 P-ELNSVKPIKLAKKVQSDYLTLTAYDPNFOHAATFTGCII-----DGNWLNNSFDTK 693  
Qy 148 -----PYVLTEVDGKLYG-----RGATDNKGPVLAWINAV-SAFRALEQDLPVN----- 190  
Db 694 FGN SGAPY--CDHDGRLVGHILGTQGLV-SQGIVI--VDALKNTFQLADQCRPQNFDMD 748  
Qy 191 -IKFIEGMEEGSVALEELVB-KEKDRFFSGVDYIYISDNLWISQ----- 234  
Db 749 FLEKVIAGTKVSHAAILKELEELREEVQFLK--KKCVTYDDYWLCQTIFGQAKGKTKKTV 806  
Qy 235 --RKPAITYGTRGNSYEMVEVKCRDQDFHSGTGGILHEPMDLVAL-----GS 282  
Db 807 RGRKHLVTKRALGKHGFMKMRMLTDEEYQNMIKGFSAEIREAVNALREQAWLNICYDN 866  
Qy 283 LVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDL EE-----YRNSSRVEKFLFDTKBEIL 338  
Db 867 DVDDGE--EDDWYDDMVETDRVNQEIDEAIERAMEDRGEFYQKKSRL-TFV---EQAM 919  
Qy 339 MHL 341  
Db 920 MHL 922  
RESULT 1310  
AAM79125  
ID AAM79125 standard; protein; 1143 AA.  
XX AAM79125;  
XX 06-NOV-2001 (first entry)  
XX Human protein SEQ ID NO 1787.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.  
XX Homo sapiens.  
XX WO200157190-A2.  
XX 09-AUG-2001.  
XX 05-FEB-2001; 2001WO-US004098.  
XX 03-FEB-2000; 2000US-00496914.  
PR 27-APR-2000; 2000US-00560875.  
PR 20-JUN-2000; 2000US-00598075.  
PR 19-JUL-2000; 2000US-00620325.  
PR 01-SEP-2000; 2000US-00654936.  
PR 15-SEP-2000; 2000US-00663561.  
PR 20-OCT-2000; 2000US-00693325.  
PR 30-NOV-2000; 2000US-00728422.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX WPI; 2001-476283/51.  
DR N-PSDB; AAK52258.  
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
PT in diagnosis and gene therapy.  
XX Claim 20; Page 4143-4146; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX SQ Sequence 1143 AA;  
Query Match 3.2%; Score 84; DB 4; Length 1143;  
Best Local Similarity 24.0%; Pred. No. 7.5e+02;  
Matches 43; Conservative 27; Mismatches 59; Indels 50; Gaps 8;  
Qy 276 LVALLGSLVDSSGHILVPGIY-DEVVPLTEEEINTYKAIHLDL EEYRNS--SRVEKFLFD 332  
Db 144 LIQCLGSGVRQAGHRL--GAHLDRLVPLVEFCN-----LDDDELRESCLQAFEAFLRK 195  
Qy 333 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 196 CPKEMGPHVPNTVSLCLQ-----YIKHDPNRYNDSDEDEEQM 232  
Qy 393 HLED-VFSKRNSNKMVSMVMTLGLHPWIANIDDTQY---LAAKRAIRTVFGTEPDMIRD 447  
Db 233 ETEDSEFSEQSEDE-----YSDDDMSWKVRRRAAKCIAALISSRPDLPLPD 279  
RESULT 1311  
AAU70675  
ID AAU70675 standard; protein; 1230 AA.  
XX AAU70675;  
XX 14-FEB-2002 (first entry)  
XX Human otoferlin.  
XX Human; mouse; otoferlin; OTOF; brain; auditory function;  
KW autosomal nonsyndromic prelingual deafness; DFNB9.  
XX Homo sapiens.  
XX WO200170972-A2.  
XX 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-IB0000578.  
XX 24-MAR-2000; 2000US-0191738P.  
XX (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;  
PI Weil D;  
XX WPI; 2001-611499/70.  
XX Novel human gene Otoferlin, underlying an autosomal recessive  
PT nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the  
PT gene, implicated in deafness.  
XX Claim 4; Fig 3; 99pp; English.  
XX The invention relates to a purified polynucleotide (I) encoding a protein  
CC sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long



CC human otoferlin isoform in brain. (I) was identified as underlying an  
CC autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for  
CC detecting deafness disease in humans and for characterising the functions  
CC of proteins and genes encoding them in auditory function. AAU70669-  
CC AAU70676 represent human and mouse otoferlin amino acid sequences of the  
CC invention  
XX  
SQ Sequence 1230 AA;  
Query Match 3.2%; Score 84; DB 4; Length 1230;  
Best Local Similarity 20.0%; Pred. No. 8.4e+02;  
Matches 90; Conservative 66; Mismatches 169; Indels 124; Gaps 24;  
QY 108 LPIPPVILAEIGSDPTKGTVCFYG-----HLDVQPADRGDGLWLTDPYV 150  
Db 695 VPLPEDVSREAGDYDSTYG--MFGIPSNDPINVLVRVYVVRATDLHPADING--KADPYI 750  
QY 151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEGM-----EBAGSVA 205  
Db 751 AIRL-GKTDIR---DKENYISKQLNPV-----FGKSFIDIASFPMESMLTVAVYDNLVG 801  
QY 206 LEELVEKEK-----DRFFS-----GV--DYIVISDNLWISQKPAITYGTRGNSYFVVEV 253  
Db 802 TDDLIGETKIDLENRFYSKHRATCGIAQTYSTHGYNIRWDRMKP-----SQILTRL 852  
QY 254 KCRDQDFHSGTGGILHEPMDLVALLGS-LVDSSG-----HILVPGI-YDEVVP--- 301  
Db 853 -CKDGKVDGPHFGPPGRVKVANRVFTGFPSEIEDENGQRKPTDEHVALLALRHWDIPRAG 911  
QY 302 --LTEEEINTYKAHLD---LEEYRNSRVEKFLFD-----TKEEILMHL 341  
Db 912 CRLVPEHVETRPLLPNDKPGIEQGRLELWVDMFPMOMPAPGTPLDISPRKPKKYELRVII 971  
QY 342 WRYPSSLIHGIEGAFDEPGTKVIPGRVIGK-----FSIR-LVPHM 381  
Db 972 WNTDEVVLEDDFFTGEKSSDIFVRGWLKQEQEDKQDTDVYHSLTGEGNFWRYLFFPD 1031  
QY 382 NVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA---NIDDTQYLAA----- 430  
Db 1032 YLAEEKIVISKESMFSDWDETEYKIPARLTQI--WDADHFSADD--FLGAIELDLNRF 1087  
QY 431 KRAIRTVFGTEPDMIRDGSTIPIAKMFQE 459  
Db 1088 PRGAKTAKQCTMEMATGEVDVPLVSIFKQ 1116  
RESULT 1312  
ADJ80171  
ID ADJ80171 standard; protein; 1236 AA.  
XX  
AC ADJ80171;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Novel human nucleic acid-associated protein #47.  
XX  
KW cytosstatic; antiarteriosclerotic; cerebroprotective; antiparkinsonian;  
KW anticonvulsant; anti-HIV; antiallergic; antibacterial; virucide;  
KW gene therapy; nucleic acid-associated protein; cancer; atherosclerosis;  
KW stroke; Parkinson's disease; epilepsy; Cushing's syndrome; AIDS; allergy;  
KW microarray element; protein-protein interaction; drug-target interaction;  
KW gene expression; chromosomal mapping; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FN WO2003038052-A2.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-US034846.  
XX  
PR 29-OCT-2001; 2001US-0348442P.  
PR 01-NOV-2001; 2001US-0335544P.

PR 05-NOV-2001; 2001US-0337535P.  
PR 09-NOV-2001; 2001US-0344650P.  
PR 15-NOV-2001; 2001US-0334762P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Becha SD, Borowsky ML, Burford N, Chawla NK, Elliott VS;  
PI Emerling BM, Forsythe IJ, Gietzen KJ, Gorvad AE, Griffin JA;  
PI Hafalia AJA, Ison CH, Lal PG, Lee EA, Lee S, Lee SY, Marquis JP;  
PI Ramkumar J, Sprague WM, Swarnakar A, Tang YT, Warren BA, Yang J;  
PI Yue H, Zebajadian Y;  
XX  
DR WPI; 2003-430514/40.  
DR N-PSDB; ADJ80229.  
XX  
PT New human nucleic acid-associated protein (NAAP) and polynucleotide,  
PT useful for diagnosing, treating, and preventing disorders associated with  
PT aberrant expression of NAAP, e.g. cancer, AIDS, stroke or infection.  
XX  
PS Claim 1; SEQ ID NO 47; 443pp; English.  
XX  
CC The invention relates to novel human nucleic acid-associated proteins and  
CC genes encoding them, sequences that have at least 90-99 % identity to the  
CC sequences; or biologically active or immunogenic fragments of these. The  
CC polypeptides and polynucleotides are useful in diagnosing, treating and  
CC preventing disorders associated with aberrant expression of NAAP, such as  
CC cell proliferative (e.g. cancer or atherosclerosis), neurological (e.g.  
CC stroke, Parkinson's disease or epilepsy), developmental (e.g. Cushing's  
CC syndrome), autoimmune/inflammatory (e.g. AIDS or allergies), or  
CC infections. These may also be used as elements on a microarray which may  
CC monitor or measure protein-protein interactions, drug-target  
CC interactions, and gene expression profiles. The polynucleotide may also  
CC be used in chromosomal mapping and in various diagnostic assays. These  
CC are also useful in assessing the effects of exogenous compounds on the  
CC expression of nucleic acids and amino acid sequences of NAAP, in  
CC facilitating drug discovery process, and in investigating the  
CC pathogenesis of diseases or medical conditions. This sequence corresponds  
CC to one of the proteins of the inventions.  
XX  
SQ Sequence 1236 AA;  
Query Match 3.2%; Score 84; DB 7; Length 1236;  
Best Local Similarity 24.0%; Pred. No. 8.5e+02;  
Matches 43; Conservative 27; Mismatches 59; Indels 50; Gaps 8;  
QY 276 LVALLGSLVDSSGHILVPGIY-DEVVPLTEEEINTYKAHLDLEEYRNS--SRVEKFLFD 332  
Db 237 LIQCLGSGVRQAGHRL--GAHLDRLVPLVEDFCN-----LDDDELRESCLOAFEAFLRK 288  
QY 333 TKEEILMHLWRYPSSLIHGIEGAFDEPGTKVIPGRVIGKFSIRLPHMNVSAVEKQVTR 392  
Db 289 CPKEMGPHVNPVNTSLCQ-----YKHDPNINYDSDEDEEQM 325  
QY 393 HLED-VFSKRNSSNMVVSMTLGLHPWIANIDDTQY---LAAKRAIRTVFGTEPDMIRD 447  
Db 326 ETEDSEFSEQESEDE-----YSDDDDMSWKVRAAKCIAALISSRPDLLPD 372  
RESULT 1313  
AAU70672  
ID AAU70672 standard; protein; 1307 AA.  
XX  
AC AAU70672;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human otoferlin #1.  
XX  
KW Human; mouse; otoferlin; OTOF; brain; auditory function;  
KW autosomal nonsyndromic prelingual deafness; DFNB9.  
XX  
OS Homo sapiens.



QY 194 IIEGMEAGSVALEELVEKDRFFS-GVDYIVISDNLWISQKPAIT-----YGTRGNS 247  
Db 467 LLENQYRVGLLRMERAI-----KERMSSVDIDTVMPHD---LINAKPAAAVREFGSSQLS 520  
QY 248 YFMVEVK-----CRD-----QDFHSGTFGGI--LHEPMADLVALL 280  
Db 521 QFMDQTNPLSEITHKRRLSALGPGLTRERAGFEVRDVHPTHYGRICPIETPEGNIGLI 580  
QY 281 GSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSRVEKFLDFTKBEILMH 340  
Db 581 NSLA-----THARVVKYGFIESPYRRVKDGKPKQDEVVYMSAMEESKH 622  
QY 341 LWRYPSSLIHGIEGAFDEPGTKTIVPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVFSK 400  
Db 623 VIAQSNIKV--AEGEIVE---DLVPGRINGEPTL-----LQKE-TVDLMDV--- 662  
QY 401 RNSSNMVVSMTGLHPWIANIDDTQYLAA---KRAIRTV-----FGTEPDMIRDG 448  
Db 663 ---SPRQVSVAAALIPFLENDANRALMGSNMQRAVPLVQSDAPLVGTGMEAVVARDS 719  
QY 449 STIPIAK 455  
Db 720 GAVVIATK 726

RESULT 1315  
ABU27289  
ID ABU27289 standard; protein; 1396 AA.  
XX  
AC ABU27289;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #12816.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Chlamydia trachomatis.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US0009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA31159.

XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 55213; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1396 AA;

Query Match 3.2%; Score 84; DB 6; Length 1396;  
Best Local Similarity 19.7%; Pred. No. 1e+03;  
Matches 82; Conservative 35; Mismatches 124; Indels 176; Gaps 16;  
QY 125 GTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDN-----KGPVLAWINAVS 178  
Db 815 GTL---NHIEVSTIRQS-----EELLPLKDRIVGRTVSENYYQPGDKSNVLAY---- 860  
QY 179 AFRALEQDLVPNIKFIIEGMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQK-- 236  
Db 861 -----AGDVLTSQAEAIDD---AGIDSVKIRSTLTCTESRRGV 895  
QY 237 -----PAITYGTRGNSYEMVEVKCRDQDFHSGTFGG----- 267  
Db 896 CAKCYGLNLANGRLIGLGEAVGIIAAQSIGEPGTQLTM-----RTFHLGGIAATSTTP 948  
QY 268 -ILHEPMADLVAL-LGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAHLDLEEYRNSR 325  
Db 949 EIVAECDGILVYDLRFVVDQEGNNLV-----LNKMGALHLVRDEGRSLSE 994  
QY 326 VEKFLFDTKEEILMHL-----WRYPSLSIHGIEGAFDEPG---TKT 363  
Db 995 YKKLLSTKSIESLATFPVELGAKILVDGAAVTAGORIAEVELHNPIICDKPGFVHYED 1054  
QY 364 VIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVVSMTGLHPWIANID 423  
Db 1055 LVEG-----VSTEKVTNKTGLVELIVKQHRGE-----LHPQIAIYA 1091  
QY 424 DTQYLAAKRAIRTVFGTEPDMIRDCGSTIPIAKMFOEIVHKSVVLIPLGAVDDGEHSQ 480  
Db 1092 DAN-----MQELV--GTYAIPSGAIIISVEEGQ 1116

RESULT 1316  
ABO71520  
ID ABO71520 standard; protein; 1501 AA.  
XX  
AC ABO71520;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #3695.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX





Db 527 NELKSRWENLLGPDYEVVATLDT-----QIADDAELQKYSKLLPIHTL 570

Qy 117 ELGSDPTKGTVCFYGHLDVQPADRGD-----GWLTPPYVLTEVDG-KLYGRGATDNKGPV 170

Db 571 RLGVEVDS---FDGHHYISSIVSGGPVDTLGLLQPEDELLELVNGMQLYK-----SRREA 622

Qy 171 LAWIN-----AVSAFRALEQDLP-----VNIKFIIEGMEERAG 202

Db 623 VSFLEKEVPPFTLVCCRLLFDDEASVDEPRRTETSLPETEVDHNMVNT-----EDDDG 677

Qy 203 SVAL-----EELVEKEKDRFFSGVDY-----IVISDNL---WISQRKPAITYGT 243

Db 678 ELALWSPVKIVELVKDCKGLGFSILDYQDPLDPTRSVIVIRSLVADGVAERSGGLLPGD 737

Qy 244 RGSNYFMVEVK--CRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVP 301

Db 738 R-----LVSVNEYCLD-----NTSLAEAVEILKAVPPLVHL---GICKPLVE 777

Qy 302 LTHEEINTYKAHLDLEEYRNSSRVEKFLFD-TKEEILMHLWRYPSLSIHGIEGAFDEPG 360

Db 778 DNEEE--SCYILH-----SSSNEDKTEFSGTIHD-----NSSLILEAPKGRDEPY 822

Qy 361 TKTVI---PGRVIGKFSIRLVPHMNVSAVEKQ-----VTRHLEDVFSKRNSSNKQV 408

Db 823 FKEELVDEPFLDLGKSF-----HSQKEIEQSKAEWEMHEFTLPRLOEMDEER-----EML 873

Qy 409 V-----SMTGLHPWIANIDDTQYLAAKRAIRTVFGT-----EPDMIRDS 449

Db 874 VDEEYELQDPSPSMELYP-LSHIQEATPVPSVNLH--FGTQWLHDNEPSESEQEARIGR 930

Qy 450 TI-----PIAKMFQEIIVHKSVVLIPLGAVDGGEHSQNEKINRWNYIEGTLKFAAFFLEM 503

Db 931 TVYSQEAQPYGYCPENVMKENFVNESLPSVPSTE--GNSQQGRFDDLENLNSLAKTSLDL 988

Qy 504 AQL 506

Db 989 GMI 991

RESULT 1318

ADJ95459

ID ADJ95459 standard; protein; 1734 AA.

XX AC ADJ95459;

XX 03-JUN-2004 (first entry)

DE Human Ubiquitin ligase E3alpha I variant.

XX Human; enzyme; ubiquitin ligase; E3alpha I; ubiquitin-proteosome pathway; gene therapy; vaccine; muscular atrophy; cachexia; catabolic disorders; cancer cachexia; renal cachexia; inflammatory cachexia; muscle wasting disorder; metabolic acidosis; uremia; burn; hyperthyroidism; Cushing's syndrome; fasting; denervation atrophy; diabetes mellitus; sepsis; AIDS wasting syndrome; SNP; single nucleotide polymorphism.

XX Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 225..246

FT /note= "Encoded by nucleotides 658-678 of SEQ ID 18 "

FT

FT Misc-difference 1573

FT /note= "May be Trp as the result of a single nucleotide polymorphism"

FT

FT Misc-difference 1665..1666

FT /note= "Encoded by nucleotides 4933-4998 of SEQ ID 18 "

FT

XX US6706505-B1.

PN 16-MAR-2004.

XX

PD

XX

PF 28-NOV-2000; 2000US-00724126.

XX

PR 08-MAR-2000; 2000US-0187911P.

XX

PA (AMGE-) AMGEN INC.

XX

PI Han H, Kwak K;

XX

DR WPI; 2004-236723/22.

DR N-PSDB; ADJ95458.

XX

PT New nucleic acid molecule, useful for preparing a composition for diagnosing, treating or preventing diseases associated with human E3approximatelya polypeptide, e.g., muscle atrophy.

PT

XX

PS Claim 19; SEQ ID NO 19; 104pp; English.

XX

CC The invention relates to a new isolated nucleic acid molecule appearing as ADJ95441(or its complement) encoding a ubiquitin ligase E3alpha I protein appearing as ADJ95442. Also included are a vector comprising the nucleic acid, a host cell comprising the vector, a process of producing a E3alpha I ubiquitin ligase polypeptide, a composition comprising the nucleic acid molecule, a reagent comprising a detectably labelled nucleotide, and a method for determining the presence of a human E3alpha I ubiquitin ligase nucleic acid in a biological sample. The nucleic acid molecule is useful for preparing a composition for diagnosing, treating or preventing diseases associated with human E3alpha I polypeptide, e.g. muscle atrophy, cachexia, catabolic disorders, cancer cachexia, renal cachexia, inflammatory cachexia, muscle wasting disorders associated with metabolic acidosis, uremia, burns, hyperthyroidism, Cushing's syndrome, fasting, denervation atrophy, diabetes mellitus, sepsis and AIDS wasting syndrome. The present sequence represents a human E3alpha I variant protein encoded by a cDNA assembled from previously isolated cDNA fragments.

CC

XX

SQ Sequence 1734 AA;

Query Match 3.2%; Score 84; DB 8; Length 1734;

Best Local Similarity 18.2%; Pred. No. 1.4e+03;

Matches 62; Conservative 52; Mismatches 107; Indels 120; Gaps 15;

Qy 248 YFMVEVKCR---DQDFHSGTGGILHEPM-----ADLVAL 279

Db 681 FYYQDVKCREEMYDKDIIMLQIGASIMDPNKFLLLVQLRYELAEAFNKTISTKDQDLIKQ 740

Qy 280 LGS�VDSSGHILVPGIYDEVVP---LTHEEINTYKAHLDLEEYRNSSRVEKFLDTK- 334

Db 741 YNTLIEMLQVLIYIVGERYVPGVGNVTKEEVTMRIIHLHCIEPMHSAIAKNLPENEN 800

Qy 335 -----EEIL--MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVE 387

Db 801 NETGLENVINKVATFKKPGVSGHGVYELKDES-----LKDFNMYF---YHYSKTQ 847

Qy 388 KQVTRHLEDVFSKRNSSNK-----MVVSMTLGLHPWIANIDDTQYLAAKRAI 434

Db 848 HSKAEHMQK--KRRKQENKDEALPPPPPPPEFCPAFSKVINL---LNCDIMMYI-----L 896

Qy 435 RTVF---GTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDGGEHSQN----- 481

Db 897 RTVFERAIDTDSNLWTEG-----MLQMAFH---ILALGLLEEKQQLQKAPEEEVTFD 945

Qy 482 -----EKNRWNYIEGTLKFAAFFLEM 503

Db 946 FYHKASRLGSSAMNIQMLLEKLGIPQLEGQKDMITWILQM 986

RESULT 1319

ADJ95459

ID ADJ95459 standard; protein; 1734 AA.

XX

AC ADJ95459;

XX

DT 16-DEC-2004 (first entry)

XX DE Variant human E3alpha1 ubiquitin ligase.

XX KW Human; E3alpha ubiquitin ligase; huE3alphai;

KW ubiquitin-proteasome pathway; chromosome 15 q; rapid muscle wasting;

KW fasting; metabolic acidosis; muscle degeneration; kidney failure;

KW renal cachexia; uremia; diabetes mellitus; sepsis; AIDS wasting syndrome;

KW cancer cachexia; negative nitrogen balance; burn; Cushing's syndrome;

KW inflammatory cachexia; hyperthyroidism; denervation atrophy;

KW protein/tissue wasting; energy-protein malnutrition; muscle atrophy;

KW gene therapy; enzyme.

XX OS Homo sapiens.

XX US2004185037-A1.

PN 23-SEP-2004.

XX 15-JAN-2004; 2004US-00758672.

XX 08-MAR-2000; 2000US-0187911P.

PR 28-NOV-2000; 2000US-00724126.

XX (HANH/) HAN H.

PA (KWAK/) KWAK K.

XX Han H., Kwak K;

XX WPI; 2004-707854/69.

DR Novel isolated human E3alpha ubiquitin ligase nucleic acid molecule

XX useful for treating and/or preventing renal cachexia or inflammatory

PT cachexia.

XX Example 9; SEQ ID NO 19; 115pp; English.

PS The present invention relates to new orthologue of human E3alpha

XX ubiquitin ligase, huE3alphai and huE3alphaiI. Most intracellular proteins

CC are degraded through the ubiquitin-proteasome pathway. Proteins are

CC marked for proteasomal degradation by conjugation of ubiquitin to the

CC protein. Conjugation of the ubiquitin molecule involves the activation by

CC E1 enzyme, subsequent transfer to E2 enzyme, which serves as a carrier,

CC and then interacts with a specific E3 ligase family member. E3 ligase

CC binds to proteins targeted for degradation and catalyses the transfer of

CC ubiquitin from the E2 carrier enzyme to the target protein. E3 ligase

CC determines the specificity of the system. The E3alpha family is the main

CC family of intracellular ligases and is involved in the N-end rule pathway

CC of protein degradation. E3alpha enzyme binds directly to the primary

CC destabilising N-terminal amino acid and catalyses ubiquitin conjugation

CC thereby targeting the protein for degradation. The human E3alpha gene is

CC located on chromosome 15 q. Increased proteolysis through the ubiquitin-

CC proteasome pathway has been determined to be a major cause of rapid

CC muscle wasting including, fasting, metabolic acidosis, muscle

CC degeneration, kidney failure, renal cachexia, uremia, diabetes mellitus,

CC sepsis, AIDS wasting syndrome, cancer cachexia, negative nitrogen

CC balance, burns, Cushing's syndrome, inflammatory cachexia,

CC hyperthyroidism, denervation atrophy, protein/tissue wasting, and energy-

CC protein malnutrition. E3alpha plays a role in the overall increase in

CC ubiquitination that is associated with and may mediate muscle atrophy in

CC catabolic and other disease states. Treatment may be administered by gene

CC therapy, cell therapy and antisense therapy methods. The patent describes

CC is a variant of human E3alphai ubiquitin ligase. The patent describes

CC this sequence as containing a Trp at position 1568 as a result of a SNP

CC in the nucleotide sequence. However, the sequence contains a Pro at

CC position 1568.

XX Sequence 1734 AA;

SQ Query Match 3.2%; Score 84; DB 8; Length 1734;

Best Local Similarity 18.2%; Pred. No. 1.4e+03;

Matches 62; Conservative 52; Mismatches 107; Indels 120; Gaps 15;

QY 248 YFMVEVKCR----DQDFHSGTGGILHEPM-----ADLVAL 279

Db 681 FYYQDVKCREMYDKDIIMLQIGASLMDPNKELLVLQRYELAEAFNKTIISTKDDQLIKQ 740

QY 280 LGSLLVDSSGHILVPGIYDEVVP-----LTEEEINTYKAIHLDL EEYRNSSRVEKELFDTK- 334

Db 741 YNTLIEEMQLVLIYVGERYPVGVGNVTKEEVTMRIHLLLCIEPMPHSAIAKNLPENEN 800

QY 335 -----EEIL--MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVE 387

Db 801 NETGLENVINKVATFKKPGVSGHGVYELKDES-----LKOFNMYF---YHYSKTQ 847

QY 388 QVTRHLEDVFSKENSNNK-----MVVSMTLGLHPWIANIDDTQYLAAKRAI 434

Db 848 HSKAEHMQK--KRRKQENKDEALPPPPPPFCFAFSKVINL----LNCDIMMYI-----L 896

QY 435 RTVF---GTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDDGEHSQN----- 481

Db 897 RTVFERAIDTDSNLWTEG-----MLQMAFH----ILALGLLEEKKQLQKAP EEEVTFD 945

QY 482 -----EKINRWNYIEGTKLFAAFFLEM 503

Db 946 FYHKASRLGSSAMNIQMLEKLGIPQLEGQKDMITWILQM 986

RESULT 1320

ABP58330

ID ABP58330 standard; protein; 1738 AA.

XX AC ABP58330;

XX 07-APR-2003 (first entry)

XX Human cell growth, differentiation and death protein CGDD-1.

DE CGDD-1; cell growth; cell differentiation; cell death; human; cytostatic;

XX antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic;

KW antianaemic; ophthalmological; auditory; anticonvulsant;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW neuroleptic; tranquilizer; immunosuppressive; anti-HIV; antiallergic;

KW antiasthmatic; antithyroid; antidiabetic; dermatological; nephrotropic;

KW antirheumatic; antiarthritic; antiulcer; vulnery; virucide;

KW antibacterial; fungicide; antiparasitic; protozoacide; antihelminthic;

KW antiinfertility; gynaecological; ubiquitin protein ligase; enzyme;

XX gene therapy.

OS Homo sapiens.

XX WO200297032-A2.

XX 05-DEC-2002.

XX 05-APR-2002; 2002WO-US011152.

XX 06-APR-2001; 2001US-0282110P.

PR 11-APR-2001; 2001US-0283294P.

PR 26-APR-2001; 2001US-0286820P.

PR 27-APR-2001; 2001US-0287228P.

PR 16-MAY-2001; 2001US-0291662P.

PR 18-MAY-2001; 2001US-0291846P.

PR 25-MAY-2001; 2001US-0293727P.

PR 01-JUN-2001; 2001US-0295263P.

PR 01-JUN-2001; 2001US-0295340P.

PR 15-JAN-2002; 2002US-0349705P.

XX (INCY-) INCYTE GENOMICS INC.

PA Azimzai Y, Au-Young JK, Batra S, Baughn MR, Becha SD;

XX Borowsky ML, Burford N, Ding L, Elliott VS, Emerling BM, Gandhi AR;

PI Gietzen KJ, Griffin JA, Hafalia AJA, Honchell CD, Lal PG, Lee SY;

PI Lu DAM, Arvizu CS, Ramkumar J, Reddy R, Sanjanwala MM, Tang YT;

PI Wallia NK, Wang YE, Warren BA, Xu Y, Yang J, Yao MG, Yue H;

PI Zebarjadian Y;

XX



DR WPI; 2003-140453/13.  
DR N-PSDB; ABZ24689.  
XX  
PT Novel human proteins associated with cell growth, differentiation and  
PT death, useful for treating, diagnosing or preventing cancer,  
PT developmental, neurological, reproductive or autoimmune/inflammatory  
PT disorders.  
XX  
PS Claim 1; Page 183-187; 238pp; English.  
XX  
CC The present sequence is the protein sequence of human CGDD-1, a novel  
CC protein associated with cell growth, differentiation and death. The  
CC sequence is predicted from Incyte clone 1351608CB1, which was isolated  
CC from a paraganglionic tumour tissue cDNA library. Structural features  
CC establish the protein as being associated with cell growth,  
CC differentiation and death, with further evidence suggesting it to be a  
CC ubiquitin protein ligase. The invention is based on novel human CGDD-1 to  
CC -21 proteins (see ABP58330-50), the polynucleotides encoding them (see  
CC ABZ24689-709), and to the use of these for the diagnosis, treatment or  
CC prevention of cell proliferative disorders including cancer,  
CC developmental disorders, neurological disorders, autoimmune disorders,  
CC reproductive disorders, and disorders of the placenta, and in the  
CC assessment of the effects of exogenous compounds on the activity and  
CC expression of proteins and nucleic acids associated with cell growth,  
CC differentiation and death  
XX  
SQ Sequence 1738 AA;  
  
Query Match 3.2%; Score 84; DB 6; Length 1738;  
Best Local Similarity 18.2%; Pred. No. 1.4e+03;  
Matches 62; Conservative 52; Mismatches 107; Indels 120; Gaps 15;  
  
QY 248 YFMVEVKCR---DQDFHSGTFFGGILHEPM-----ADLVAL 279  
Db 665 FYYQDVKCREEMYDKDIIMLQIGASLMDPNKFLLLVLRVELAEAFNKTISTKDQLIKQ 724  
QY 280 LGSIVDSSGHILVPGIYDEVVP---LTEEEINTYKAHLDLEEYRNSRVEKFLFDTK- 334  
Db 725 YNTLIEEMQLVLIYIVGERYVPGVGNVTKEEVTMREIIHLLCIEPMPHSAIAKNLPENEN 784  
QY 335 -----EEIL--MHLWRYPSSLIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 785 NETGLENVINKVATFKKPGVSGHGVYELKDES-----LKDFNMYF---YHYSKTQ 831  
QY 388 KQVTRHLEDVFSKRNSSNK-----MVVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 832 HSKAEHMOK--KRRQKENKDEALPPPPPPPEFCPAFSKVINL-----LNCDIMMYI-----L 880  
QY 435 RTVF---GTEPDMIRDGSTIPIAKMFQEIIVHKSIVLPLGAVDDGEHSQN----- 481  
Db 881 RTVFERAIDTDSNLWTEG-----MLQMAFH---ILALGLLEEKQLQKAPEEEVTFD 929  
QY 482 -----EKINRWNYIEGTKLFAAFFLEM 503  
Db 930 FYHKASRLGSSAMNIQMLEKLKGIPQLEGQKDMITWILQM 970  
  
RESULT 1321  
ADJ95442  
ID ADJ95442 standard; protein; 1749 AA.  
XX  
AC ADJ95442;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human Ubiquitin ligase E3alpha I.  
XX  
KW Human; enzyme; ubiquitin ligase; E3alpha I; ubiquitin-proteosome pathway;  
KW gene therapy; vaccine; muscular atrophy; cachexia; catabolic disorders;  
KW cancer cachexia; renal cachexia; inflammatory cachexia;  
KW muscle wasting disorder; metabolic acidosis; uremia; burn;  
KW hyperthyroidism; Cushing's syndrome; fasting; denervation atrophy;  
KW diabetes mellitus; sepsis; AIDS wasting syndrome; SNP;

KW single nucleotide polymorphism.  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1568  
FT /note= "May be Arg as the result of a single nucleotide  
FT polymorphism"  
XX  
PN US6706505-B1.  
XX  
PD 16-MAR-2004.  
XX  
PF 28-NOV-2000; 2000US-00724126.  
XX  
PR 08-MAR-2000; 2000US-0187911P.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Han H, Kwak K;  
XX  
XX WPI; 2004-236723/22.  
DR N-PSDB; ADJ95441.  
XX  
PT New nucleic acid molecule, useful for preparing a composition for  
PT diagnosing, treating or preventing diseases associated with human  
PT E3approximately polypeptide, e.g., muscle atrophy.  
XX  
PS Claim 1; SEQ ID NO 2; 104pp; English.  
XX  
CC The invention relates to a new isolated nucleic acid molecule appearing  
CC as ADJ95441(or its complement) encoding a ubiquitin ligase E3alpha I  
CC protein appearing as ADJ95442. Also included are a vector comprising the  
CC nucleic acid, a host cell comprising the vector, a process of producing a  
CC E3alpha I ubiquitin ligase polypeptide, a composition comprising the  
CC nucleic acid molecule, a reagent comprising a detectably labelled  
CC nucleotide, and a method for determining the presence of a human E3alpha  
CC I ubiquitin ligase nucleic acid in a biological sample. The nucleic acid  
CC molecule is useful for preparing a composition for diagnosing, treating  
CC or preventing diseases associated with human E3alpha I polypeptide, e.g.  
CC muscle atrophy, cachexia, catabolic disorders, cancer cachexia, renal  
CC cachexia, inflammatory cachexia, muscle wasting disorders associated with  
CC metabolic acidosis, uremia, burns, hyperthyroidism, Cushing's syndrome,  
CC fasting, denervation atrophy, diabetes mellitus, sepsis and AIDS wasting  
CC syndrome. The present sequence represents human E3alpha I.  
XX  
SQ Sequence 1749 AA;  
  
Query Match 3.2%; Score 84; DB 8; Length 1749;  
Best Local Similarity 18.2%; Pred. No. 1.5e+03;  
Matches 62; Conservative 52; Mismatches 107; Indels 120; Gaps 15;  
  
QY 248 YFMVEVKCR---DQDFHSGTFFGGILHEPM-----ADLVAL 279  
Db 676 FYYQDVKCREEMYDKDIIMLQIGASLMDPNKFLLLVLRVELAEAFNKTISTKDQLIKQ 735  
QY 280 LGSIVDSSGHILVPGIYDEVVP---LTEEEINTYKAHLDLEEYRNSRVEKFLFDTK- 334  
Db 736 YNTLIEEMQLVLIYIVGERYVPGVGNVTKEEVTMREIIHLLCIEPMPHSAIAKNLPENEN 795  
QY 335 -----EEIL--MHLWRYPSSLIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 796 NETGLENVINKVATFKKPGVSGHGVYELKDES-----LKDFNMYF---YHYSKTQ 842  
QY 388 KQVTRHLEDVFSKRNSSNK-----MVVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 843 HSKAEHMOK--KRRQKENKDEALPPPPPPPEFCPAFSKVINL-----LNCDIMMYI-----L 891  
QY 435 RTVF---GTEPDMIRDGSTIPIAKMFQEIIVHKSIVLPLGAVDDGEHSQN----- 481  
Db 892 RTVFERAIDTDSNLWTEG-----MLQMAFH---ILALGLLEEKQLQKAPEEEVTFD 940  
QY 482 -----EKINRWNYIEGTKLFAAFFLEM 503

Db 941 FYHKASRLGSSAMNIQMLLEKLGIPQLEGQKDMITWILQM 981

RESULT 1322  
ADS86864  
ID ADS86864 standard; protein; 1749 AA.  
XX  
AC ADS86864;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Human E3alpha ubiquitin ligase, hE3alphaI protein sequence.  
XX  
KW Human; E3alpha ubiquitin ligase; huE3alphaI;  
KW ubiquitin-proteasome pathway; chromosome 15 q; rapid muscle wasting;  
KW fasting; metabolic acidosis; muscle degeneration; kidney failure;  
KW renal cachexia; uremia; diabetes mellitus; sepsis; AIDS wasting syndrome;  
KW cancer cachexia; negative nitrogen balance; burn; Cushing's syndrome;  
KW inflammatory cachexia; hyperthyroidism; denervation atrophy;  
KW protein/tissue wasting; energy-protein malnutrition; muscle atrophy;  
KW gene therapy; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN US2004185037-A1.  
XX  
PD 23-SEP-2004.  
XX  
PF 15-JAN-2004; 2004US-00758672.  
XX  
PR 08-MAR-2000; 2000US-0187911P.  
PR 28-NOV-2000; 2000US-00724126.  
XX  
PA (HANH/) HAN H.  
PA (KWAK/) KWAK K.  
XX  
PI Han H, Kwak K;  
XX  
DR WPI; 2004-707854/69.  
DR N-PSDB; ADS86863.  
XX  
PT Novel isolated human E3alpha ubiquitin ligase nucleic acid molecule  
PT useful for treating and/or preventing renal cachexia or inflammatory  
PT cachexia.  
XX  
PS Claim 13; SEQ ID NO 2; 115pp; English.  
XX  
CC The present invention relates to new orthologue of human E3alpha  
CC ubiquitin ligase, huE3alphaI and huE3alphaII. Most intracellular proteins  
CC are degraded through the ubiquitin-proteasome pathway. Proteins are  
CC marked for proteasomal degradation by conjugation of ubiquitin to the  
CC protein. Conjugation of the ubiquitin molecule involves the activation by  
CC E1 enzyme, subsequent transfer to E2 enzyme, which serves as a carrier,  
CC and then interacts with a specific E3 ligase family member. E3 ligase  
CC binds to proteins targeted for degradation and catalyses the transfer of  
CC ubiquitin from the E2 carrier enzyme to the target protein. E3 ligase  
CC determines the specificity of the system. The E3alpha family is the main  
CC family of intracellular ligases and is involved in the N-end rule pathway  
CC of protein degradation. E3alpha enzyme binds directly to the primary  
CC destabilising N-terminal amino acid and catalyses ubiquitin conjugation  
CC thereby targeting the protein for degradation. The human E3alpha gene is  
CC located on chromosome 15 q. Increased proteolysis through the ubiquitin-  
CC proteasome pathway has been determined to be a major cause of rapid  
CC muscle wasting including, fasting, metabolic acidosis, muscle  
CC degeneration, kidney failure, renal cachexia, uremia, diabetes mellitus,  
CC sepsis, AIDS wasting syndrome, cancer cachexia, negative nitrogen  
CC balance, burns, Cushing's syndrome, inflammatory cachexia,  
CC hyperthyroidism, denervation atrophy, protein/tissue wasting, and energy-  
CC protein malnutrition. E3alpha plays a role in the overall increase in  
CC ubiquitination that is associated with and may mediate muscle atrophy in  
CC catabolic and other disease states. Treatment may be administered by gene  
CC therapy, cell therapy and antisense therapy methods. The present sequence

CC is human E3alphaI protein sequence.  
XX  
SQ Sequence 1749 AA;  
Query Match 3.2%; Score 84; DB 8; Length 1749;  
Best Local Similarity 18.2%; Pred. No. 1.5e+03;  
Matches 62; Conservative 52; Mismatches 107; Indels 120; Gaps 15;  
QY 248 YFMVEVKCR---DQDFHSGTGGILHEPM-----ADLVAL 279  
Db 676 FYYQDVKCREEMYDKDIIMLQIGASLMDPNKFLULLVQLQRYELAEAFNKTISTKDQDLIKQ 735  
QY 280 LGS�VDSSGHILVPGIYDEVVP---LTEEEINITYKAHLDLEEYRNSSSRVEKFLDTK- 334  
Db 736 YNTLIEEMLOVLIVIGERYVPGVGNVTKEEVTMRIHLLCIEPMPHSAIAKNLPENEN 795  
QY 335 -----EEIL--MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 796 NETGLENVINKVATFKKPGVSGHGVYELKDES-----LKDFNMVF---YHYSKTQ 842  
QY 388 QQVTRHLEDVFSKRNSSNK-----MVVSMTLGLHPWIANIDDTQYLAAKRAI 434  
Db 843 HSKAEHMQK--KRRKQENKDEALPPPPPEFCPAFSKVINL-----LNCDIMMYI-----L 891  
QY 435 RTVF---GTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGSEHSQN----- 481  
Db 892 RTVFERAIDTDSNLWTEG-----MLQMAFH---ILALGLLEEKQQLQKAPEEVTFD 940  
QY 482 -----EKINRWNYIEGTKLFFAAFFLEM 503  
Db 941 FYHKASRLGSSAMNIQMLLEKLGIPQLEGQKDMITWILQM 981  
RESULT 1323  
ADM26543  
ID ADM26543 standard; protein; 1849 AA.  
XX  
AC ADM26543;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Hyperthermophile Methanopyrus kandleri protein #1149.  
XX  
KW hyperthermophile; protein stability enhancement;  
KW protein activity enhancement.  
XX  
OS Methanopyrus kandleri.  
XX  
PN WO2003076575-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 04-MAR-2003; 2003WO-US006664.  
XX  
PR 04-MAR-2002; 2002US-0361742P.  
PR 14-MAY-2002; 2002US-0380423P.  
PR 16-SEP-2002; 2002US-0410974P.  
XX  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
XX  
PI Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;  
XX  
DR WPI; 2003-748383/70.  
DR N-PSDB; ADM27081.  
XX  
PT New isolated nucleic acids encoding any of about 1700 Methanopyrus  
PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
PT as diagnostic agents.  
XX  
PS Claim 31; SEQ ID NO 1149; 1023pp; English.  
XX  
CC The invention comprises the amino acid sequence of proteins from the





```
RESULT 1325
ABG19121
ID  ABG19121 standard; protein; 1883 AA.
XX
AC  ABG19121;
XX
DT  18-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #19112.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US008631.
XX
PR  31-MAR-2000; 2000US-00540217.
PR  23-AUG-2000; 2000US-00649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
DR  N-PSDB; AAS83308.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity..
XX
PS  Claim 20; SEQ ID NO 49480; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC  sequences. (I) is useful as hybridisation probes, polymerase chain
CC  reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC  and in recombinant production of (II). The polynucleotides are also used
CC  in diagnostics as expressed sequence tags for identifying expressed
CC  genes. (I) is useful in gene therapy techniques to restore normal
CC  activity of (II) or to treat disease states involving (II). (II) is
CC  useful for generating antibodies against it, detecting or quantitating a
CC  polypeptide in tissue, as molecular weight markers and as a food
CC  supplement. (II) and its binding partners are useful in medical imaging
CC  of sites expressing (II). (I) and (II) are useful for treating disorders
CC  involving aberrant protein expression or biological activity. The
CC  polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC  amino acid sequences of the invention. Note: The sequence data for this
CC  patent did not appear in the printed specification, but was obtained in
CC  electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 1883 AA;

Query Match
Best Local Similarity 3.2%; Score 84; DB 4; Length 1883;
Matches 67; Conservative 42; Mismatches 100; Indels 86; Gaps 18;

QY  84 TLQRLGARV---ASVDM-----GPOQLPDGQSLPIPP-----VILAEIGSDPTK 124
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db  549 TIQQLSLTSSGSAVDLCTIQAVSLLPGEPPQKIPTGVGPLPEGTGVLILGR-SSLNLK 607
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
QY  125 GTVCFYGHLD-----VQPADRGDGLWLTDPYVL---TEVDGKLYGRGA 163
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db  608 GVQIHTSVVDSYKGEIQLVISSIPWSASPRDRIQLLLLPYIKGNSBIK-RIGGLVS 666
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
```

```
QY  164 TDNKGVLAWINAVSAFRALEQDLPVNIKFIIEGMEAGSVALEELVEKEKDRFFSGVDY 223
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db  667 TDPTGKAAYWASQVS-----ENRPV-CKAIIOGKQ-----FGLVD-----TGADV 706
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
QY  224 IVISDNLWISQ--RKPAIT-----YGTRGNSYFMVEV-KCRDQDFHSGTGGILHEPMDL 276
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db  707 SIIALNQWPKNWLKQKAVTGLVGIGTASEVYQSMELHCLGPDNQESTV-----QPMITS 761
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
QY  277 VALLGSLVDSSGHILV----PGIYDEVVPLTTEEINTYKAIHLDLEEYRNSSRVE 327
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db  762 IPL-----NLWGRDLLQQWEKPVVWVNWQWPLPKQKL---EALHLLANEQLEKGHIE 808
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|

RESULT 1326
AAU70673
ID  AAU70673 standard; protein; 1997 AA.
XX
AC  AAU70673;
XX
DT  14-FEB-2002 (first entry)
XX
DE  Human otoferlin #2.
XX
KW  Human; mouse; otoferlin; OTOF; brain; auditory function;
KW  autosomal nonsyndromic prelingual deafness; DFNB9.
XX
OS  Homo sapiens.
XX
PN  WO200170972-A2.
XX
PD  27-SEP-2001.
XX
PF  23-MAR-2001; 2001WO-IB000578.
XX
PR  24-MAR-2000; 2000US-0191738P.
XX
PA  (INSP ) INST PASTEUR.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI  Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;
PI  Weil D;
XX
DR  WPI; 2001-611499/70.
DR  N-PSDB; AAS95026.
XX
PT  Novel human gene Otoferlin, underlying an autosomal recessive
PT  nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the
PT  gene, implicated in deafness.
XX
PS  Disclosure; Fig 14F; 99pp; English.
XX
CC  The invention relates to a purified polynucleotide (I) encoding a protein
CC  sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long
CC  human otoferlin isoform in brain. (I) was identified as underlying an
CC  autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for
CC  detecting deafness disease in humans and for characterising the functions
CC  of proteins and genes encoding them in auditory function. AAU70669-
CC  AAU70676 represent human and mouse otoferlin amino acid sequences of the
CC  invention
XX
SQ  Sequence 1997 AA;
```

```
Query Match
Best Local Similarity 3.2%; Score 84; DB 4; Length 1997;
Matches 90; Conservative 66; Mismatches 169; Indels 124; Gaps 24;

QY  108 LPIPPVILAEIGSDPTKGTVCFYG-----HLDVQPADRGDGLWLTDPYV 150
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db  1462 VPLPEDVSREAGYDSTYG--MFOGIPSNPDINLVVRVVVRATDLHPADING--KADPYI 1517
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
QY  151 LTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGM-----EEAGSVA 205
   |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
```

Db 1518 AIRL-CKTDIR---DKENYISKQLNPV-----FGKSFDIEASFPMESMLTVAVDWDLVG 1568  
Qy 206 LEELVEKEK-----DRFFS-----GV-DYIVISDNLWISQKPKPAITYGTRGNSYFMVEV 253  
Db 1569 TDDLIGETKIDLENRFYSKHRATCGIAQTYSTHGYNWRDPMKP-----SQILTRL 1619  
Qy 254 KCRDQDFHSGTGGILHEPMDLVALLGS-LVDSSG-----HILVPGI-YDEVVP--- 301  
Db 1620 -CKDGKVDGPHFGPPGRVKVANRVFTGPSEIEDENGQRKPTDEHVALLALRHWDIPRAG 1678  
Qy 302 --LTEEEINTYKAIHLD--LLEEYRNSRVEKFLFD-----TKEEILMHL 341  
Db 1679 CRLVPEHVETRPLLNPDKPGIEQGRLELWDMFPMMPAPCTPLDISPRKPKKYELRVII 1738  
Qy 342 WRYPSLSIHGIEGAFDEPGTKTIPGRVIGK-----FSIR-LVPHM 381  
Db 1739 WNTDEVLEDDDDFFTGKSSDIFVRGWLKGQEDKQDTDVHYHSLTGEGNFWRYLFFPD 1798  
Qy 382 NVSAVEKQVTRHLEDVFSKRNSNMVSMTLGLHPWIA---NIDDTQYLAA----- 430  
Db 1799 YLAAEEKIVISKESMFSWDETEYKIPARLTLOI--WDADHFSADD--FLGAIELDLNRF 1854  
Qy 431 KRAIRTVFGTEPDMIRDGSGTIPIAKMFOE 459  
Db 1855 PRGAKTAKQCTMEMATGEVDVPLVSIFKQ 1883

RESULT 1327  
ABG12556  
ID ABG12556 standard; protein; 2002 AA.  
XX  
AC ABG12556;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #12547.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.

XX WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS76743.

XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 42915; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2002 AA;

Query Match 3.2%; Score 84; DB 4; Length 2002;  
Best Local Similarity 22.7%; Pred. No. 1.8e+03;  
Matches 67; Conservative 42; Mismatches 100; Indels 86; Gaps 18;  
Qy 84 TLQRLGARV---ASVDM-----GPOQLPDGQSLPIPP---VILAEIGSDPTK 124  
Db 570 TIQQLSLTSGSAAVDLCTIQAVSLLPGEPPQKIPTGVYGPLPEGTVGLILGR-SSLNLK 628  
Qy 125 GTVCFYGHLD-----VQPADRGDWLTDPYVL---TEVDGKLYGRGA 163  
Db 629 GVQIHTSVVDSYKGEIQLVISSIPWSASPRDRIAQLLLLPYIKGNSEIK-RIGGLVS 687  
Qy 164 TDNKG PVLAWINAVSAFRALEQDLVPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDY 223  
Db 688 TDPTGKAAYWASQVS-----ENRPV-CKAIIQKQ-----FEGDVD-----TGADV 727  
Qy 224 IVISDNLWISQ--RKPAIT----YGTRGNSYFMVEV-KCRDQDFHSGTGGILHEPMADL 276  
Db 728 SIIALNQWPXNWLKQKAVTGLVGIGTASEVYQSMELHCLGPDNQESTV-----QPMITS 782  
Qy 277 VALLGSLVDSSGHILV----PGIYDEVVPLTSEEINTYKAIHLDLLEEYRNSRVE 327  
Db 783 IPL-----NLWGRDLLQWQEKPVWVNQWPLPKQKL---EALHLLANEQLEKGHIE 829

RESULT 1328  
ABG67242  
ID ABG67242 standard; protein; 2165 AA.  
XX  
AC ABG67242;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Respiratory syncytial virus L protein, mutant #12.  
XX  
KW Respiratory syncytial virus; RSV; attenuated phenotype; antigenome;  
KW G protein; F protein; M2-2 gene; expression vector; vaccine; L protein;  
KW mutant; mutein.  
XX  
OS Respiratory syncytial virus.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 620 /note= "Wild type Glu subsituted by Ala"  
FT Misc-difference 621 /note= "Wild type Arg subsituted by Ala"  
XX  
PN WO200244334-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 28-NOV-2001; 2001WO-US044819.  
XX  
PR 28-NOV-2000; 2000US-00724416.  
XX  
PA (AVIR-) AVIRON INC.

XX Jin H, Tang R, Li S, Bryant M;  
PI WPI; 2002-508507/54.  
XX Isolated infectious respiratory syncytial virus particle, useful as a  
PT vaccine, has an attenuated phenotype comprising the viral genome that has  
PT a heterologous sequence encoding a G and F protein and a mutation in the  
PT M2-2 gene.  
XX  
PS Example 9; Page; 150pp; English.  
XX  
CC The invention describes an isolated infectious respiratory syncytial  
CC virus (RSV) particle with an attenuated phenotype comprising an RSV  
CC antigenome or genome, where the genome or antigenome has a heterologous  
CC sequence encoding a G and F protein, and a mutation in the M2-2 gene. The  
CC RSV particle is useful as expression vector or vaccine. This is the amino  
CC acid sequence of the RSV L protein used in the creation of the  
CC recombinant RSV particle of the invention. Note: This sequence does not  
CC appear in the specification but has been created from the wild type  
CC sequence shown in ABG67228 using information given in the invention  
XX  
SQ Sequence 2165 AA;  
  
Query Match 3.2%; Score 84; DB 5; Length 2165;  
Best Local Similarity 17.6%; Pred. No. 2e+03;  
Matches 90; Conservative 78; Mismatches 177; Indels 166; Gaps 24;  
  
QY 9 AASLLAVLLLLLLERGMFSSPPPPALLEKF-----QYIDLHQDEFVQTLKE 55  
Db 620 AAELSVGRMFAMQPGMFRQVQ---ILA EKMI AENILQFPFESLTRYGDLEQLKLE-LKA 675  
  
QY 56 WVAIESDS-----VQPVPRFRQEL-FRMAVAADTLQRLGARVASVDMGPQ 100  
Db 676 GISNKSRYNDYNNYISKSIITDLSKFNQAFRYETSCISDVLDL-----HG VQ 727  
  
QY 101 QLPDQGSLPIPPVILAE LSGDPTKGTVCFYGHLDVQPADRGDGLWTDPIV-----LTEV 154  
Db 728 SLFSWLHLTIPHVTI-----ICTYRH-----APPYIGHIVDLNNV 763  
  
QY 155 DGK----LYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELV 210  
Db 764 DEQSGLYRYHMGGIEGCQKLWTEAISLLDLISLKGKFSITALINGDNQ--SIDISKPI 821  
  
QY 211 EKEKDRFFSGVDYIIVISDNLWISQRKPA-ITYGTRGNSYFMVEVKCRDQDFHSGTF--GG 267  
Db 822 RLMEGQTHAQADYLLALNSLKLKYKEYAGIGHKLKGTETYI----SRDMQFMSKTIQHG 877  
  
QY 268 ILHEPMADLVALLGSLVDSSGHILVPGIYDE-----VVP LTEEEINTYKAIHLDLEEY 320  
Db 878 VYYPASIKKVLRVGPWINT-----ILDDFKVSLSIGSLTQE-----LEY 917  
  
QY 321 RNSSRVEKFLDFTKEEILMHLWRYP SLI----HGIEGAFDEPGTKTVIPGRVIGKFSIR 376  
Db 918 RGESLLCSLIF-----RNVWLYNQIALQLKNHAL-----CNNKLYLD 954  
  
QY 377 LVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVMSMTLGLHPWIANIDDTQYLAAKRAIRT 436  
Db 955 IL-----KVLKHLKTFEFLNDIDTALTLYMNL---PMLFGGDPNLL-----YRS 996  
  
QY 437 VEGTEPDMIRDGSTIPIAKMFQEI VHKSVVL 467  
Db 997 FYRRTPDFL TEA-----IVHSVFIL 1016  
  
RESULT 1329  
ABG00402  
ID ABG00402 standard; protein; 2383 AA.  
XX  
AC ABG00402;  
XX  
DT 13-FEB-2002 (first entry)  
XX

DE Novel human diagnostic protein #393.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX WO200175067-A2.  
PN  
XX 11-OCT-2001.  
PD  
XX 30-MAR-2001; 2001WO-US008631.  
PF  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
PA Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS64589.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 30761; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2383 AA;  
  
Query Match 3.2%; Score 84; DB 4; Length 2383;  
Best Local Similarity 22.7%; Pred. No. 2.4e+03;  
Matches 67; Conservative 42; Mismatches 100; Indels 86; Gaps 18;  
  
QY 84 TLQRLGARV---ASVDM-----GPOQLPDGQSLPIPP-----VILAE LGS DPTK 124  
Db 951 TIQQLSLTTSGSAAVDLCTIQAVSLLPGEPPQKIPTGVYGPLPEGTGLILGR-SSLNLK 1009  
  
QY 125 GTVCFYGHLD-----VQPADRGDGLWTDPIV L-----TEVDGKLYGRGA 163  
Db 1010 GVQIHTSVVSDSYKGEIQLVISSSIPWSASPRDRIAQLLLPYIKGGSNSEIK-RIGGLVS 1068  
  
QY 164 TDNKG PVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEDRFFSGVDY 223  
Db 1069 TDPTGKAAYWASQVS-----ENRPV-CKAIIQKQ-----FGLVD-----TGADV 1108  
  
QY 224 IVIDNLWISQ--RKPAIT-----YGTRGNSYFMVEV-KCRDQDFHSGTGGILHEPMADL 276  
Db 1109 SIIALNQWPKNWLKQKAVTGLVGIGTASEVYQSMEILHCLGPDNQESTV-----QPMITS 1163







Db 1035 STVPLPNCNVKQLQNLKLTSLQIHENNLLIPTQSELIN-----HVDLVSTQNSD-MKPFM 1088  
Qy 331 FDTKEEILMHLWRYPs-----LSIHGIEGAFDEPGTKTVIPG-----RVIGKFSIRLV 378  
Db 1089 MTLIKDYLSEDVRFSTNNVLMLLSSIHPIGTSF---GRVTAESGYRIRYYIVGTDKISID 1145  
Qy 379 PHMNVSAVEKQVTRHLEDV 397  
Db 1146 ADTGELILKERFYRNLDI 1164

RESULT 1333  
ABU52622  
ID ABU52622 standard; protein; 4299 AA.  
XX  
AC ABU52622;  
XX  
DT 04-MAR-2003 (first entry)  
XX Human NOVX protein, NOV28.  
DE  
XX Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy;  
KW obesity; infectious disease; anorexia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidaemia; metabolic disturbance;  
KW metabolic syndrome X; wasting disorder; cancer; gene therapy.

XX Homo sapiens.  
OS  
XX  
XX WO200281518-A2.  
PN  
XX  
XX PD 17-OCT-2002.  
XX  
XX PF 21-FEB-2002; 2002WO-US005374.  
XX  
PR 21-FEB-2001; 2001US-0270220P.  
PR 21-FEB-2001; 2001US-0270523P.  
PR 23-FEB-2001; 2001US-0270797P.  
PR 23-FEB-2001; 2001US-0270810P.  
PR 08-MAR-2001; 2001US-0274295P.  
PR 16-MAR-2001; 2001US-0276400P.  
PR 16-MAR-2001; 2001US-0276677P.  
PR 26-MAR-2001; 2001US-0278796P.  
PR 04-APR-2001; 2001US-0281521P.  
PR 25-APR-2001; 2001US-0286548P.  
PR 17-MAY-2001; 2001US-0291765P.  
PR 10-AUG-2001; 2001US-0311595P.  
PR 13-AUG-2001; 2001US-0311980P.  
PR 10-SEP-2001; 2001US-0318526P.  
PR 17-SEP-2001; 2001US-0322712P.  
PR 18-OCT-2001; 2001US-0330307P.

XX (CURA-) CURAGEN CORP.  
PA  
XX  
PI Pena CEA, Shinkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA;  
PI Vernet CAM, Malyankar UL, Guo X, Gusev VY, Casman SJ, Boldog FL;  
PI Furtak K, Tchernev VT, Patturajan M, Gangolli EA, Padigar M, Liu X;  
PI Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD;  
XX  
DR WPI; 2003-046859/04.  
DR N-PSDB; ABX70677.  
XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,  
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious  
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and  
PT cancer.

XX  
PS Claim 1; Page 227-228; 479pp; English.  
XX  
CC The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a,  
CC 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15,  
CC 16a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABU52578-ABU52624), a

CC variant of NOVX, a mature form of NOVX, and a variant of the mature form  
CC of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding  
CC NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX  
CC NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining  
CC the presence or amount of NOVX or NOVX NA in a sample, and identifying an  
CC agent that binds or modulates the expression or activity of NOVX. NOVX,  
CC NOVX NA or ab is useful for treating or preventing a NOVX-associated  
CC disorder in a subject, preferably human. Ab is useful for determining the  
CC presence or amount of NOVX in a sample. NOVX is useful for identifying an  
CC agent that binds to NOVX. NOVX, NOVX NA or ab is useful for treating  
CC metabolic disorders, diabetes, cardiomyopathy, obesity, infectious  
CC disease, anorexia, neurodegenerative disorders, Alzheimer's disease,  
CC Parkinson's disease, immune disorders, haematopoietic disorders, and  
CC various dyslipidaemias, metabolic disturbances associated with obesity,  
CC the metabolic syndrome X and wasting disorders associated with chronic  
CC diseases, various cancers, endocrine, connective tissue, blood, vascular,  
CC skin, renal, bone, brain, muscle disorders, or bacterial, fungal,  
CC protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening  
CC assays, detection assays, predictive medicine, and in methods of  
CC treatment. NOVX is useful as immunogen, to screen for potential  
CC ant/agonist compounds, and as bait protein in a two-hybrid or three-  
CC hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to  
CC detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX  
CC activity. The cell is useful for producing non-human transgenic animals.  
CC Ab is useful for isolating, and purifying NOVX and to monitor protein  
CC levels in tissue as part of a clinical testing procedure. The present  
CC sequence represents a NOVX protein  
XX  
SQ Sequence 4299 AA;

Query Match 3.2%; Score 84; DB 6; Length 4299;  
Best Local Similarity 19.8%; Pred. No. 5.9e+03;  
Matches 93; Conservative 67; Mismatches 159; Indels 150; Gaps 24;

Qy 72 QELFRMMAVAADTLQRLGARVASVDMGPQ-----LPDQSLPIPPVILAELGSDPTK 124  
Db 2648 ETLVSLRVHTVDDIQIAAALAQ-C-MGPSRELVCVRSCLK--QTLHKLEAMMLILOAETTA 2704  
Qy 125 GTVCFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE 184  
Db 2705 GT-----VTPTAIGDS-----ILNITGDLIHLASSDVRAPQPSLGAEPSRMVA 2749  
Qy 185 QD----LPVNIKFIEGM---EEAGSVALEELVEKEK-----D 215  
Db 2750 SQAYNLTSALMRILMRSRVLNNEEPLTLAGEEIVAQCKSDPRSLLCYGGAPGPGCHFISIP 2809  
Qy 216 RFFSG-----VDYIVISD-----NLWISQRKPAITYGTRGNSYFMVE----- 252  
Db 2810 EAFSGALANLSDVVQLIFLVDNSNPPFPFGYISNYTVSTKVASMAFQTQAGAIPIERLASE 2869  
Qy 253 ----VKC-RDQDF----HSGTFGGILHEPMADLVALLGSLVDSS-----GHILVP 293  
Db 2870 RAITVKVPNNSDWAARGHRSSANSVWVQPQASVGAV--TLDSSNPAAVLHLQLNYTLDD 2927  
Qy 294 GIYDEVVPLTEEEINTYKAHLDLEEYRN-----SSRVEKFLDFTKEEILMHLWRYPsL 347  
Db 2928 GHY-----LSEEPYLAIVLHSEPRPNEHNCSARRIRP----- 2962  
Qy 348 SIHGIEGAFDEPGTKTVIPGR--VIGKFSIRLVPHMNVSAVEKQVTRH--LEDVFSKRNS 403  
Db 2963 --ESLQGADHRPYTFFISPSGRDPAGSYHLNLSHFRWSALQVSVGLYTSLCQYFSEED- 3019  
Qy 404 SNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR--TVFGTE----PDMIR 446  
Db 3020 ----MWRTEGLLP----LEETSPROAVCLTRHLTAFGASLFPVPPSHVR 3060

RESULT 1334  
AAE31508  
ID AAE31508 standard; protein; 131 AA.  
XX  
AC AAE31508;  
XX



DT 24-FEB-2003 (first entry)  
 XX  
 DE Latex Hev b8 profilin V protein.  
 XX  
 KW Profilin; therapy; allergy; immunoassay; latex.  
 XX  
 OS Hevea brasiliensis.  
 XX  
 PN WO200270005-A1.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 27-FEB-2002; 2002WO-US005911.  
 XX  
 PR 28-FEB-2001; 2001US-0272149P.  
 XX  
 PA (IMMV-) IMMVARX INC.  
 XX  
 PI Babich M;  
 XX  
 DR WPI; 2003-046731/04.  
 XX  
 PT Purified multimeric forms of plant profilin, for use in a diagnostic test  
 PT for allergies and to hypersensitize a mammal, comprises plant profilin  
 PT monomers each comprising a sequence containing a cysteine.  
 XX  
 PS Claim 10; Page 16; 37pp; English.  
 XX  
 CC The invention relates to purified multimeric forms of plant profilin used  
 CC in diagnosis and treatment of allergies. Multimeric profilin, or a  
 CC functional equivalent of it, is used in a diagnostic test for allergies  
 CC and is used to hypersensitize a mammal. It is also used in immunoassays  
 CC and for screening patients to determine profilin allergenicity. The  
 CC present sequence is latex Hev b8 profilin protein  
 XX  
 SQ Sequence 131 AA;  
  
 Query Match 3.2%; Score 83.5; DB 6; Length 131;  
 Best Local Similarity 23.7%; Pred. No. 29;  
 Matches 40; Conservative 24; Mismatches 46; Indels 59; Gaps 9;  
  
 QY 144 WLT--DPYVLTEVDG-KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGME 200  
 | | | : : : : | : | : | : : : : : : : : : : : : : : : : : : :  
 Db 3 WQTVYDDHLMCDIDGRLTAATAIIGHDGSVWQAQSSGFQPKSDE-----VAAVMKDFDE 56  
  
 QY 201 AGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP-AITYGTRGNSYFMVEVKCRDQD 259  
 | | | | | | | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 57 PGSAPTGL-----HLGGTKYMWI-----QGEPGAVIRGKKS----- 89  
  
 QY 260 FHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEIN 308  
 | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 90 -----GGI-----TVKKTGQALIIGIYDE--PLTPGQCN 116  
  
 RESULT 1335  
 ABU34953  
 ID ABU34953 standard; protein; 137 AA.  
 XX  
 AC ABU34953;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #20480.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Moraxella catarrhalis.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.



CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC specific for P. acnes proteins. These antibodies can be used to  
CC downregulate expression and activity of P. acnes polypeptides and  
CC therefore treat P. acnes infections. The antibodies may also be used as  
CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 235 AA;

Query Match 3.2%; Score 83.5; DB 4; Length 235;  
Best Local Similarity 23.2%; Pred. No. 72;  
Matches 66; Conservative 33; Mismatches 114; Indels 71; Gaps 13;  
QY 55 EWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVI 114  
Db 6 EWFRLARGDPLPGDKIVVHLHGAAAHMQTARKNAGARAAALDAGVHDPDVEEL----- 59  
QY 115 LAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVDGKLYG-----RGATDN 166  
Db 60 -----AAYFLLCCTEGHL-IGHCDFGD---AHPIVRALLEKFLAGLERVDRRCRVAHDG 108  
QY 167 KGPVLAWINAVSAFRALEQDL-----PVNIKFIIEGMEEAGSVALEELVEKE-KDRFF 218  
Db 109 GVLVLSVLNDKTAADGVESALDHDFLARPGGERHAV-GMKREGPVAVKDVGKRDVKGKGNLP 167  
QY 219 SGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVK-CRDQDFHSGTGGILHEPMADLV 277  
Db 168 TAMDSI-----QSDTAIIIGDRRGSSRLIRVDGGRIFAFQTQQDGGL--RPVS--- 213  
QY 278 ALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAHLDLEEYR 321  
Db 214 -----VPGRSQRA-----EELRTHAG---DLRPYR 235

RESULT 1338  
ABM56389  
ID ABM56389 standard; protein; 235 AA.  
AC ABM56389;  
XX  
DT 20-OCT-2003 (first entry)  
XX Propionibacterium acnes predicted ORF-encoded polypeptide #21065.  
DE Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
XX immunostimulant; immune response; vaccine.  
KW Propionibacterium acnes.  
OS  
XX WO2003033515-A1.  
PN  
XX  
PD 24-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032727.  
XX  
PR 15-OCT-2001; 2001US-00978825.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
PI Barth B, Vallieve-Douglas J;  
XX  
DR WPI; 2003-381789/36.  
DR N-PSDB; ACF64536.  
XX

PT New Propionibacterium acnes polypeptides and polynucleotides encoding the  
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
or for stimulating an immune response specific for a P. acnes protein.  
XX  
PS Example 1; SEQ ID NO 21065; 1481pp; English.  
XX

CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
CC encoding a Propionibacterium acnes protein. The invention also relates to  
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
CC immunogenic fragments of P. acnes polypeptides. The invention  
CC additionally encompasses expression vectors and host cells comprising a  
CC polynucleotide of the invention; antibodies against polypeptides of the  
CC invention; fusion proteins comprising a polypeptide of the invention; a  
CC method for stimulating an immune response specific for a P. acnes  
CC polypeptide and an isolated T cell population comprising T cells prepared  
CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
CC antigen-presenting cells that express the polypeptide); a method and kit  
CC for detecting or determining the presence or absence of P. acnes in a  
CC patient; and a method for inhibiting the development of P. acnes in a  
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations or antigen-presenting cells that express the  
CC polypeptides are useful for diagnosing, preventing or treating acne  
CC vulgaris, or for stimulating an immune response specific for a P. acnes  
CC protein. The polynucleotides can also be used as probes or primers for  
CC nucleic acid hybridisation. The vaccine composition is useful for the  
CC stimulation of an immune response against P. acnes, or for treating acne,  
CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence represents a polypeptide predicted to be encoded by an ORF (open  
CC reading frame) contained within the P. acnes polynucleotides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 235 AA;

Query Match 3.2%; Score 83.5; DB 6; Length 235;  
Best Local Similarity 23.2%; Pred. No. 72;  
Matches 66; Conservative 33; Mismatches 114; Indels 71; Gaps 13;  
QY 55 EWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVI 114  
Db 6 EWFRLARGDPLPGDKIVVHLHGAAAHMQTARKNAGARAAALDAGVHDPDVEEL----- 59  
QY 115 LAELGSDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVDGKLYG-----RGATDN 166  
Db 60 -----AAYFLLCCTEGHL-IGHCDFGD---AHPIVRALLEKFLAGLERVDRRCRVAHDG 108  
QY 167 KGPVLAWINAVSAFRALEQDL-----PVNIKFIIEGMEEAGSVALEELVEKE-KDRFF 218  
Db 109 GVLVLSVLNDKTAADGVESALDHDFLARPGGERHAV-GMKREGPVAVKDVGKRDVKGKGNLP 167  
QY 219 SGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVK-CRDQDFHSGTGGILHEPMADLV 277  
Db 168 TAMDSI-----QSDTAIIIGDRRGSSRLIRVDGGRIFAFQTQQDGGL--RPVS--- 213  
QY 278 ALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAHLDLEEYR 321  
Db 214 -----VPGRSQRA-----EELRTHAG---DLRPYR 235

RESULT 1339  
ABB54173  
ID ABB54173 standard; protein; 285 AA.  
XX  
AC ABB54173;  
XX  
DT 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
XX  
DE Lactococcus lactis protein ispA.  
XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.



XX Lactococcus lactis; IL1403.  
OS  
XX FR2807446-A1.  
PN  
XX 12-OCT-2001.  
PD  
XX 11-APR-2000; 2000FR-00004630.  
PF  
XX 11-APR-2000; 2000FR-00004630.  
PR  
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
PA  
XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
PI  
XX WPI; 2002-043418/06.  
DR  
XX New nucleotide sequence useful in the identification or Lactococcus  
XX lactis and related species.  
PT  
XX Claim 6; SEQ ID NO 875; 2504pp; French.  
PS  
XX The present invention is related to a Lactococcus lactis nucleotide  
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
CC acid sequence is useful in the detection and/or amplification of nucleic  
CC acid sequence, particularly to identify Lactococcus lactis or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO200177334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 285 AA;

Query Match 3.2%; Score 83.5; DB 5; Length 285;  
Best Local Similarity 20.4%; Pred. No. 97;  
Matches 52; Conservative 43; Mismatches 95; Indels 65; Gaps 11;  
QY 171 LAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRF-----FSG 220  
Db 43 LLFLNLLEAFDLELSKAHYHVAALAE-MIHTGSLIHDDLPAMDNDYRRGQLTNHKKFDE 101  
QY 221 VDIYIVISDNLMWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALL 280  
Db 102 ATAILAGDTLFFD---PFFILSTADLSAEIIVALTRELAFASGSYG-----MVA-- 147  
QY 281 GSLVDSSGHILVPGIYDEVVPLTE-EEINTYKAIHL-----DLEEYRN 322  
Db 148 GOILDMAGE-----GKELTLAEIEQIHLKTRLLTFFPFAAGIVAQKSTDEVEKLRQ 200  
QY 323 SSRVEKFLFDTKBEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 201 VGQILGLAFQIRDDIL-----DVTATFAELG-KT--PGKDILEEKSTYVAHLG 245  
QY 383 VSAVEKQVTRHLEDV 397  
Db 246 LEGAKKSLTGNLSEV 260

RESULT 1340  
ADS29358  
ID ADS29358 standard; protein; 285 AA.  
XX  
AC ADS29358;  
XX 02-DEC-2004 (first entry)  
DT  
XX Bacterial polypeptide #18391.  
DE  
XX Recombinant DNA construct; transformed plant; improved plant property;  
KW

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
XX (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
PI  
XX WPI; 2004-061375/06.  
DR  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
PT  
XX Claim 1; SEQ ID NO 18391; 122pp; English.  
PS  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 285 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 285;  
Best Local Similarity 20.4%; Pred. No. 97;  
Matches 52; Conservative 43; Mismatches 95; Indels 65; Gaps 11;  
QY 171 LAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRF-----FSG 220  
Db 43 LLFLNLLEAFDLELSKAHYHVAALAE-MIHTGSLIHDDLPAMDNDYRRGQLTNHKKFDE 101  
QY 221 VDIYIVISDNLMWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMDLVALL 280  
Db 102 ATAILAGDTLFFD---PFFILSTADLSAEIIVALTRELAFASGSYG-----MVA-- 147  
QY 281 GSLVDSSGHILVPGIYDEVVPLTE-EEINTYKAIHL-----DLEEYRN 322



PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
PR	10-AUG-1999;	99US-0148171P.
PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
PR	16-AUG-1999;	99US-0149368P.
PR	17-AUG-1999;	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.
PR	20-AUG-1999;	99US-0149723P.
PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149930P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 3.2%; Score 83.5; DB 3; Length 336;		
Best Local Similarity 22.4%; Pred. No. 1.3e+02;		
Matches	54; Conservative	35; Mismatches 87; Indels 65; Gaps 14;
QY	38	VFOYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDM 97
Db	111	IFIYYQL--DNYIQNHRRYVKRSRD-----QQLLHGLEY-----SHTSSCE- 149
QY	98	GPQQLPDGQSLPIPP--VILAELGSDPTKGTVCFYGHLDVQPADRGD-GWLTD----- 147
Db	150	-PESSNG--LPVPCGLIAWSMFND----TFTFSRERTKLNVRNNIAWKSDREHKFGK 202
QY	148	-PYVLTEVDGKLYGRGATDNKGPV-----LAWINAVS--AFRAL-----EQDLPVNIKFI 194
Db	203	NVYPINFQNTLIGGAKLDPKLPLSDQEDFIVWMRAAALLSFRKLYGRIEEDL----- 255
QY	195	IEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRP--AITYGTRGNSYFMVE 252
Db	256	-----EPGKVVEVNLNMNNYNTYSFSGQKKLILSTSNWLGRNDFLGITYLVVGSSSVVIS 310
QY	253	V 253
Db	311	I 311
RESULT 1342		
AAG23021		
ID	AAG23021	standard; protein; 342 AA.
XX	AC	AAG23021;
XX	DT	17-OCT-2000 (first entry)
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 26172.
XX	KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	KW	termination sequence.
XX	OS	Arabidopsis thaliana.
XX	PN	EP1033405-A2.
XX	PD	06-SEP-2000.
XX	PF	25-FEB-2000; 2000EP-00301439.
XX	PR	25-FEB-1999; 99US-0121825P.
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PR 22-JUL-1999; 99US-0145089P.  
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PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
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PR 27-JUL-1999; 99US-0145919P.  
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PR 12-AUG-1999; 99US-0148341P.  
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PR 27-AUG-1999; 99US-0151065P.  
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PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
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PR 23-SEP-1999; 99US-0155486P.  
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PR 21-OCT-1999; 99US-0160770P.  
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PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
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PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
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PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.

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PR 28-OCT-1999;    99US-0161920P.
PR 28-OCT-1999;    99US-0161992P.
PR 28-OCT-1999;    99US-0161993P.
PR 29-OCT-1999;    99US-0162142P.

Query Match          3.2%;   Score 83.5;   DB 3;   Length 342;
Best Local Similarity 22.4%;   Pred. No. 1.3e+02;
Matches 54; Conservative 35; Mismatches 87; Indels 65; Gaps 14;

QY 38 VFQYIDLHQDEFVQTLKEWVAIESDSVPVPRFRQELFRMMAVAADTLQLGARVASVDM 97
      :|:| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 117 IFIYYQL--DNYQNHRRYVKRSR-----QQLLHGLEY-----SHTSSCE- 155

QY 98 GPQLPDGOSLPIPP--VILAEIGSDPTKGTVCFYGHLDVQPADRGD-GWLTD----- 147
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Db 156 -PEESSNG--LPIVPCGLIAWSMFND----TFTFSRERTKLNVSRNNIAWKSDREHKFGK 208

QY 148 -PYVLTEVDGKLYGRGATDNKGPV-----LAWINAVS---AFRAL-----EQDLFVNIKFI 194
      | | : | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 209 NVYPINFQNGTLIGGAKLDPKLPSDQEDFIVWMRAALLSPRKLYGRIEEDL----- 261

QY 195 IEGMEEAGSVALLEELVEKEKRFFSGVDYIVISDNLWISQRKP--AITYGTRGNSYFMVE 252
      -----| | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 262 ----EPGKVVEVNLMMNNTYSFSGOKKLILSTSNWLGGRNDFLGITYLVVGSSVVVIS 316

QY 253 V 253
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Db 317 I 317

RESULT 1343
AAG23020
ID AAG23020 standard; protein; 343 AA.
XX
AC AAG23020;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26171.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999;    99US-0121825P.
PR 05-MAR-1999;    99US-0123180P.
PR 09-MAR-1999;    99US-0123548P.
PR 23-MAR-1999;    99US-0125788P.
PR 25-MAR-1999;    99US-0126264P.
PR 29-MAR-1999;    99US-0126785P.
PR 01-APR-1999;    99US-0127462P.
PR 06-APR-1999;    99US-0128234P.
PR 08-APR-1999;    99US-0128714P.
PR 16-APR-1999;    99US-0129845P.
PR 19-APR-1999;    99US-0130077P.
PR 21-APR-1999;    99US-0130449P.
PR 23-APR-1999;    99US-0130510P.
PR 23-APR-1999;    99US-0130891P.
PR 28-APR-1999;    99US-0131449P.
PR 30-APR-1999;    99US-0132048P.
PR 30-APR-1999;    99US-0132407P.
PR 04-MAY-1999;    99US-0132484P.
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PR 23-JUL-1999; 99US-0145145P.  
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PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
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PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
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PR 04-AUG-1999; 99US-0147204P.  
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PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
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PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
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PR 29-OCT-1999; 99US-0162142P.

Query Match 3.2%; Score 83.5; DB 3; Length 343;  
Best Local Similarity 22.4%; Pred. No. 1.3e+02;  
Matches 54; Conservative 35; Mismatches 87; Indels 65; Gaps 14;

QY 38 VFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDM 97  
Db 118 IFIYYQL--DNYIQNHRRYVKSRSD-----QQLLHGLEY-----SHTSSCE- 156  
QY 98 GPQQLPDGQSLPIPP--VILAEIGSDPTKGTVCFYGHLDVQPADRGD--GWLTD----- 147  
Db 157 -PEESSNG--LPIVPCGLIAWSMFND----TTFPSRERTKLNVSNNIAWKSDBEHKFGK 209  
QY 148 -PYVLTEVDGKLYRGATDNKGPV-----LAWINAVS--AFRAL----EQDLPVNIKFI 194  
Db 210 NVYPINFQNGTLIGGAKLDPKLPLSDQEDFIVWRAAALLSFRKLYGRIEEDL----- 262  
QY 195 IEGMEEAGSVALEBELVEKEKDRFFSGVDYIVISDNLWISQRP--AITYGTRGNSYFMVE 252  
Db 263 -----EPGKVVEVNLMMNNYNTYSFSGQKKLILSTSNWLGGRNDFLGITYLVGSSSVVIS 317  
QY 253 V 253  
Db 318 I 318

RESULT 1344  
ADA36700  
ID ADA36700 standard; protein; 344 AA.  
XX  
AC ADA36700;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Acinetobacter baumannii protein #3861.  
XX  
KW Acinetobacter baumannii; bacterial disease; antibiotic; vaccine;  
KW plant biocontrol agent.  
XX  
OS Acinetobacter baumannii.  
XX  
PN US6562958-B1.  
XX  
PD 13-MAY-2003.  
XX  
PF 04-JUN-1999; 99US-00328352.  
XX  
PR 09-JUN-1998; 98US-0088701P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Breton G, Bush D;  
XX  
DR WPI; 2003-576092/54.  
DR N-PSDB; ADA32574.  
XX  
PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
PT for diagnosing a bacterial disease, as components of antibacterial  
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
PT plants.



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XX      Example; SEQ ID NO 7987; 328pp; English.
PS
XX
CC      The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC      The A. baumannii nucleic acids and polypeptides are useful as reagents
CC      for diagnosing a bacterial disease, as components of antibacterial
CC      vaccines, as targets for antibacterial drugs, to detect the presence of
CC      A. baumannii and other Acinetobacter species in a sample, in screening
CC      compounds for the ability to interfere with the A. baumannii life cycle
CC      or to inhibit A. baumannii infection, and as biocontrol agents for
CC      plants. The present sequence represents the amino acid sequence of an A.
CC      baumannii protein.
XX
SQ      Sequence 344 AA;

      Query Match          3.2%; Score 83.5; DB 6; Length 344;
      Best Local Similarity 20.7%; Pred. No. 1.3e+02;
      Matches 82; Conservative 46; Mismatches 138; Indels 131; Gaps 21;

QY      109 PIPPVILAE LSGDPTKGTVCFYGHLDVQPADRG--DGWLTDPYVLTEDVGKLYGRGATDN 166
Db      13 PKVTVILANLGT-PDEATV-----PAVRRFLKQFLSDPRVI-EI----- 49

QY      167 KGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEGSV--ALEELV-----EKE 213
Db      50 --PKFIWRIILNLF-----VLPRPRKRVAHAYASVWSTDSPNREIVFEQTQRVQAYLERE 102

QY      214 KDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDF-----HSGT 264
Db      103 NKQF----DLTVL-----PAMTYGNPGIDAVLEKLAHPQEHVILLPLFPQYSAT 148

QY      265 FGGILHEPMADLVALLSGSLVDSSGHILVPGIYDE--VVPLTTEEINTYKAIHLDLEEVN 322
Db      149 STAPLYDAFAKWIPTQRNL---PGLTIKDYYQHMPFIQALAESVLAYQAQH----- 197

QY      323 SSRVEKFLFDTKKEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382
Db      198 -GKPEKLL-----MSFHGIPQPYADKGDPPYADRCRITAKLVAAEL---- 236

QY      383 VSAVEKQVTRHLEDVFSKRNSNKMVWSM--TLGLHPWIANIDDTQYLA--AKRAIRTVF 438
Db      237 -----HLKD-----DEWATSFQSRFGKQEWVKPYTD-QLLQDWAKQGVKSQV 277

QY      439 GTEPDMIRD-----GSTIPIAKMFQRIVHKSVVLIP 469
Db      278 VLSPAFSADCLTLEELAIAQNAELFQEAAGGSYAYIP 314

RESULT 1345
AAAY66633
ID      AAAY66633 standard; protein; 367 AA.
XX
AC      AAAY66633;
XX
DT      05-APR-2000 (first entry)
XX
DE      Membrane-bound protein PRO189.
XX
KW      Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW      pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS      Homo sapiens.
XX
PN      WO9963088-A2.
XX
PD      09-DEC-1999.
XX
PF      02-JUN-1999; 99WO-US012252.
XX
PR      02-JUN-1998; 98US-0087607P.
PR      02-JUN-1998; 98US-0087609P.
PR      02-JUN-1998; 98US-0087759P.
PR      03-JUN-1998; 98US-0087827P.
PR

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PR      04-JUN-1998; 98US-0088021P.
PR      04-JUN-1998; 98US-0088025P.
PR      04-JUN-1998; 98US-0088028P.
PR      04-JUN-1998; 98US-0088029P.
PR      04-JUN-1998; 98US-0088030P.
PR      04-JUN-1998; 98US-0088033P.
PR      04-JUN-1998; 98US-0088326P.
PR      05-JUN-1998; 98US-0088167P.
PR      05-JUN-1998; 98US-0088202P.
PR      05-JUN-1998; 98US-0088212P.
PR      05-JUN-1998; 98US-0088217P.
PR      09-JUN-1998; 98US-0088655P.
PR      10-JUN-1998; 98US-0088722P.
PR      10-JUN-1998; 98US-0088730P.
PR      10-JUN-1998; 98US-0088734P.
PR      10-JUN-1998; 98US-0088738P.
PR      10-JUN-1998; 98US-0088740P.
PR      10-JUN-1998; 98US-0088741P.
PR      10-JUN-1998; 98US-0088742P.
PR      10-JUN-1998; 98US-0088810P.
PR      10-JUN-1998; 98US-0088811P.
PR      10-JUN-1998; 98US-0088824P.
PR      10-JUN-1998; 98US-0088825P.
PR      10-JUN-1998; 98US-0088826P.
PR      11-JUN-1998; 98US-0088858P.
PR      11-JUN-1998; 98US-0088861P.
PR      11-JUN-1998; 98US-0088863P.
PR      11-JUN-1998; 98US-0088876P.
PR      12-JUN-1998; 98US-0089090P.
PR      12-JUN-1998; 98US-0089105P.
PR      16-JUN-1998; 98US-0089440P.
PR      16-JUN-1998; 98US-0089512P.
PR      16-JUN-1998; 98US-0089514P.
PR      17-JUN-1998; 98US-0089532P.
PR      17-JUN-1998; 98US-0089538P.
PR      17-JUN-1998; 98US-0089598P.
PR      17-JUN-1998; 98US-0089599P.
PR      17-JUN-1998; 98US-0089600P.
PR      17-JUN-1998; 98US-0089653P.
PR      18-JUN-1998; 98US-0089801P.
PR      18-JUN-1998; 98US-0089907P.
PR      18-JUN-1998; 98US-0089908P.
PR      19-JUN-1998; 98US-0089947P.
PR      19-JUN-1998; 98US-0089948P.
PR      19-JUN-1998; 98US-0089952P.
PR      22-JUN-1998; 98US-0090246P.
PR      22-JUN-1998; 98US-0090252P.
PR      22-JUN-1998; 98US-0090254P.
PR      23-JUN-1998; 98US-0090349P.
PR      23-JUN-1998; 98US-0090355P.
PR      24-JUN-1998; 98US-0090429P.
PR      24-JUN-1998; 98US-0090431P.
PR      24-JUN-1998; 98US-0090435P.
PR      24-JUN-1998; 98US-0090444P.
PR      24-JUN-1998; 98US-0090445P.
PR      24-JUN-1998; 98US-0090461P.
PR      24-JUN-1998; 98US-0090472P.
PR      24-JUN-1998; 98US-0090535P.
PR      24-JUN-1998; 98US-0090538P.
PR      24-JUN-1998; 98US-0090540P.
PR      24-JUN-1998; 98US-0090557P.
PR      25-JUN-1998; 98US-0090676P.
PR      25-JUN-1998; 98US-0090678P.
PR      25-JUN-1998; 98US-0090688P.
PR      25-JUN-1998; 98US-0090690P.
PR      25-JUN-1998; 98US-0090691P.
PR      25-JUN-1998; 98US-0090694P.
PR      25-JUN-1998; 98US-0090695P.
PR      25-JUN-1998; 98US-0090696P.
PR      26-JUN-1998; 98US-0090862P.
PR      26-JUN-1998; 98US-0090863P.
PR      01-JUL-1998; 98US-0091358P.
PR      01-JUL-1998; 98US-0091360P.

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PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2001-032160/04.  
DR N-PSDB; AAF44089.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
PT to cause targeted cell death.  
XX  
PS Claim 12; Fig 6; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
CC be used for targeted delivery of bioactive molecules, such as toxins,  
CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
CC DNA. They may also be used to produce transgenic animals which are used  
CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
CC and protein sequence can be used for tissue typing and in treating  
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
CC AAF44470 represent PCR primers and hybridisation probes used in the  
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
CC AAB65300 represent human PRO polynucleotide and protein sequences given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 4; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

Qy 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEHINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQXCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
Qy 323 SSRVEKFLDFTKEEILMLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
Qy 383 VSAVEKQVTRHLEDVFSKRNSNMVMSMTLGLHPWIANIDTQY-----LAA 430  
Db 101 -----EDQFQEAQTSPLAKHTSQAI-----LQVLAAEDFTIFKAMVQKNIEMQLQA 149  
Qy 431 KRAIRTVFGPEPDMIRDGSI-----PIAKMFOEIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
Qy 485 NRWNYYIEGFK 494  
Db 200 KRKKQLSEAK 209

RESULT 1347  
ABG34032  
ID ABG34032 standard; protein; 367 AA.  
XX  
AC ABG34032;  
XX  
DT 15-JUL-2002 (first entry)  
DE Human Pro peptide #3.  
XX  
KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;  
KW tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200224888-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US027099.  
XX  
PR 01-SEP-2000; 2000US-0229896P.  
PR 05-SEP-2000; 2000US-0230621P.  
PR 22-SEP-2000; 2000US-0235147P.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 12-JAN-2001; 2001US-0261878P.  
PR 16-JAN-2001; 2001US-0261910P.  
PR 16-JAN-2001; 2001US-0261939P.  
PR 16-JAN-2001; 2001US-0262150P.  
PR 25-JAN-2001; 2001US-0264395P.  
PR 02-FEB-2001; 2001US-0266421P.  
PR 09-FEB-2001; 2001US-0267623P.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 09-MAR-2001; 2001US-0274399P.  
PR 03-APR-2001; 2001US-0280982P.  
PR 04-APR-2001; 2001US-0282129P.  
PR 04-APR-2001; 2001US-0282199P.  
PR 09-MAY-2001; 2001US-0290589P.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2002-362426/39.  
DR N-PSDB; ABK69963.  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or for  
PT genetic analysis of individuals with genetic disorders.  
XX  
PS Claim 11; Fig 6; 218pp; English.  
XX  
CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The invention  
CC also comprises a method for producing the proteins of the invention by  
CC recombinant means and antibodies specific for the protein of the  
CC invention. The antibody may be used for detecting the PRO proteins of the  
CC invention and may be used to modify their activity. polynucleotides may  
CC be used as hybridisation probes for a cDNA library to isolate the full-  
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation  
CC probes for mapping the gene which encodes that PRO and for genetic  
CC analysis of individuals with genetic disorders, in assays to identify  
CC other proteins or molecules involved in binding reaction, to generate  
CC transgenic animals or knock-out animals which in turn are useful in the  
CC development and screening of therapeutically useful reagents, for







PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
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PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
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PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

DR WPI; 2003-247083/24.  
DR N-PSDB; ABX80110.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments.

XX Claim 12; Fig 6; 648pp; English.

PS The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpetiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries, and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein

XX Sequence 367 AA;

Query Match

Best Local Similarity 3.2%; Score 83.5; DB 6; Length 367;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;







PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX

PA (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-288106/28.  
DR N-PSDB; ABX90087.  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes.  
XX  
PS Claim 12; Fig 6; 650pp; English.  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein electrophoresis,  
CC and the isolated nucleic acids may be used for recombinantly expressing  
CC those markers. The PRO polypeptides and nucleic acids may also be used in  
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for  
CC PRO, and in affinity purification of PRO from recombinant cell culture or  
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO  
CC polynucleotides of the invention. Note: The sequence data for this patent  
CC is also available in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 6; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
Qy 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN 322  
Db 28 PILDVFEQKCEVNCCKGHVITPGSPPEVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
Qy 323 SSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
Qy 383 VSAVEKQVTRHLEDVFSKRNSNMVSVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEACTSPLAKHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
Qy 431 KRAITVFGTEPDMIRDGSTI-----PIAKMFOEIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
Qy 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1352  
ABU13862  
ID ABU13862 standard; protein; 367 AA.  
XX  
AC ABU13862;  
XX  
DT 26-FEB-2003 (first entry)  
XX  
DE Human PRO189 polypeptide.  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;



KW genetic disorder; antibacterial; immunosuppressive.

XX Homo sapiens.

OS US2002103125-A1.

PN 01-AUG-2002.

XX 20-NOV-2001; 2001US-00989731.

PF 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

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PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

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PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.

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PR 17-JUN-1998; 98US-0089599P.

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PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 06-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 30-MAR-2000; 2000WO-US008439.

PR 15-MAY-2000; 2000WO-US013358.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH LTD.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;

WPI; 2003-102117/09.  
N-PSDB; ABX63933.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 12; Fig 6; 649pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. ABU13860-ABU14006 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at [seqdata.uspto.gov/psipsDIDEntry.html](http://seqdata.uspto.gov/psipsDIDEntry.html)

Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 6; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;









DT	10-SEP-2003	(first entry)	
XX			
DE	Human	PRO189 polypeptide.	
XX			
KW	Human; PRO	polypeptide; secreted protein; transmembrane protein; genetic disorder; antibacterial; immunosuppressive.	
KW			
XX	Homo sapiens.		
OS			
XX			
PN	US2002127576-A1.		
XX			
PD	12-SEP-2002.		
XX			
PF	14-NOV-2001; 2001US-00991073.		
XX			
PR	16-JUN-1997; 97US-0049787P.		
PR	17-OCT-1997; 97US-0062250P.		
PR	05-NOV-1997; 97WO-US020069.		
PR	12-NOV-1997; 97US-0065186P.		
PR	13-NOV-1997; 97US-0065311P.		
PR	24-NOV-1997; 97US-0066770P.		
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PR	20-MAR-1998; 98US-0078910P.		
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PR	28-MAY-1998; 98US-0087106P.		
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PR	02-JUN-1998; 98US-0087759P.		
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PR	11-JUN-1998; 98US-0088876P.		
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PR	18-JUN-1998; 98US-0089801P.		
PR	18-JUN-1998; 98US-0089907P.		
PR	18-JUN-1998; 98US-0089908P.		
PR	16-SEP-1998; 98WO-US019330.		
PR	17-SEP-1998; 98WO-US019437.		
PR	07-OCT-1998; 98WO-US021141.		
PR	01-DEC-1998; 98WO-US025108.		
PR	05-JAN-1999; 99WO-US000106.		
PR	08-MAR-1999; 99WO-US005028.		
PR	02-JUN-1999; 99WO-US012252.		
PR	15-SEP-1999; 99WO-US021090.		
PR			
PR	15-SEP-1999; 99WO-US021547.		
PR	30-NOV-1999; 99WO-US028313.		
PR	01-DEC-1999; 99WO-US028301.		
PR	01-DEC-1999; 99WO-US028634.		
PR	16-DEC-1999; 99WO-US030095.		
PR	20-DEC-1999; 99WO-US030911.		
PR	06-JAN-2000; 2000WO-US000219.		
PR	06-JAN-2000; 2000WO-US000376.		
PR	11-FEB-2000; 2000WO-US003565.		
PR	18-FEB-2000; 2000WO-US004341.		
PR	22-FEB-2000; 2000WO-US004414.		
PR	24-FEB-2000; 2000WO-US004914.		
PR	24-FEB-2000; 2000WO-US005004.		
PR	02-MAR-2000; 2000WO-US005841.		
PR	10-MAR-2000; 2000WO-US006319.		
PR	15-MAR-2000; 2000WO-US006884.		
PR	20-MAR-2000; 2000WO-US007377.		
PR	30-MAR-2000; 2000WO-US008439.		
PR	15-MAY-2000; 2000WO-US013358.		
PR	17-MAY-2000; 2000WO-US013705.		
PR	22-MAY-2000; 2000WO-US014042.		
PR	30-MAY-2000; 2000WO-US014941.		
PR	02-JUN-2000; 2000WO-US015264.		
PR	28-JUL-2000; 2000WO-US020710.		
PR	11-AUG-2000; 2000WO-US022031.		
PR	23-AUG-2000; 2000WO-US023522.		
PR	24-AUG-2000; 2000WO-US023328.		
PR	08-NOV-2000; 2000WO-US030952.		
PR	01-DEC-2000; 2000WO-US032678.		
PR	28-FEB-2001; 2001WO-US006520.		
PR	01-JUN-2001; 2001WO-US017800.		
PR	20-JUN-2001; 2001WO-US019692.		
PR	29-JUN-2001; 2001WO-US021066.		
PR	09-JUL-2001; 2001WO-US021735.		
PR	28-AUG-2001; 2001US-00941992.		
XX			
PA	(GETH )	GENENTECH INC.	
XX			
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;		
PI	Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;		
PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;		
PI	Zhang Z;		
XX			
DR	WPI; 2003-340824/32.		
DR	N-PSDB; ACD44123.		
XX			
PT	Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346		
PT	and PRO1375, which stimulate proliferation of stimulated T-lymphocytes		
PT	and are therapeutically useful for enhancing immune responses.		
XX			
PS	Claim 12; Fig 6; 661pp; English.		
XX			
CC	The present invention relates to the isolation of novel human PRO		
CC	polypeptides, and the polynucleotide sequences encoding them. The PRO		
CC	polypeptides are secreted and transmembrane proteins. The PRO		
CC	polypeptides are useful for detecting other PRO polypeptides, for linking		
CC	bioactive molecules to cells expressing PRO polypeptides, for modulating		
CC	biological activities of cells expressing PRO polypeptides, and for for		
CC	identifying agonists or antagonists. The polynucleotide sequences		
CC	encoding PRO polypeptides are useful as hybridisation probes, in		
CC	chromosome and gene mapping, in the generation of antisense RNA and DNA,		
CC	in the preparation of PRO polypeptides, for generating transgenic animals		
CC	or knockout animals, to construct hybridisation probes for mapping the		
CC	gene which encodes the PRO polypeptide, and for the genetic analysis of		
CC	individuals with genetic disorders, in gene therapy, for chromosome		
CC	identification, as chromosome markers, and for generating probes for PCR,		
CC	Northern analysis, Southern analysis and Western analysis. ABO25891-		
CC	ABO26037 represent the human PRO polypeptides of the invention. Note: The		
CC	sequence data for this patent was obtained in electronic format directly		
CC	from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html		
XX			
SQ	Sequence 367 AA;		









XX Novel human secreted or transmembrane protein PRO189.  
DE Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2003027985-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 14-NOV-2001; 2001US-00990562.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
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PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
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PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
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PR 10-AUG-1998; 98US-0095916P.  
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PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
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PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.



PR 26-AUG-1998; 98US-0097955P.  
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PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
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PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
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PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
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PR 15-SEP-1999; 99WO-US021090.  
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PR 08-OCT-1999; 99US-0158663P.  
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PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
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PR 15-MAY-2000; 2000WO-US013358.  
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PR 30-MAY-2000; 2000WO-US014941.

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Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
Qy 383 VSAVEKQVTRHLEDVFSKRNSNMVSVMTGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
Qy 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
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ABU92111  
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XX  
DT 16-JUL-2003 (first entry)  
XX  
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XX  
KW Human; secreted and transmembrane protein; PRO; nootropic;  
KW neuroprotective; antiparkinsonian; cytostatic; gene therapy;  
KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
PN US2003017476-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 20-NOV-2001; 2001US-00989724.  
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PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
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PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.







CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
CC useful for detecting PRO polypeptides and for linking a bioactive  
CC molecule to a cell expressing the above polypeptides, where the bioactive  
CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
CC causes the death of the cell. The polypeptide is useful for identifying  
CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
CC PRO, as a molecular weight marker for protein electrophoresis purposes  
CC and the PRO polynucleotide is useful for recombinantly expressing those  
CC markers. The polynucleotide is also useful as a hybridisation probe, in  
CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
CC the preparation of PRO polypeptide, for generating transgenic animals or  
CC knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, to construct hybridisation  
CC probes for mapping the gene which encodes PRO and for the genetic  
CC analysis of individuals with genetic disorders, in gene therapy, for  
CC chromosome identification, as a chromosome marker and for generating  
CC probes for PCR, Northern analysis, Southern analysis and Western  
CC analysis. This sequence represents a human PRO polypeptide of the  
CC invention  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 6; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

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Db 28 PILDVEQKCEVNCCKGHVITPGSPVPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSPLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSNMVSMVTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFORIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGVLPDCLTDGSDVWSDLEHEEMKILREVLRS-----KKEYDQEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1361.  
ABU81569  
ID ABU81569 standard; protein; 367 AA.  
XX  
AC ABU81569;  
XX  
DT 24-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO189.  
XX  
KW Human; secreted and transmembrane protein; gene therapy; PRO; PRO943;  
KW PRO183; PRO184; PRO185; PRO331; PRO1133; PRO363; PRO5723; PRO1387;  
KW PRO1114; PRO3301; PRO9940; PRO1181; PRO7170; PRO361; PRO846;  
KW bioactive molecule; toxin; radiolabel; antibody; cell death; cancer;  
KW autoimmune disease; chromosome mapping; gene mapping; transgenic animal;  
KW knockout animal; septic shock.  
XX  
OS Homo sapiens.  
XX  
FN US2002177164-A1.  
XX  
PD 28-NOV-2002.  
XX  
PF 20-NOV-2001; 2001US-00989293.  
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PR 30-NOV-1999; 99WO-US028313.  
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PR 16-DEC-1999; 99WO-US030095.  
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PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.



AC ADA37519;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO189.  
XX  
KW PRO; secreted protein; transmembrane protein;  
KW hypertrophy of neonatal heart; angiogenesis;  
KW vascular endothelial growth factor; VEGF-stimulated proliferation;  
KW endothelial cell; T-lymphocyte proliferation; retinal neuron;  
KW c-fos induction; adipocyte cell; chondrocyte differentiation;  
KW pancreatic beta-cell precursor differentiation; gene therapy; tumour;  
KW cancer; human; colon cancer; lung cancer; breast cancer;  
KW rod photoreceptor cell.  
XX  
OS Homo sapiens.  
XX  
PN US2003008297-A1.  
PD  
XX 09-JAN-2003.  
XX  
PF 15-NOV-2001; 2001US-00997653.  
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(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;

WPI; 2003-531419/50.

N-PSDB; ADA37518.

New isolated PRO183, PRO184, PRO361 or PRO846 nucleic acid and secreted transmembrane polypeptides, useful as targets for the diagnosis and treatment of cancers, such as lung and breast cancers.

Claim 12; Fig 6; 660pp; English.

The invention relates to an isolated nucleic acid molecule comprising the full-length coding sequence of the DNA ATCC Accession Numbers given in the specification, or comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 147 PRO polypeptides, or an extracellular domain of the polypeptide; or (b) any of 147 nucleotide sequences fully defined in the specification. Also included are the PRO proteins (or their extracellular domains with or without their associated extracellular domains), expression vectors, host cells, PRO chimaeric proteins, anti-PRO antibodies, methods of detecting polypeptide in a sample, methods of linking a bioactive molecule to a cell expressing a polypeptide and methods of modulating at least one biological activity of a cell expressing the polypeptide. The PRO polypeptides or







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PR 17-AUG-1999; 99US-0149396P.  
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Query Match 3.2%; Score 83.5; DB 6; Length 367;  
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Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
  
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Db 101 ----EDQFQACTSPLAKTHTSQAI-----LQVLAAEDFTIFKAMMVQKNIEMQLQA 149  
  
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RESULT 1368  
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XX Human PRO189 polypeptide.  
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XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
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XX

OS Homo sapiens.  
XX US2003054987-A1.  
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XX 20-MAR-2003.  
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PF 14-NOV-2001; 2001US-00990443.  
XX  
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Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

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Dd	84	-ELVEKLL-----EGYLKEIGIN-----	100
Qy	383	VSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQY-----LAA	430
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Db 84 -ELVEKLL-----EGYLKEIGIN-----100  
Qy 383 VSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEACTSPLAKHTTSQAI-----LQPVLAABDFTIFKAMMVQKNIEMQLQA 149  
Qy 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFQEIYVHKSVVLIPLGAVDDGSHSQNEKI 484  
Db 150 IRIIQERNGLVPDCLTDGSDVVSDLEHEEMKILREVLRKS-----KEYDQEEER 199  
Qy 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1374  
ADA38449  
ID ADA38449 standard; protein; 367 AA.  
XX  
AC ADA38449;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO189.  
XX  
KW PRO; secreted protein; transmembrane protein; gene therapy; tumour;  
KW cancer; human; colon cancer; lung cancer; breast cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003059780-A1.  
PD  
XX 27-MAR-2003.  
PF 14-NOV-2001; 2001US-00991854.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
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PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
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PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.





XX 20-NOV-2003 (first entry)

DE Human secreted/transmembrane polypeptide PRO189.

XX Human; PRO; secreted protein; transmembrane protein;

KW endothelial cell tube formation; chondrocyte cell differentiation;

KW microvascular endothelial cell; tumour; lung tumour; colon tumour;

KW breast tumour; prostate tumour; rectal tumour; kidney tumour;

KW liver tumour; cytostatic; vaccine.

XX Homo sapiens.

OS US2003073190-A1.

XX 17-APR-2003.

XX 09-SEP-2002; 2002US-00238283.

XX 01-JUL-1998; 98US-0091358P.

PR 02-JUN-1999; 99WO-US012252.

PR 20-JUL-1999; 99US-0144758P.

PR 28-JUL-1999; 99US-0146222P.

PR 25-AUG-1999; 99US-00380137.

PR 30-MAR-2000; 2000WO-US008439.

PR 02-JUN-2000; 2000WO-US015264.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX WPI; 2003-585304/55.

DR N-PSDB; ADA43586.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or

PT PRO21383, useful in molecular biology, chromosome and gene mapping, in

PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 11; Fig 6; 352pp; English.

PS The invention relates to an isolated secreted/transmembrane (PRO)

CC polypeptide, having at least 80% sequence identity to a sequence selected

CC from any one of the 57 amino acid sequences given in specification, or to

CC a sequence encoded by a nucleic acid molecule selected from any one of

CC the nucleic acids deposited under any of the ATCC accession numbers given

CC in specification, or a sequence having at least 80% identity to PRO

CC lacking its associated signal peptide, an extracellular domain of PRO

CC with or without its associated signal peptide. Also included are vectors,

CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding

CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and

CC an oligonucleotide probe derived from any one of the above nucleotide

CC sequences. PRO6018 polypeptide is useful for stimulating the

CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

CC and PRO21383 polypeptides are useful for stimulating the proliferation of

CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

CC polypeptides are useful for inhibiting the proliferation of human

CC microvascular endothelial cells. PRO polypeptides are useful for

CC detecting the presence of tumour in a mammal, including tumours of lung,

CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,

CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and

CC PRO34274 polypeptides are useful for inducing endothelial cell tube

CC formation. PRO or the antibody are useful in the preparation of a

CC medicament for treating a condition responsive to PRO polypeptide. The

CC oligonucleotide probes are useful for isolating genomic and cDNA

CC nucleotide sequences, for measuring or detecting the expression of an

CC associated gene, and as antisense probes. PRO nucleic acid is useful as a

CC hybridisation probe, in chromosome and gene mapping, in the generation of

CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and

CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The

CC present sequence represents a PRO protein.

XX SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 7; Length 367;

Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSGHILVPGIYDEV-----VPLT---EEEINTYKAHLDLEERYN 322

Db 28 PILDFVEQKCEVNCCKGSHVITPGSPVILVACVPLVFDDEESKLTYTEIH---QYK- 83

QY 323 SSRVEKFLFDTKKEEILMHLWRYPSSLIHGIEGADEFPGTKTVIPGRVIGKFSIRLVPHMN 382

Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIANIDDTQY-----LAA 430

Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMQLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFOQIVHKSVWLIPLGAVDGGEHSQNEKI 484

Db 150 IRIQERNGVLPDCLTDGSDVVSLEHEEMKILREVLRS-----KEEYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1378

ABO53108

ID ABO53108 standard; protein; 367 AA.

XX ABO53108;

XX 14-OCT-2003 (first entry)

DE Human secreted/transmembrane protein PRO189.

XX Human; secreted protein; transmembrane protein; PRO;

KW adrenal cortical capillary endothelial cell; angiogenesis; wound healing;

KW diabetes; obesity; hyper-insulinaemia; hypo-insulinaemia;

KW chondrocyte redifferentiation; bone disorder; cartilage disorder;

KW sports injury; arthritis; kidney mesangial cell proliferation;

KW kidney disorder; Berger disease; neuropathy; coeliac disease;

KW dermatitis herpetiformis; Crohn's disease; tumour; cancer.

XX Homo sapiens.

XX US2003044806-A1.

PD 06-MAR-2003.

XX 15-NOV-2001; 2001US-00998156.

XX 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

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PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 04-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
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PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
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PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
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PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US028634.  
PR 20-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 11-FEB-2000; 2000WO-US000376.  
PR 18-FEB-2000; 2000WO-US003565.  
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PR 16-JUN-1997; 97US-0049787P.  
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PR 10-JUL-1998; 98US-0092472P.  
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PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
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PR 11-AUG-1998; 98US-0096146P.  
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PR 13-AUG-1998; 98US-0096413P.  
PR 17-AUG-1998; 98US-0096757P.  
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PR 20-AUG-1998; 98US-0097218P.  
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PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.

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PR	26-JUL-1999;	99US-0145698P.	KW	
PR	28-JUL-1999;	99US-0146222P.	XX	
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PR	15-SEP-1999;	99WO-US021090.	XX	Homo sapiens.
PR	15-SEP-1999;	99WO-US021547.	PN	US2003049638-A1.
PR	08-OCT-1999;	99US-0158663P.	XX	
PR	30-NOV-1999;	99WO-US028313.	PD	13-MAR-2003.
PR	01-DEC-1999;	99WO-US028301.	XX	
PR	01-DEC-1999;	99WO-US028634.	PF	16-NOV-2001; 2001US-00991157.
PR	16-DEC-1999;	99WO-US030095.	XX	
PR	20-DEC-1999;	99WO-US030911.	PR	16-JUN-1997; 97US-0049787P.
PR	05-JAN-2000;	2000WO-US000219.	PR	17-OCT-1997; 97US-0062250P.
PR	06-JAN-2000;	2000WO-US000376.	PR	05-NOV-1997; 97WO-US020069.
PR	11-FEB-2000;	2000WO-US003565.	PR	12-NOV-1997; 97US-0065186P.
PR	18-FEB-2000;	2000WO-US004341.	PR	13-NOV-1997; 97US-0065311P.
PR	22-FEB-2000;	2000WO-US004414.	PR	24-NOV-1997; 97US-0066770P.
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PR	24-FEB-2000;	2000WO-US005004.	PR	20-MAR-1998; 98US-0078910P.
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PR	15-MAR-2000;	2000WO-US006884.	PR	07-MAY-1998; 98US-0084600P.
PR	20-MAR-2000;	2000WO-US007377.	PR	28-MAY-1998; 98US-0087106P.
PR	30-MAR-2000;	2000WO-US008439.	PR	02-JUN-1998; 98US-0087607P.
PR	15-MAY-2000;	2000WO-US013358.	PR	02-JUN-1998; 98US-0087609P.
PR	22-MAY-2000;	2000WO-US014042.	PR	03-JUN-1998; 98US-0087827P.
PR	30-MAY-2000;	2000WO-US014941.	PR	04-JUN-1998; 98US-0088021P.
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PR	23-JUN-2000;	2000US-0213637P.	PR	04-JUN-1998; 98US-0088028P.
PR	28-JUL-2000;	2000WO-US020710.	PR	04-JUN-1998; 98US-0088030P.
PR	11-AUG-2000;	2000WO-US022031.	PR	04-JUN-1998; 98US-0088033P.
PR	23-AUG-2000;	2000WO-US023522.	PR	04-JUN-1998; 98US-0088326P.
Query Match 3.2%; Score 83.5; DB 7; Length 367;			PR	05-JUN-1998; 98US-0088167P.
Best Local Similarity 22.0%; Pred. No. 1.4e+02;			PR	05-JUN-1998; 98US-0088202P.
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;			PR	05-JUN-1998; 98US-0088212P.
QY	272 PMADLVALLGSLVDSGHILVPGIYDEV-----VPLT---EEINTYKAIHLDLEEYRN 322		PR	05-JUN-1998; 98US-0088217P.
Db	28 PILDVEQKCEVNCCKGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83		PR	09-JUN-1998; 98US-0088655P.
QY	323 SSRVEKFLFDTKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382		PR	10-JUN-1998; 98US-0088734P.
Db	84 -ELVEKLL-----EGYLKEIGIN----- 100		PR	10-JUN-1998; 98US-008738P.
QY	383 VSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430		PR	10-JUN-1998; 98US-0088742P.
Db	101 -----EDQFOEACTSPLAKHTHSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQQA 149		PR	10-JUN-1998; 98US-0088810P.
QY	431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFOEIVHKSVWLIPGLGAVDDGEHSQNEKI 484		PR	10-JUN-1998; 98US-0088824P.
Db	150 IRIQERNGLVPDCLTDGSDVVSDDLEHEEMKILREVLRKS-----KBEYDQEEER 199		PR	10-JUN-1998; 98US-0088826P.
QY	485 NRWNYIEGTK 494		PR	11-JUN-1998; 98US-0088858P.
Db	200 KRKKQLSEAK 209		PR	11-JUN-1998; 98US-0088861P.
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XX			PR	16-JUN-1998; 98US-0089512P.
AC	ADA06297;		PR	16-JUN-1998; 98US-0089514P.
XX			PR	17-JUN-1998; 98US-0089532P.
DT	29-JAN-2004 (revised)		PR	17-JUN-1998; 98US-0089538P.
DT	06-NOV-2003 (first entry)		PR	17-JUN-1998; 98US-0089598P.
XX	Human secreted/transmembrane PRO polypeptide #3.		PR	17-JUN-1998; 98US-0089599P.
DE			PR	17-JUN-1998; 98US-0089600P.
XX			PR	17-JUN-1998; 98US-0089653P.
KW	human; tissue typing; cardiac insufficiency disorder; angiogenesis;		PR	18-JUN-1998; 98US-0089907P.
KW	wound healing; tumour; immune response; retinal disorder; retinal injury;		PR	18-JUN-1998; 98US-0089908P.
KW	sight loss; age-related macular degeneration; AMD; kidney disorder;		PR	19-JUN-1998; 98US-0089947P.
KW	mesangial cell function; Berger disease; nephropathy; dermatitis;		PR	19-JUN-1998; 98US-0089948P.





DT 20-NOV-2003 (first entry)  
XX Human secreted/transmembrane protein PRO189.  
DE  
XX  
KW PRO; secreted protein; transmembrane protein;  
KW hypertrophy of neonatal heart; angiogenesis;  
KW vascular endothelial growth factor; VEGF-stimulated proliferation;  
KW endothelial cell; T-lymphocyte proliferation; retinal neuron;  
KW c-fos induction; adipocyte cell; chondrocyte differentiation;  
KW pancreatic beta-cell precursor differentiation; gene therapy; tumour;  
KW cancer; human; colon cancer; lung cancer; breast cancer;  
KW rod photoreceptor cell.  
XX  
OS Homo sapiens.  
XX  
PN US2003059782-A1.  
XX  
PD 27-MAR-2003.  
XX  
PF 15-NOV-2001; 2001US-00997628.  
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PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
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PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
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PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.

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PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.

Query Match      3.2%; Score 83.5; DB 7; Length 367;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
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QY      323 SSRVEKFLFDTKKEEILMHLWRYPSPSLSIHGIEGAFDEPGTKTIVIPGRVIGKFSIRLVPHMN 382
Db      84  -ELVEKLL-----EGYLKEIGIN-----100

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QY      431 KRAIRTVFGTEPDMIRDGTI-----PIAKMFOEIVHKSWWLIPLGAVDDGGRHSQNEKI 484
Db      150 IRIIQERNGLVPDCLTGDSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199

QY      485 NRWNYIEGTK 494
Db      200 KRKKQLSEAK 209

RESULT 1395
ADC56141
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AC ADC56141;
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DT 18-DEC-2003 (first entry)
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DE Human PRO polypeptide #3.
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KW Human; PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;
KW insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;
KW thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;
KW polycystic kidney disease; renal tumour; antidiabetic; antianaemic;
KW cytosstatic; cardiant; vulnery; antiinflammatory; anorectic.
XX
OS Homo sapiens.
XX
PN US2003064375-A1.
XX
PD 03-APR-2003.
XX
PF 15-NOV-2001; 2001US-00997857.
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PR 16-JUN-1997; 97US-0049787P.
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PR 12-NOV-1997; 97US-0065186P.
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107-JUL-1998; 98US-0091978P.
107-JUL-1998; 98US-0091982P.
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PR 05-NOV-1997; 97WO-US020069.  
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PR 01-DEC-1998; 98WO-US025108.  
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PR 05-JAN-1999; 99WO-US000106.  
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PR	17-AUG-1999;	99US-0149396P.
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PR	22-FEB-2000;	2000WO-US004414.
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PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-2000;	2000WO-US013358.
PR	17-MAY-2000;	2000WO-US013705.
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QY	323 SSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382	
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QY	383 VSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQY-----LAA 430	
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Db	200 KRKKQLSEAK 209	
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DT	18-DEC-2003 (first entry)	
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KW	vascular endothelial growth factor; VEGF-stimulated proliferation;	
KW	endothelial cell; T-lymphocyte proliferation; retinal neuron;	
KW	c-fos induction; adipocyte cell; chondrocyte differentiation;	
KW	pancreatic beta-cell precursor differentiation; gene therapy; tumour;	
KW	cancer; human; colon cancer; lung cancer; breast cancer;	
KW	rod photoreceptor cell.	
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OS	Homo sapiens.	

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PD	10-APR-2003.	
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XX	14-NOV-2001; 2001US-00993748.	
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PR	24-JUN-1998;	98US-0090540P.





KW cancer; human.

XX

OS Homo sapiens.

XX

PN US2003073193-A1.

XX

PD 17-APR-2003.

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PF 16-SEP-2002; 2002US-00245147.

XX

PR 04-APR-2001; 2001US-0282199P.

PR

PR 29-AUG-2001; 2001WO-US027099.

PR

PR 18-JUL-2002; 2002US-00197942.

XX

XX (GETH ) GENENTECH INC.

XX

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX

DR WPI; 2003-730023/69.

DR

DR N-PSDB; ADC23349.

XX

PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or

PT PRO21383, useful in molecular biology, chromosome and gene mapping and in

PT gene therapy.

XX

PS Claim 11; SEQ ID NO 6; 308pp; English.

XX

CC This invention relates to a novel isolated and secreted PRO polypeptide.

CC PRO is a transmembrane protein involved in the formation, differentiation

CC and maintenance of multicellular organisms, and more particularly the

CC proliferation, differentiation and migration of individual cells. The

CC invention describes screening compounds to identify PRO polypeptide

CC agonists and antagonists, anti-PRO antibodies, and immunoconjugates

CC comprising an antibody conjugated to a cytotoxic agent. Specifically, the

CC heterologous protein of the chimeric polypeptide is an epitope tag or an

CC Fc region of an immunoglobulin. Through the use of gene therapy, the PRO

CC polypeptide is useful for preparing cytostatic compositions for

CC diagnosing or treating cancer. The polypeptide is also useful as a

CC molecular weight marker for protein electrophoresis purposes. This

CC polypeptide sequence is a human PRO polypeptide, encoded by a native

CC clone of the cDNA library of the invention.

XX

SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 7; Length 367;

Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

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QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMN 382

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QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430

Db 101 -----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGEHSQNEKI 484

Db 150 IRIIQERNGLVPLDCLTDGSDVVDLEHEEMKILREVLRS-----KEEYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1399

ADC26043

ID ADC26043 standard; protein; 367 AA.

XX

AC ADC26043;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human PRO189 protein.

XX

XX PRO; cytostatic; cancer; sports-related joint problem;

KW articular cartilage defect; osteoarthritis; rheumatoid arthritis;

KW tissue typing; gene therapy; foetal haemoglobin induction; transgenic;

KW human.

XX

OS Homo sapiens.

XX

PN US2003073194-A1.

XX

PD 17-APR-2003.

XX

PF 16-SEP-2002; 2002US-00245730.

XX

PR 02-JUN-1998; 98US-0087607P.

PR

PR 02-JUN-1999; 99WO-US012252.

PR

PR 25-AUG-1999; 99US-00380137.

PR

PR 30-MAY-2000; 2000WO-US014941.

PR

PR 29-AUG-2001; 2001WO-US027099.

PR

PR 18-JUL-2002; 2002US-00197942.

XX

XX (GETH ) GENENTECH INC.

PA

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX

XX WPI; 2003-708428/67.

DR

DR N-PSDB; ADC26042.

XX

PT New secreted and transmembrane PRO polypeptides useful in stimulating the

PT proliferation or differentiation of chondrocyte cells and detecting the

PT presence of a tumor in a mammal.

XX

PS Claim 11; SEQ ID NO 6; 308pp; English.

XX

CC The invention relates to a novel isolated PRO polypeptide. The

CC polypeptide of the invention demonstrates cytostatic activity and may be

CC useful during the preparation of a composition for diagnosing or treating

CC sports-related joint problems, including articular cartilage defects,

CC osteoarthritis and rheumatoid arthritis. Furthermore, the polypeptides

CC may be utilised during tissue typing, gene therapy, foetal haemoglobin

CC induction and the production of transgenic animals. The current sequence

CC is that of the human PRO protein of the invention.

XX

SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 7; Length 367;

Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN 322

Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83

QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTIPGRVIGKFSIRLVPHMN 382

Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430

Db 101 -----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGEHSQNEKI 484

Db 150 IRIIQERNGLVPLDCLTDGSDVVDLEHEEMKILREVLRS-----KEEYDQEEER 199

Qy 485 NRWNYEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1400  
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XX  
AC ADC14308;  
XX  
DT 18-DEC-2003 (first entry)  
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XX  
KW human; secreted and transmembrane protein; PRO; nootropic;  
KW neuroprotective; antiparkinsonian; cytostatic; gene therapy;  
KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
PN US2003082546-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 28-AUG-2001; 2001US-00941992.  
XX  
PR 06-NOV-1996; 96US-00743698.  
PR 16-JUN-1997; 97US-0049787P.  
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PR 17-OCT-1997; 97US-0062250P.  
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PR 12-NOV-1997; 97US-0065186P.  
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PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
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PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
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PR 02-MAR-2000; 2000WO-US005841.  
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Query Match

3.2%; Score 83.5; DB 7; Length 367;









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Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430

Db 101 ----EDQFOEACTSPAKTHTSQAI-----LQPVLAADFTIFKAMMVQKNVEMQLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFORIVHKSVWLIPGLGAVDDGEHSQNEKI 484

Db 150 IRIIQERNGVLPDCLTDGSDVVSdleHEEMKILREVLRS-----KREYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1404

ADC82198

ID ADC82198 standard; protein; 367 AA.

XX

AC ADC82198;

XX

DT 01-JAN-2004 (first entry)

XX

DE Human PRO polypeptide #3.

XX

KW Human; PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;

KW insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;

KW thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;

KW polycystic kidney disease; renal tumour; antidiabetic; antianaemic;

KW cytostatic; cardiant; vulnerary; antiinflammatory; anorectic.

XX

OS Homo sapiens.

XX

PN US2003059833-A1.

XX

PD 27-MAR-2003.

XX

PF 15-NOV-2001; 2001US-00997440.

XX

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

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QY	485 NRWNYIEGTK 494	
Db	200 KRKKQLSEAK 209	
RESULT 1409		
ADD55939		
ID	ADD55939 standard; protein; 367 AA.	
XX		
AC	ADD55939;	
XX		
DT	15-JAN-2004 (first entry)	
XX		
DE	Human PRO polypeptide #3.	
XX		
KW	Human; PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;	
KW	insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;	
KW	thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;	
KW	polycystic kidney disease; renal tumour; antidiabetic; antianaemic;	
KW	cytostatic; cardiant; vulnerary; antiinflammatory; anorectic.	
XX		
OS	Homo sapiens.	
XX		
PN	US2003077594-A1.	
XX		
PD	24-APR-2003.	
XX		
PF	14-NOV-2001; 2001US-00993583.	
XX		
PR	16-JUN-1997; 97US-0049787P.	
PR	17-OCT-1997; 97US-0062250P.	
PR	05-NOV-1997; 97WO-US020069.	
PR	12-NOV-1997; 97US-0065186P.	
PR	13-NOV-1997; 97US-0065311P.	
PR	24-NOV-1997; 97US-0066770P.	
PR	25-FEB-1998; 98US-0075945P.	
PR	20-MAR-1998; 98US-0078910P.	

PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088036P.  
PR 04-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090542P.  
PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
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PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.

PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.

PR	16-DEC-1999;	99WO-US030095.	
PR	20-DEC-1999;	99WO-US030911.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
PR	11-FEB-2000;	2000WO-US000356S.	
PR	18-FEB-2000;	2000WO-US004341.	
PR	22-FEB-2000;	2000WO-US004414.	
PR	24-FEB-2000;	2000WO-US004914.	
PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	10-MAR-2000;	2000WO-US006319.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	20-MAR-2000;	2000WO-US007377.	
PR	30-MAR-2000;	2000WO-US008439.	
PR	15-MAY-2000;	2000WO-US013358.	
PR	17-MAY-2000;	2000WO-US013705.	
PR	22-MAY-2000;	2000WO-US014042.	
PR	30-MAY-2000;	2000WO-US014941.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	23-JUN-2000;	2000US-0213637P.	
PR	28-JUL-2000;	2000WO-US020710.	
PR	11-AUG-2000;	2000WO-US022031.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
Query Match 3.2%; Score 83.5; DB 7; Length 367;			
Best Local Similarity 22.0%; Pred. No. 1.4e+02;			
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;			
QY	272	PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN	322
Db	28	PILDFVEQKEVCKGKHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK-	83
QY	323	SSRVEKFLFDTKKEIILMHLWRYPSLSIHGIEGAPDEPGTKVIPGRVIGKFSIRLVPHMN	382
Db	84	-ELVEKLL-----EGYLKEIGIN-----	100
QY	383	VSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQY-----LAA	430
Db	101	-----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMQLQA	149
QY	431	KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVKHSVVLPLGAVDDGEHSQNEKI	484
Db	150	IRIIQERNGLVPCLTGSDVVSdleHEEMKILREVLRS-----KEEYDQEEER	199
QY	485	NRWNYIEGTK	494
Db	200	KRKQLSEAK	209
RESULT 1410			
ADD54377			
ID	ADD54377	standard; protein; 367 AA.	
XX			
AC	ADD54377;		
XX			
DT	15-JAN-2004	(first entry)	
XX			
DE	Human PRO	polypeptide #3.	
XX			
KW	Human; PRO;	pancreatic beta-cell precursor cell; pancreatic beta-cell;	
KW	insulin deficiency;	diabetes mellitus; haemoglobin-associated disorder;	
KW	thalassaemia;	endothelial cell growth; cancer; cystic renal dysplasia;	
KW	polycystic kidney disease;	renal tumour; antidiabetic; antianaemic;	
KW	cytostatic;	cardiant; vulnery;	antiinflammatory; anorectic.
XX			
OS	Homo sapiens.		
XX			
PN	US2002132253-A1.		
XX			
PD	19-SEP-2002.		
XX			
PF	14-NOV-2001;	2001US-00991163.	

XX			
PR	16-JUN-1997;	97US-0049787P.	
PR	17-OCT-1997;	97US-0062250P.	
PR	05-NOV-1997;	97WO-US020069.	
PR	12-NOV-1997;	97US-0065186P.	
PR	13-NOV-1997;	97US-0065311P.	
PR	24-NOV-1997;	97US-0066770P.	
PR	25-FEB-1998;	98US-0075945P.	
PR	20-MAR-1998;	98US-0078910P.	
PR	28-APR-1998;	98US-0083322P.	
PR	07-MAY-1998;	98US-0084600P.	
PR	28-MAY-1998;	98US-0087106P.	
PR	02-JUN-1998;	98US-0087607P.	
PR	02-JUN-1998;	98US-0087759P.	
PR	03-JUN-1998;	98US-0087827P.	
PR	04-JUN-1998;	98US-0088021P.	
PR	04-JUN-1998;	98US-0088026P.	
PR	04-JUN-1998;	98US-0088028P.	
PR	04-JUN-1998;	98US-0088029P.	
PR	04-JUN-1998;	98US-0088030P.	
PR	04-JUN-1998;	98US-0088033P.	
PR	04-JUN-1998;	98US-0088326P.	
PR	05-JUN-1998;	98US-0088167P.	
PR	05-JUN-1998;	98US-0088202P.	
PR	05-JUN-1998;	98US-0088212P.	
PR	05-JUN-1998;	98US-0088217P.	
PR	09-JUN-1998;	98US-0088655P.	
PR	10-JUN-1998;	98US-0088734P.	
PR	10-JUN-1998;	98US-0088738P.	
PR	10-JUN-1998;	98US-0088742P.	
PR	10-JUN-1998;	98US-0088810P.	
PR	10-JUN-1998;	98US-0088824P.	
PR	10-JUN-1998;	98US-0088826P.	
PR	11-JUN-1998;	98US-0088858P.	
PR	11-JUN-1998;	98US-0088861P.	
PR	11-JUN-1998;	98US-0088876P.	
PR	12-JUN-1998;	98US-0089105P.	
PR	16-JUN-1998;	98US-0089440P.	
PR	16-JUN-1998;	98US-0089512P.	
PR	16-JUN-1998;	98US-0089514P.	
PR	17-JUN-1998;	98US-0089532P.	
PR	17-JUN-1998;	98US-0089538P.	
PR	17-JUN-1998;	98US-0089598P.	
PR	17-JUN-1998;	98US-0089599P.	
PR	17-JUN-1998;	98US-0089600P.	
PR	17-JUN-1998;	98US-0089653P.	
PR	18-JUN-1998;	98US-0089801P.	
PR	18-JUN-1998;	98US-0089907P.	
PR	18-JUN-1998;	98US-0089908P.	
PR	16-SEP-1998;	98WO-US019330.	
PR	17-SEP-1998;	98WO-US019437.	
PR	07-OCT-1998;	98WO-US021141.	
PR	01-DEC-1998;	98WO-US025108.	
PR	05-JAN-1999;	99WO-US000106.	
PR	08-MAR-1999;	99WO-US005028.	
PR	02-JUN-1999;	99WO-US012252.	
PR	15-SEP-1999;	99WO-US021090.	
PR	15-SEP-1999;	99WO-US021547.	
PR	30-NOV-1999;	99WO-US028313.	
PR	01-DEC-1999;	99WO-US028301.	
PR	01-DEC-1999;	99WO-US028634.	
PR	16-DEC-1999;	99WO-US030095.	
PR	20-DEC-1999;	99WO-US030911.	
PR	06-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
PR	11-FEB-2000;	2000WO-US003565.	
PR	18-FEB-2000;	2000WO-US004341.	
PR	22-FEB-2000;	2000WO-US004414.	
PR	24-FEB-2000;	2000WO-US004914.	
PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	





CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
CC represents a human PRO polypeptide of the invention.

XX  
SQ Sequence 367 AA;  
  
Query Match 3.2%; Score 83.5; DB 7; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
  
QY 323 SSRVEKFLFDTKKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEAactsPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
  
QY 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFOEIVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 150 IRIQERNGVLPDCLTDGSDVVDLEHEEMKILREVLRS-----KEEYDQEEER 199  
  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1412  
ADE11176  
ID ADE11176 standard; protein; 367 AA.  
XX ADE11176;  
XX 29-JAN-2004 (first entry)  
XX Human PRO polypeptide #3.  
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN US2003073191-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 09-SEP-2002; 2002US-00238370.  
XX  
XX 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 25-AUG-1999; 99US-00380137.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
XX WPI; 2003-657650/62.  
DR

DR N-PSDB; ADE11175.  
XX  
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.  
XX  
PS Claim 11; SEQ ID NO 6; 307pp; English.  
XX  
CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
CC represents a human PRO polypeptide of the invention.

XX  
SQ Sequence 367 AA;  
  
Query Match 3.2%; Score 83.5; DB 7; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
  
QY 323 SSRVEKFLFDTKKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEAactsPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
  
QY 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFOEIVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 150 IRIQERNGVLPDCLTDGSDVVDLEHEEMKILREVLRS-----KEEYDQEEER 199  
  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1413  
ADE26531  
ID ADE26531 standard; protein; 367 AA.  
XX  
AC ADE26531;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO189.  
XX  
KW human; secreted and transmembrane protein; PRO; nootropic;  
KW neuroprotective; antiparkinsonian; cytostatic; gene therapy;  
KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease.  
XX  
OS Homo sapiens.

XX US2003087304-A1.  
PN  
XX  
PD 08-MAY-2003.  
XX  
PF 15-NOV-2001; 2001US-00997333.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
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PR 04-JUN-1998; 98US-0088025P.  
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PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
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PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.











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Db 150 IRIIQERNGLVPLDCLTDGSDVVDLEHEEMKILREVLRKS-----KKEYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1418

ADD88223

ID ADD88223 standard; protein; 367 AA.

XX

AC ADD88223;

DT 29-JAN-2004 (first entry)

XX Human PRO polypeptide #3.

DE

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX Homo sapiens.

OS

XX US2003073189-A1.

PN

XX 17-APR-2003.

PD

XX 09-SEP-2002; 2002US-00238183.

PF

XX 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1999; 99WO-US012252.

PR 25-AUG-1999; 99US-00380137.

PR 30-MAY-2000; 2000WO-US014941.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX WPI; 2003-576478/54.

DR N-PSDB; ADD88222.

XX New PRO nucleic acid, useful for the manufacture of a medicament for

PT diagnosing or treating tumor or for measuring or detecting expression of

PT an associated gene.

XX Claim 11; SEQ ID NO 6; 308pp; English.

PS

XX The invention relates to isolated human PRO polypeptides (secreted and

CC transmembrane polypeptides) and the polynucleotides encoding them. The

CC invention also relates to an antibody which specifically binds to a PRO

CC polypeptide, a method for stimulating the release of tumour necrosis

CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the

CC proliferation or differentiation of chondrocyte cells and a method for

CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,

CC colon, breast, prostate, rectal, cervical and liver tumours). The

CC polynucleotides are useful in molecular biology, including uses as

CC hybridisation probes, in chromosome and gene mapping, in generating

CC antisense RNA and DNA and in gene therapy. The polynucleotides may also

CC be used in preparing PRO polypeptides by recombinant techniques and in

CC generating either transgenic animals or knock-out animals which are

CC useful in the development and screening of therapeutically useful

CC reagents. The PRO polypeptides or antibodies are used in preparing a

CC medicament for treating a condition responsive to the polypeptides or

CC antibodies, such as tumours, for stimulating and inhibiting proliferation

CC of human microvascular endothelial cells, for inducing endothelial cell

CC tube formation and for treating sports-related joint problems, articular

CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence

CC represents a human PRO polypeptide of the invention.

XX Sequence 367 AA;

SQ

Query Match 3.2%; Score 83.5; DB 7; Length 367;

Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

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QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382

Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDDTQY-----LAA 430

Db 101 ----EDQFOEACTSPLAKHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGHSQNEKI 484

Db 150 IRIIQERNGLVPLDCLTDGSDVVDLEHEEMKILREVLRKS-----KKEYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1419

ADE25998

ID ADE25998 standard; protein; 367 AA.

XX

AC ADE25998;

XX 29-JAN-2004 (first entry)

DT

XX Novel human secreted and transmembrane protein PRO189.

DE

XX human; secreted and transmembrane protein; PRO; nootropic;

KW neuroprotective; antiparkinsonian; cytostatic; gene therapy;

KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;

KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease.

XX Homo sapiens.

OS

XX US2003087305-A1.

PN 08-MAY-2003.

XX 15-NOV-2001; 2001US-00997384.

PF 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

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PR 25-FEB-1998; 98US-0075945P.

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PR 28-APR-1998; 98US-0083322P.

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PR 04-JUN-1998; 98US-0088021P.

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PR 05-JAN-2000; 2000WO-US000219.  
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PR 22-FEB-2000; 2000WO-US004414.

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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.

Query Match      3.2%; Score 83.5; DB 7; Length 367;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

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QY 323 SSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382
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QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIANIDDTQY-----LAA 430
Db 101 ----EDQFQEAactsPLAKHTTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRGDSTI-----PIAKMFEIVHKSVVLIPLGAVDDGSHSQNEKI 484
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRKS-----KBEYDQEEER 199

QY 485 NRWNYIEGTK 494
Db 200 KRKKQLSEAK 209

RESULT 1420
ADD90804
ID ADD90804 standard; protein; 367 AA.
XX
AC ADD90804;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO189.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2003073188-A1.
XX
PD 17-APR-2003.
XX
PF 06-SEP-2002; 2002US-00237535.
XX
PR 07-JUL-1998; 98US-0091978P.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
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PA (GETH ) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2003-585303/55.
DR N-PSDB; ADD90803.
XX
PT New PRO polypeptide, useful for the manufacture of a medicament for
PT diagnosing or treating tumors.
XX
PS Claim 11; SEQ ID NO 6; 295pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 367 AA;
```

```
Query Match      3.2%; Score 83.5; DB 7; Length 367;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN 322
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83

QY 323 SSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIANIDDTQY-----LAA 430
Db 101 ----EDQFQEAactsPLAKHTTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRGDSTI-----PIAKMFEIVHKSVVLIPLGAVDDGSHSQNEKI 484
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRKS-----KBEYDQEEER 199

QY 485 NRWNYIEGTK 494
Db 200 KRKKQLSEAK 209
```



RESULT 1421  
ADF66935  
ID ADF66935 standard; protein; 367 AA.  
XX  
AC ADF66935;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human PRO189 amino acid sequence SEQ ID NO:8.  
XX  
KW antiinflammatory; antiarteriosclerotic; cardiant; antiinfertility;  
KW anti-HIV; cytostatic; antidiabetic; gene therapy; inflammatory disease;  
KW organ failure; atherosclerosis; cardiac injury; infertility;  
KW birth defect; premature aging; AIDS; cancer; diabetic complication;  
KW chromosome mapping; gene mapping; tissue typing; human.  
XX  
OS Homo sapiens.  
XX  
PN US2002198148-A1.  
XX  
PD 26-DEC-2002.  
XX  
PF 14-NOV-2001; 2001US-00990436.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
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PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
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PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2003-370797/35.  
DR N-PSDB; ADF66934.  
XX  
PT New secreted and transmembrane nucleic acids and polypeptides, designated  
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or  
PT cancer.  
XX  
PS Claim 12; SEQ ID NO 8; 651pp; English.  
XX  
CC The present invention describes an isolated PRO nucleic acid (I). Also  
CC described: (1) a vector comprising (I); (2) a host cell comprising the  
CC vector in (I); (3) producing PRO polypeptides by culturing the host cell  
CC under conditions suitable for the expression of the polypeptide and  
CC recovering the polypeptide from the cell culture; (4) an isolated  
CC polypeptide (II) which is encoded by (I); (5) a chimeric molecule  
CC comprising (II) fused to a heterologous amino acid sequence; (6) an  
CC antibody that specifically binds to (II); (7) detecting (M1) a PRO943,  
CC PRO183, PRO184, PRO185, PRO331, PRO1133, PRO363, PRO5723, PRO1387,

CC PRO1114, PRO1181, PRO3301, PRO9940, PRO7170, PRO361, or PRO846  
CC polypeptide in a sample suspected of containing the polypeptide; and (8)  
CC modulating at least one biological activity of a cell expressing any of  
CC the polypeptides described in (M1). (I) has antiinflammatory,  
CC antiarteriosclerotic, cardiant, antiinfertility, anti-HIV, cytostatic and  
CC antidiabetic activities, and can be used in gene therapy. The nucleic  
CC acids and polypeptides are useful for treating inflammatory diseases,  
CC organ failure, atherosclerosis, cardiac injury, infertility, birth  
CC defects, premature aging, AIDS, cancer, or diabetic complications. The  
CC nucleic acids are useful as hybridisation probes, in chromosome and gene  
CC mapping, and in generating antisense RNA or DNA. The polypeptides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both  
CC are useful in tissue typing. The present sequence is used in the  
CC exemplification of the present invention.

XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 7; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKATHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEACTIONPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVLPDCLTDGSDVSDLEHEEMKILREVLRS-----KKEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1422

ADF99359

ID ADF99359 standard; protein; 367 AA.

XX ADF99359;

XX 26-FEB-2004 (first entry)

DE Human secreted/transmembrane polypeptide PRO189.

XX Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.

OS Homo sapiens.

XX US2003078401-A1.

XX 24-APR-2003.

XX 16-SEP-2002; 2002US-00245033.

XX 11-FEB-2000; 2000WO-US003565.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2003-743856/70.  
XX N-PSDB; ADF99358.

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful  
PT in gene therapy, chromosome identification, tissue typing, or as  
PT hybridization probes in chromosome and gene mapping.

XX Claim 11; SEQ ID NO 6; 209pp; English.

CC The invention relates to an isolated secreted/transmembrane (PRO)  
CC polypeptide, having at least 80% sequence identity to a sequence selected  
CC from any one of the 57 amino acid sequences given in specification, or to  
CC a sequence encoded by a nucleic acid molecule selected from any one of  
CC the nucleic acids deposited under any of the ATCC accession numbers given  
CC in specification, or a sequence having at least 80% identity to PRO  
CC lacking its associated signal peptide, an extracellular domain of PRO  
CC with or without its associated signal peptide. Also included are vectors,  
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,  
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
CC an oligonucleotide probe derived from any one of the above nucleotide  
CC sequences. PRO6018 polypeptide is useful for stimulating the  
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.

XX Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 7; Length 367;

Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKATHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEACTIONPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVLPDCLTDGSDVSDLEHEEMKILREVLRS-----KKEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1423







DE Human PRO polypeptide #3.  
XX  
KW Human; PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;  
KW insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;  
KW thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;  
KW polycystic kidney disease; renal tumour; antidiabetic; antianaemic;  
KW cytostatic; cardiant; vulnery; antiinflammatory; anorectic.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2003050457-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 16-NOV-2001; 2001US-00991172.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
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PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
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PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
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PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.







QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSQVWLIPLGAVDDGHSQNEKI 484  
Db 150 IRIIQERNGLVLPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209  
RESULT 1428  
ADE51657  
ID ADE51657 standard; protein; 367 AA.  
XX  
AC ADE51657;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane polypeptide PRO189.  
XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX US2003104560-A1.  
PN  
XX  
PD 05-JUN-2003.  
XX  
PF 09-SEP-2002; 2002US-00238325.  
XX  
PR 01-JUL-1998; 98US-0091358P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 20-JUL-1999; 99US-0144758P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 25-AUG-1999; 99US-00380137.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-008997/01.  
DR N-PSDB; ADE51656.  
XX  
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
PT in gene therapy, as diagnostic markers for the presence of cancerous  
PT tumors, or as therapeutic targets for treating tumors, osteoarthritis or  
PT thalassemia.  
XX  
XX Claim 11; SEQ ID NO 6; 303pp; English.  
PS  
XX The invention relates to an isolated secreted/transmembrane (PRO)  
CC polypeptide, having at least 80% sequence identity to a sequence selected  
CC from any one of the 57 amino acid sequences given in specification, or to  
CC a sequence encoded by a nucleic acid molecule selected from any one of  
CC the nucleic acids deposited under any of the ATCC accession numbers given  
CC in specification, or a sequence having at least 80% identity to PRO  
CC lacking its associated signal peptide, an extracellular domain of PRO  
CC with or without its associated signal peptide. Also included are vectors,  
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,  
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
CC an oligonucleotide probe derived from any one of the above nucleotide

CC sequences. PRO6018 polypeptide is useful for stimulating the  
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEIILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIANIDTQY-----LAA 430  
Db 101 ----EDQFQEAQTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSQVWLIPLGAVDDGHSQNEKI 484  
Db 150 IRIIQERNGLVLPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1429

ADE51773

ID ADE51773 standard; protein; 367 AA.

XX  
AC ADE51773;

XX  
DT 29-JAN-2004 (first entry)

XX  
DE Human secreted/transmembrane polypeptide PRO189.

XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.

OS Homo sapiens.

XX US2003104561-A1.

XX  
PN 05-JUN-2003.

XX  
PF 09-SEP-2002; 2002US-00238346.

XX  
PR 09-FEB-1999; 99US-0119342P.

PR 29-OCT-1999; 99US-0162506P.





CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEAactsPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDCSTI-----PIAKMFQEIHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVPLDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1431  
ADE37515  
ID ADE37515 standard; protein; 367 AA.  
XX  
AC ADE37515;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane polypeptide PRO189.  
XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003104565-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 13-SEP-2002; 2002US-00243446.  
XX  
PR 25-JAN-2001; 2001US-0264395P.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-009002/01.

DR N-PSDB; ADE37514.  
XX  
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
PT in gene therapy, as diagnostic markers for the presence of cancerous  
PT tumors, or as therapeutic targets for treating tumors, osteoarthritis or  
PT thalassemia.  
XX  
PS Claim 11; SEQ ID NO 6; 301pp; English.  
XX  
CC The invention relates to an isolated secreted/transmembrane (PRO)  
CC polypeptide, having at least 80% sequence identity to a sequence selected  
CC from any one of the 57 amino acid sequences given in specification, or to  
CC a sequence encoded by a nucleic acid molecule selected from any one of  
CC the nucleic acids deposited under any of the ATCC accession numbers given  
CC in specification, or a sequence having at least 80% identity to PRO  
CC lacking its associated signal peptide, an extracellular domain of PRO  
CC with or without its associated signal peptide. Also included are vectors,  
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
CC an oligonucleotide probe derived from any one of the above nucleotide  
CC sequences. PRO6018 polypeptide is useful for stimulating the  
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEAactsPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDCSTI-----PIAKMFQEIHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVPLDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1432  
ADD95286  
ID ADD95286 standard; protein; 367 AA.  
XX



CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
CC represents a human PRO polypeptide of the invention.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEAactsPLAKTHTSQAI-----LQPVLAAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGSHSQNEKI 484  
Db 150 IRIIQERNGLVPCDCLTDGSDVSDLEHEEMKILREVLRKS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1434  
ADE76075  
ID ADE76075 standard; protein; 367 AA.  
XX  
AC ADE76075;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human PRO polypeptide #3.  
XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN US2003124665-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 16-SEP-2002; 2002US-00245810.  
XX  
PR 15-SEP-2000; 2000US-0232887P.

PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-009145/01.  
DR N-PSDB; ADE76074.  
XX  
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,  
PT in tissue typing, and in chromosome identification.  
XX  
PS Claim 11; SEQ ID NO 6; 301pp; English.  
XX

CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
CC represents a human PRO polypeptide of the invention.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEAactsPLAKTHTSQAI-----LQPVLAAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGSHSQNEKI 484  
Db 150 IRIIQERNGLVPCDCLTDGSDVSDLEHEEMKILREVLRKS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1435  
ADE39398  
ID ADE39398 standard; protein; 367 AA.  
XX  
AC ADE39398;  
XX







XX OS Homo sapiens.

XX PN US2003138903-A1.

XX PD 24-JUL-2003.

XX PF 12-SEP-2002; 2002US-00243431.

XX PR 20-JUL-1999; 99US-0144790P.

XX PR 15-MAY-2000; 2000WO-US013358.

XX PR 29-AUG-2001; 2001WO-US027099.

XX PR 18-JUL-2002; 2002US-00197942.

XX PA (GETH ) GENENTECH INC.

XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

XX PI Fong S;

XX DR WPI; 2004-009305/01.

XX DR N-PSDB; ADE19663.

XX PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful

XX PT in gene therapy, as diagnostic markers for the presence of cancerous

XX PT tumors, or as therapeutic targets for treating tumors, osteoarthritis or

XX PT thalassemia.

XX PS Claim 11; SEQ ID NO 6; 300pp; English.

XX CC The invention relates to isolated human PRO polypeptides (secreted and

XX CC transmembrane polypeptides) and the polynucleotides encoding them. The

XX CC invention also relates to an antibody which specifically binds to a PRO

XX CC polypeptide, a method for stimulating the release of tumour necrosis

XX CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the

XX CC proliferation or differentiation of chondrocyte cells and a method for

XX CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,

XX CC colon, breast, prostate, rectal, cervical and liver tumours). The

XX CC polynucleotides are useful in molecular biology, including uses as

XX CC hybridisation probes, in chromosome and gene mapping, in generating

XX CC antisense RNA and DNA and in gene therapy. The polynucleotides may also

XX CC be used in preparing PRO polypeptides by recombinant techniques and in

XX CC generating either transgenic animals or knock-out animals which are

XX CC useful in the development and screening of therapeutically useful

XX CC reagents. The PRO polypeptides or antibodies are used in preparing a

XX CC medicament for treating a condition responsive to the polypeptides or

XX CC antibodies, such as tumours, for stimulating and inhibiting proliferation

XX CC of human microvascular endothelial cells, for inducing endothelial cell

XX CC tube formation and for treating sports-related joint problems, articular

XX CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence

XX CC represents a human PRO polypeptide of the invention.

XX SQ Sequence 367 AA;

Query Match

Best Local Similarity 3.2%; Score 83.5; DB 8; Length 367;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAIHLDLEEYRN 322

Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83

QY 323 SSRVEKFLDFTKBEILMHLWRYPSSLTHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382

Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDDTQY-----LAA 430

Db 101 -----EDQFQEACTSPAKTHTSQAI-----LQPVLAAEFTIFKAMVMQKNIEMQLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484

Db 150 IRIIQERNGLVPLDCLTDGSDVSDLEHEEMKILREVLRKS-----KEEYDQEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1439

ID ADE77242

XX 12-SEP-2002; 2002US-00243431.

AC ADE77242;

XX 29-JAN-2004 (first entry)

XX Human secreted/transmembrane polypeptide PRO189.

XX Human; PRO; secreted protein; transmembrane protein;

XX endothelial cell tube formation; chondrocyte cell differentiation;

XX microvascular endothelial cell; tumour; lung tumour; colon tumour;

XX breast tumour; prostate tumour; rectal tumour; kidney tumour;

XX liver tumour; cytostatic; vaccine.

OS Homo sapiens.

XX US2003124666-A1.

XX 03-JUL-2003.

XX 16-SEP-2002; 2002US-00245910.

XX 01-APR-1999; 99US-0127372P.

XX 29-OCT-1999; 99US-0162506P.

XX 02-DEC-1999; 99WO-US028551.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

XX Fong S;

XX WPI; 2004-009146/01.

XX N-PSDB; ADE77241.

XX New PRO polypeptide and nucleic acid encoding the polypeptide, for use in

XX gene therapy, chromosome identification, tissue typing, or as

XX hybridization probes in chromosome and gene mapping.

XX Claim 11; SEQ ID NO 6; 301pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)

XX polypeptide, having at least 80% sequence identity to a sequence selected

XX from any one of the 57 amino acid sequences given in specification, or to

XX a sequence encoded by a nucleic acid molecule selected from any one of

XX the nucleic acids deposited under any of the ATCC accession numbers given

XX in specification, or a sequence having at least 80% identity to PRO

XX lacking its associated signal peptide, an extracellular domain of PRO

XX with or without its associated signal peptide. Also included are vectors,

XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding

XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

XX PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and

XX an oligonucleotide probe derived from any one of the above nucleotide

XX sequences. PRO6018 polypeptide is useful for stimulating the

XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

XX and PRO21383 polypeptides are useful for stimulating the proliferation of

XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

XX polypeptides are useful for inhibiting the proliferation of human

XX microvascular endothelial cells. PRO polypeptides are useful for

XX detecting the presence of tumour in a mammal, including tumours of lung,

XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,

XX PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and



CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.

XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFTDKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGHSQNEKI 484  
Db 150 IRIIQERNGLVPCDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1440

AD65350  
ID ADE65350 standard; protein; 367 AA..

XX  
AC ADE65350;

XX 29-JAN-2004. (first entry)

XX Human PRO polypeptide #3.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX OS Homo sapiens.

XX US2003119116-A1.

XX 26-JUN-2003.

XX 11-SEP-2002; 2002US-00241860.

XX 01-APR-1999; 99US-0127372P.

XX 29-OCT-1999; 99US-0162506P.

XX 02-DEC-1999; 99WO-US028551.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX WPI; 2004-009092/01.

DR N-PSDB; ADE65349.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
PT PRO21383, for use in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 11; SEQ ID NO 6; 30lpp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
CC represents a human PRO polypeptide of the invention.

XX Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFTDKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGHSQNEKI 484  
Db 150 IRIIQERNGLVPCDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1441

AD65350

ID ADE75959 standard; protein; 367 AA.

XX ADE75959;

XX 29-JAN-2004 (first entry)

XX Human PRO polypeptide #3.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;

KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;



```
XX SQ      Sequence 367 AA;
      Query Match      3.2%; Score 83.5; DB 8; Length 367;
      Best Local Similarity 22.0%; Pred. No. 1.4e+02;
      Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 323 SSRVEKFLFDTKKEIIMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 101 -----EDQFQEACTIONPLAKTHTSQA-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGSHSQNEKI 484
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 150 IRIIQERNGLVLPDCLTDGSDVSDLEHEEMKILREVLRKS-----KKEYDQEEER 199
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 485 NRWNYIEGTK 494
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 200 KRKKQLSEAK 209

RESULT 1443
ADE64480
ID ADE64480 standard; protein; 367 AA.
XX
AC ADE64480;
XX
DT 29-JAN-2004 (first entry)
DE Human PRO polypeptide #3.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
OS Homo sapiens.
XX
XX US2003119114-A1.
XX
PD 26-JUN-2003.
XX
PF 09-SEP-2002; 2002US-00238261.
XX
PR 27-MAR-1998; 98US-0079689P.
PR 08-MAR-1999; 99WO-US005028.
PR 25-AUG-1999; 99US-00380138.
PR 30-MAY-2000; 2000WO-US014941.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2004-009090/01.
DR N-PSDB; ADE64479.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
```

```
PS XX      Claim 11; SEQ ID NO 6; 301pp; English.
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polypeptide of the invention.
XX
SQ      Sequence 367 AA;
      Query Match      3.2%; Score 83.5; DB 8; Length 367;
      Best Local Similarity 22.0%; Pred. No. 1.4e+02;
      Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 323 SSRVEKFLFDTKKEIIMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQY-----LAA 430
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 101 -----EDQFQEACTIONPLAKTHTSQA-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSIVLPLGAVDDGSHSQNEKI 484
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 150 IRIIQERNGLVLPDCLTDGSDVSDLEHEEMKILREVLRKS-----KKEYDQEEER 199
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 485 NRWNYIEGTK 494
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 200 KRKKQLSEAK 209

RESULT 1444
ADE38815
ID ADE38815 standard; protein; 367 AA.
XX
AC ADE38815;
XX
DT 29-JAN-2004 (first entry)
DE Human PRO polypeptide #3.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
XX US2003096363-A1.
XX
PD 22-MAY-2003.
```







KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour; adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; KW microvascular endothelial cell; endothelial cell tube formation; KW sports-related joint problem; articular cartilage defect; osteoarthritis; KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX Homo sapiens.

OS US2003108996-A1.

XX 12-JUN-2003.

PF 11-SEP-2002; 2002US-00242653.

XX 27-APR-1999; 99US-0131271P.

PR 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99WO-US028551.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC; PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z; PI Fong S;

XX WPI; 2004-009014/01.

DR N-PSDB; ADE38698.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO21383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

XX Claim 11; SEQ ID NO 6; 308pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

XX SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367; Best Local Similarity 22.0%; Pred. No. 1.4e+02; Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLLEYRN 322

Db 28 PILDVFEQKCEVNCCKGGHVTGSPPEVILVACVFLVFDDEESKLTYTEIH---QEYK- 83

QY 323 SSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382

Db 84 -ELVEKLL-----EGYLKKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWTIANIDDTQY-----LAA 430

Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTTFKAMMVQKNIEMLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFOEIVHKSVLLPLCAVDDGEHSQNEKI 484

Db 150 IRIIQERNGLVPDCLTDGSDVVSLEHEMKILREVLRS-----KEEYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1448

ADE37399

ID ADE37399 standard; protein; 367 AA.

XX ADE37399;

AC ADE37399;

XX 29-JAN-2004 (first entry)

DE Human secreted/transmembrane polypeptide PRO189.

XX Human; PRO; secreted protein; transmembrane protein; KW endothelial cell tube formation; chondrocyte cell differentiation; KW microvascular endothelial cell; tumour; lung tumour; colon tumour; KW breast tumour; prostate tumour; rectal tumour; kidney tumour; KW liver tumour; cytostatic; vaccine.

XX Homo sapiens.

OS US2003104563-A1.

XX 05-JUN-2003.

XX 12-SEP-2002; 2002US-00243124.

XX 20-JAN-2000; 2000US-0177118P.

PR 10-NOV-2000; 2000WO-US030873.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC; PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z; PI Fong S;

XX WPI; 2004-009000/01.

DR N-PSDB; ADE37398.

XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, as diagnostic markers for the presence of cancerous tumors, or as therapeutic targets for treating tumors, osteoarthritis or thalassemia.

XX Claim 11; SEQ ID NO 6; 303pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of











RESULT 1453	
ADD89119	
ID	ADD89119 standard; protein; 367 AA.
XX	
AC	ADD89119;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human PRO polypeptide #3.
XX	
KW	Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW	tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW	adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW	microvascular endothelial cell; endothelial cell tube formation;
KW	sports-related joint problem; articular cartilage defect; osteoarthritis;
KW	rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX	
OS	Homo sapiens.
XX	
PN	US2003138897-A1.
XX	
PD	24-JUL-2003.
XX	
PF	11-SEP-2002; 2002US-00242074.
XX	
PR	02-AUG-2000; 2000US-0222695P.
PR	20-JUN-2001; 2001WO-US019692.
PR	29-AUG-2001; 2001WO-US027099.
PR	18-JUL-2002; 2002US-00197942.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI	Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI	Fong S;
XX	
DR	WPI; 2004-009299/01.
DR	N-PSDB; ADD89118.
XX	
PT	New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT	PRO21383, for use in molecular biology, chromosome and gene mapping, in
PT	generating antisense RNA and DNA, and in gene therapy.
XX	
PS	Claim 11; SEQ ID NO 6; 301pp; English.
XX	
CC	The invention relates to isolated human PRO polypeptides (secreted and
CC	transmembrane polypeptides) and the polynucleotides encoding them. The
CC	invention also relates to an antibody which specifically binds to a PRO
CC	polypeptide, a method for stimulating the release of tumour necrosis
CC	factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC	proliferation or differentiation of chondrocyte cells and a method for
CC	detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC	colon, breast, prostate, rectal, cervical and liver tumours). The
CC	polynucleotides are useful in molecular biology, including uses as
CC	hybridisation probes, in chromosome and gene mapping, in generating
CC	antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC	be used in preparing PRO polypeptides by recombinant techniques and in
CC	generating either transgenic animals or knock-out animals which are
CC	useful in the development and screening of therapeutically useful
CC	reagents. The PRO polypeptides or antibodies are used in preparing a
CC	medicament for treating a condition responsive to the polypeptides or
CC	antibodies, such as tumours, for stimulating and inhibiting proliferation
CC	of human microvascular endothelial cells, for inducing endothelial cell
CC	tube formation and for treating sports-related joint problems, articular
CC	cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC	represents a human PRO polypeptide of the invention.
XX	
SQ	Sequence 367 AA;
Query Match	3.2%; Score 83.5; DB 8; Length 367;
Best Local Similarity	22.0%; Pred. No. 1.4e+02;
Matches	55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY	272	PMADLVALGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN	322
Db	28	PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK-	83
QY	323	SSRVEKFLFDTKKEIILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN	382
Db	84	-ELVEKLL-----EGYLKEIGIN-----	100
QY	383	VSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQY-----LAA	430
Db	101	-----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA	149
QY	431	KRAIRTVFGTEPDMIRDGSI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI	484
Db	150	IRIIQERNGVLPDCLTDGSDVSDLEHEEMKILREVLRS-----KKEYDQEEER	199
QY	485	NRWNYIEGTK	494
Db	200	KRKKQLSEAK	209
RESULT 1454			
ADD88886			
ID	ADD88886	standard; protein; 367 AA.	
XX			
AC	ADD88886;		
DT	29-JAN-2004	(first entry)	
XX			
DE	Human PRO polypeptide #3.		
XX			
KW	Human; PRO; secreted polypeptide; transmembrane polypeptide;		
KW	tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;		
KW	adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;		
KW	microvascular endothelial cell; endothelial cell tube formation;		
KW	sports-related joint problem; articular cartilage defect; osteoarthritis;		
KW	rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003138899-A1.		
XX			
PD	24-JUL-2003.		
XX			
PF	11-SEP-2002; 2002US-00242574.		
XX			
PR	25-MAY-1999;	99US-0135725P.	
PR	29-OCT-1999;	99US-0162506P.	
PR	02-DEC-1999;	99WO-US028551.	
PR	29-AUG-2001;	2001WO-US027099.	
PR	18-JUL-2002;	2002US-00197942.	
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;		
PI	Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;		
PI	Fong S;		
XX			
DR	WPI; 2004-009301/01.		
DR	N-PSDB; ADD88885.		
XX			
PT	New PRO polypeptide and nucleic acid encoding it, for use in gene		
PT	therapy, chromosome identification, tissue typing, or as hybridization		
PT	probes in chromosome and gene mapping.		
XX			
PS	Claim 11; SEQ ID NO 6; 301pp; English.		
XX			
CC	The invention relates to isolated human PRO polypeptides (secreted and		
CC	transmembrane polypeptides) and the polynucleotides encoding them. The		
CC	invention also relates to an antibody which specifically binds to a PRO		
CC	polypeptide, a method for stimulating the release of tumour necrosis		
CC	factor-alpha (TNF-alpha) from human blood, a method for stimulating the		
CC	proliferation or differentiation of chondrocyte cells and a method for		



KW Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX US2003124667-A1.
PN
XX
XX 03-JUL-2003.
PD
XX 18-SEP-2002; 2002US-00246098.
PF
XX 16-JAN-2001; 2001US-0262150P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2004-009147/01.
DR N-PSDB; ADE77357.
DR
XX
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX
XX Claim 11; SEQ ID NO 6; 301pp; English.
PS
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
XX SQ Sequence 367 AA;
Query Match 3.2%; Score 83.5; DB 8; Length 367;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;
QY 272 PMADLVALLGSLVSSGHILVPGIYDEV-----VPLT-----EEINTYKAIHLDLEBYRN 322

Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVFDDEESKLTYTEIH---QEYK- 83
QY 323 SSRVEKFLFDTKKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100
QY 383 VSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWIANIDDTQY-----LAA 430
Db 101 ----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTTFKAMMVQKNIEMLQA 149
QY 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFOEIVHKSVVLLPLGAVDDGEHSQNEKI 484
Db 150 IRIIQERNGLVDPDCLTDGSDVVSLEHEMKILREVLRKS-----KEEYDQEEER 199
QY 485 NRWNYIEGTK 494
Db 200 KRKKQLSEAK 209
RESULT 1457
ADE65234
ID ADE65234 standard; protein; 367 AA.
XX
AC ADE65234;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PRO polypeptide #3.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX US2003119113-A1.
XX
XX 26-JUN-2003.
XX
XX 06-SEP-2002; 2002US-00237471.
XX
XX 20-JUL-1999; 99US-0144758P.
PR 15-MAR-2000; 2000WO-US006884.
PR 02-JUN-2000; 2000WO-US015264.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2004-009089/01.
DR N-PSDB; ADE65233.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, for use in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 11; SEQ ID NO 6; 301pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,



CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
XX represents a human PRO polypeptide of the invention.

SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKAIHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGHVITPGSPPEVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEIILMHLWRYPSPLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGVLPDCLTDGSDVVSdleHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1458  
ADE39282  
ID ADE39282 standard; protein; 367 AA.  
XX  
AC ADE39282;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human PRO polypeptide #3.  
XX  
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN US2003119115-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 09-SEP-2002; 2002US-00238324.  
XX  
PR 17-MAY-2000; 2000WO-US013705.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-009091/01.  
DR N-PSDB; ADE39281.  
XX  
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.  
XX  
PS Claim 11; SEQ ID NO 6; 301pp; English.  
XX  
CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
XX represents a human PRO polypeptide of the invention.

SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKAIHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGHVITPGSPPEVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEIILMHLWRYPSPLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGVLPDCLTDGSDVVSdleHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1459  
ADE38467  
ID ADE38467 standard; protein; 367 AA.  
XX  
AC ADE38467;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane polypeptide PRO189.  
XX Human; PRO; secreted protein; transmembrane protein;  
KW

KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX US2003104559-A1.  
PN  
XX  
XX 05-JUN-2003.  
XX  
XX 06-SEP-2002; 2002US-00237636.  
XX  
XX 27-MAR-1998; 98US-0079689P.  
PR 08-MAR-1999; 99WO-US005028.  
PR 25-AUG-1999; 99US-00380138.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
XX WPI; 2004-008996/01.  
DR N-PSDB; ADE38466.  
XX  
XX New secreted and transmembrane PRO polypeptide and nucleic acid, useful  
PT in gene therapy, as diagnostic markers for the presence of cancerous  
PT tumors, or as therapeutic targets for treating tumors, osteoarthritis or  
PT thalassemia.  
XX  
XX Claim 11; SEQ ID NO 6; 301pp; English.  
PS  
XX  
XX The invention relates to an isolated secreted/transmembrane (PRO)  
CC polypeptide, having at least 80% sequence identity to a sequence selected  
CC from any one of the 57 amino acid sequences given in specification, or to  
CC a sequence encoded by a nucleic acid molecule selected from any one of  
CC the nucleic acids deposited under any of the ATCC accession numbers given  
CC in specification, or a sequence having at least 80% identity to PRO  
CC lacking its associated signal peptide, an extracellular domain of PRO  
CC with or without its associated signal peptide. Also included are vectors,  
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,  
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and  
CC an oligonucleotide probe derived from any one of the above nucleotide  
CC sequences. PRO6018 polypeptide is useful for stimulating the  
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080  
CC and PRO21383 polypeptides are useful for stimulating the proliferation of  
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEILMHLWRYPSPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSNMVSMILGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEA CTSLAKTHTSQAI-----LQPVLA AEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIOERNGLVPCDCLTGDSDVSDLEHEEMKILREVLRS-----KBEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209  
RESULT 1460  
ADF35134  
ID ADF35134 standard; protein; 367 AA.  
XX ADF35134;  
XX  
DT 12-FEB-2004 (first entry)  
XX Human PRO189 polypeptide.  
DE  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW transgenic; tumour; cytostatic.  
KW Homo sapiens.  
XX  
XX US2003194760-A1.  
PD 16-OCT-2003.  
XX  
PF 16-NOV-2001; 2001US-00991150.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090472P.  
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PR 24-JUN-1998; 98US-0090542P.  
PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.

PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
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PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
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PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
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PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-JUN-2000; 2000US-0213637P.



PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 08-NOV-2000; 2000WO-US030952.

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

Qy 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGHVITPGSPPEPVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
Qy 323 SSRVEKFLDFTKEEILMHLWRYPSSLHIGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
Qy 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMQLQA 149  
Qy 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEI VHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIQERNGVLPDCLTDGSDVVDLEHEEMKILREVLRS-----KEEYDQEEER 199  
Qy 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1461  
ADG11384  
ID ADG11384 standard; protein; 367 AA.  
XX  
AC ADG11384;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human PRO189 polypeptide.  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW transgenic; tumour; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003228655-A1.  
XX  
PD 11-DEC-2003.  
XX  
PF 20-NOV-2001; 2001US-00989733.  
XX  
PR 10-AUG-1998; 98US-0095916P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 25-AUG-1999; 99US-00380137.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Baton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2004-081070/08.  
DR N-PSDB; ADG11383.  
XX  
PT New PRO polypeptide useful in diagnosing or treating cardiac  
PT insufficiency disorders, retinal disorders, kidney disorders, obesity,

PT diabetes, cancer, thalassemia, or arthritis.  
XX  
PS Claim 12; SEQ ID NO 8; 648pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for  
CC identifying agonists or antagonists. The PRO polypeptide or the antibody  
CC may be used in preparing a medicament for treating a condition responsive  
CC to the polypeptide or antibody, such as tumours, and in various  
CC diagnostic assays. The polynucleotide sequences encoding PRO polypeptides  
CC are useful as hybridisation probes, in chromosome and gene mapping, in  
CC the generation of antisense RNA and DNA, in the preparation of PRO  
CC polypeptides, for generating transgenic animals or knockout animals, and  
CC in gene therapy. The present sequence represents a human PRO polypeptide  
CC of the invention. Note: The sequence data for this patent was obtained in  
CC electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsDIDentry.html.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
Qy 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGHVITPGSPPEPVILVACVPLVFDDEESKLTYTEIH---QEYK- 83  
Qy 323 SSRVEKFLDFTKEEILMHLWRYPSSLHIGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
Qy 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMQLQA 149  
Qy 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEI VHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIQERNGVLPDCLTDGSDVVDLEHEEMKILREVLRS-----KEEYDQEEER 199  
Qy 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1462  
ADG11020  
ID ADG11020 standard; protein; 367 AA.  
XX  
AC ADG11020;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human secreted/transmembrane polypeptide PRO189.  
XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003170809-A1.  
XX  
PD 11-SEP-2003.  
XX  
PF 16-SEP-2002; 2002US-00244972.  
XX



CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKEEILMHLWRYPSSLHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNKMVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFQEIHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQBEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1464  
ADH31432  
ID ADH31432 standard; protein; 367 AA.  
XX ADH31432;  
XX 11-MAR-2004 (first entry)  
XX Human PRO polypeptide #3.  
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN US2003119139-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 18-SEP-2002; 2002US-00246080.  
XX  
XX 02-FEB-2001; 2001US-0266421P.  
PR 09-FEB-2001; 2001US-0267623P.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;

XX  
DR WPI; 2004-096601/10.  
DR N-PSDB; ADH31431.  
XX  
PT Fifty seven nucleic acids encoding PRO polypeptides, useful for  
PT stimulating chondrocyte proliferation, particularly for treating e.g.  
PT lung or breast tumors.  
XX  
PS Claim 11; SEQ ID NO 6; 303pp; English.  
XX  
CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
XX represents a human PRO polypeptide of the invention.  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKEEILMHLWRYPSSLHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNKMVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFOEACTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFQEIHKSVVLIPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQBEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1465  
ADH38680  
ID ADH38680 standard; protein; 367 AA.

XX ADH38680;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human secreted/transmembrane polypeptide PRO189.  
XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;













Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430

Db 101 -----EDQFQEAECTSPLAKTHTSQAI-----LQPVLAAEDFTIFKAMVQKNTEMQLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGHSQNEKI 484

Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----K EYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1471

ADH26832

ID ADH26832 standard; protein; 367 AA.

XX

AC ADH26832;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human secreted/transmembrane polypeptide PRO189.

XX

KW Human; PRO; secreted protein; transmembrane protein;

KW endothelial cell tube formation; chondrocyte cell differentiation;

KW microvascular endothelial cell; tumour; lung tumour; colon tumour;

KW breast tumour; prostate tumour; rectal tumour; kidney tumour;

KW liver tumour; cytostatic; vaccine.

XX

OS Homo sapiens.

XX

PN US2003119134-A1.

XX

PD 26-JUN-2003.

XX

PF 16-SEP-2002; 2002US-00245852.

XX

PR 12-JAN-1999; 99US-0115554P.

PR 30-NOV-1999; 99WO-US028313.

PR 11-AUG-2000; 2000WO-US022031.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX

DR WPI; 2004-096596/10.

DR N-PSDB; ADH26831.

XX

PT Fifty seven nucleic acids encoding PRO polypeptides, useful for

PT stimulating Tumor Necrosis Factor alpha or chondrocyte proliferation,

PT particularly for treating e.g. lung or breast tumors.

XX

PS Claim 11; SEQ ID NO 6; 301pp; English.

XX

CC The invention relates to an isolated secreted/transmembrane (PRO)

CC polypeptide, having at least 80% sequence identity to a sequence selected

CC from any one of the 57 amino acid sequences given in specification, or to

CC a sequence encoded by a nucleic acid molecule selected from any one of

CC the nucleic acids deposited under any of the ATCC accession numbers given

CC in specification, or a sequence having at least 80% identity to PRO

CC lacking its associated signal peptide, an extracellular domain of PRO

CC with or without its associated signal peptide. Also included are vectors,

CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding

CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and

CC an oligonucleotide probe derived from any one of the above nucleotide

CC sequences. PRO6018 polypeptide is useful for stimulating the

CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

CC and PRO21383 polypeptides are useful for stimulating the proliferation of

CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

CC polypeptides are useful for inhibiting the proliferation of human

CC microvascular endothelial cells. PRO polypeptides are useful for

CC detecting the presence of tumour in a mammal, including tumours of lung,

CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,

CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and

CC PRO34274 polypeptides are useful for inducing endothelial cell tube

CC formation. PRO or the antibody are useful in the preparation of a

CC medicament for treating a condition responsive to PRO polypeptide. The

CC oligonucleotide probes are useful for isolating genomic and cDNA

CC nucleotide sequences, for measuring or detecting the expression of an

CC associated gene, and as antisense probes. PRO nucleic acid is useful as a

CC hybridisation probe, in chromosome and gene mapping, in the generation of

CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and

CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The

CC present sequence represents a PRO protein.

XX

SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;

Best Local Similarity 22.0%; Pred. No. 1.4e+02;

Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEEINTYKAHLDLEEYRN 322

Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVFDDEESKLTYTEIH---Q EYK- 83

QY 323 SSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382

Db 84 -ELVEKLL-----EGYLKEIGIN----- 100

QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430

Db 101 -----EDQFQEAECTSPLAKTHTSQAI-----LQPVLAAEDFTIFKAMVQKNTEMQLQA 149

QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGHSQNEKI 484

Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----K EYDQEEER 199

QY 485 NRWNYIEGTK 494

Db 200 KRKKQLSEAK 209

RESULT 1472

ADH38100

ID ADH38100 standard; protein; 367 AA.

XX

AC ADH38100;

XX

DT 11-MAR-2004 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO189.

XX

KW human; PRO; membrane bound protein; membrane bound receptor;

KW cell proliferation; cell migration; cell differentiation;

KW mitogenic factor; survival factor; cytotoxic factor;

KW differentiation factor; neuropeptide; hormone; cell receptor;

KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX

OS Homo sapiens.

XX

PN US2003119123-A1.

XX

PD 26-JUN-2003.

XX

PF 12-SEP-2002; 2002US-00243326.

XX

PR 17-AUG-1999; 99US-0149327P.

PR 15-MAY-2000; 2000WO-US013358.



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PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX (GETH ) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2004-106467/11.
DR N-PSDB; ADH38099.
XX Isolated nucleic acid molecule encoding a secreted and transmembrane PRO
PT polypeptide e.g., PRO6071, PRO4487, is useful in the treatment of cancer.
XX Claim 1; SEQ ID NO 6; 302pp; English.
XX This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
XX SQ Sequence 367 AA;
Query Match 3.2%; Score 83.5; DB 8; Length 367;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEINTYKAHLDLEEYRN 322
Db 28 PILDFVEQKEVCKGKHVITPGSPVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83
QY 323 SSRVEKFLDPTKEEILMHLWRYPSSLHIGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVMTLGLHPWIANIDDTQY-----LAA 430
Db 101 ----EDQFQEAQTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149
QY 431 KRAIRTVFGTEPDMIRDGSI-----PIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKI 484
Db 150 IRIIQERNGLVPLDCLTDGSDVSDLEHEEMKILREVLRS-----KKEYDQEEER 199
QY 485 NRWNYIEGTK 494
Db 200 KRKKQLSEAK 209
RESULT 1473
ADH38796
ID ADH38796 standard; protein; 367 AA.
XX ADH38796;
AC ADH38796;
XX 11-MAR-2004 (first entry)
DT
```

```
XX Human secreted/transmembrane polypeptide PRO189.
DE
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2003119141-A1.
XX
PD 26-JUN-2003.
XX
PF 18-SEP-2002; 2002US-00246305.
XX
PR 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX (GETH ) GENENTECH INC.
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2004-096603/10.
DR N-PSDB; ADH38795.
DR
XX Fifty seven nucleic acids encoding PRO polypeptides, useful for
PT stimulating chondrocyte proliferation, particularly for treating e.g.
PT lung or breast tumors.
XX
PS Claim 11; SEQ ID NO 6; 301pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 367 AA;
Query Match 3.2%; Score 83.5; DB 8; Length 367;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
```















RESULT 1480  
ADH29194

ADH29194  
ID ADH29194 standard: protein; 367 AA.

ID ADH29194 standard; protein; 367 AA.

AC ADH29194;

11-MAR-2004 (first entry)

Human secreted/transmembrane polypeptide PRO189.

Human; PRO; secreted protein; transmembrane protein;  
endothelial cell tube formation; chondrocyte cell differentiation;  
microvascular endothelial cell; tumour; lung tumour; colon tumour;  
breast tumour; prostate tumour; rectal tumour; kidney tumour;  
liver tumour; cytostatic; vaccine.

OS Homo sapiens.

US2003119136-A1.

PD 26-JUN-2003:

16-SEP-2002: 2002US-00245881.

PR 17-AUG-1999: 99US-0149327P.

PR 15-MAY-2000; 2000WO-US013358.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

PA (GETH ) GENENTECH INC.

...  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
PI

WPI; 2004-096598/10.  
N-PSDB; ADH29193.

DR N-PSDB; ADH29193.

Fifty seven nucleic acids encoding PRO polypeptides, useful for stimulating Tumor Necrosis Factor alpha or chondrocyte proliferation, particularly for treating e.g. lung or breast tumors.

PS Claim 11: SEQ ID NO 6; 301pp; English.

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation of chondrocyte cells. PRO1313, PRO20080 proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acids useful as







CC is often transmitted by secreted polypeptides (for example mitogenic  
CC factors, survival factors, cytotoxic factors, differentiation factors,  
CC neuropeptides and hormones) which are received and interpreted by diverse  
CC cell receptors or membrane bound proteins. These membrane bound proteins  
CC and receptors may be of use as pharmaceutical and diagnostic agents, such  
CC as in the blocking of receptor-ligand interactions. The current invention  
CC provides the amino acid sequences of novel human membrane bound receptors  
CC and proteins, along with the cDNA sequences encoding them. The novel  
CC proteins of the invention may have cytostatic activities through the  
CC stimulation of chondrocytes. The nucleic acids of the invention may be  
CC useful for the manufacture of a medicament for diagnosing or treating a  
CC tumour in a mammal. In addition, they may be useful for measuring or  
CC detecting the expression of a tumour associated gene. The present  
CC sequence is a human PRO protein of the invention.

XX Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEPILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEAactsPLAKHTTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1485  
ADH52445  
ID ADH52445 standard; protein; 367 AA.  
XX ADH52445;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO189.  
XX  
KW human; PRO; membrane bound protein; membrane bound receptor;  
KW cell proliferation; cell migration; cell differentiation;  
KW mitogenic factor; survival factor; cytotoxic factor;  
KW differentiation factor; neuropeptide; hormone; cell receptor;  
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX Homo sapiens.

XX US2003119129-A1.

XX 26-JUN-2003.

XX 17-SEP-2002; 2002US-00245479.

XX 10-AUG-1999; 99US-0148188P.

XX 15-MAY-2000; 2000WO-US013358.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

XX

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-096591/10.  
DR N-PSDB; ADH52444.  
XX  
PT Fifty seven nucleic acids encoding PRO polypeptides, useful for  
PT stimulating Tumor Necrosis Factor alpha or chondrocyte proliferation,  
PT particularly for treating e.g. lung or breast tumors, or arthritis in a  
PT mammal.  
XX  
PS Claim 1; SEQ ID NO 6; 303pp; English.

XX  
CC This invention relates to novel nucleic acids encoding human PRO secreted  
CC and transmembrane proteins. Extracellular proteins play important roles  
CC in the formation, differentiation and maintenance of multicellular  
CC organisms. The fate of many individual cells (for example proliferation,  
CC migration or differentiation) is typically governed by information  
CC received from other cells and the immediate environment. The information  
CC is often transmitted by secreted polypeptides (for example mitogenic  
CC factors, survival factors, cytotoxic factors, differentiation factors,  
CC neuropeptides and hormones) which are received and interpreted by diverse  
CC cell receptors or membrane bound proteins. These membrane bound proteins  
CC and receptors may be of use as pharmaceutical and diagnostic agents, such  
CC as in the blocking of receptor-ligand interactions. The current invention  
CC provides the amino acid sequences of novel human membrane bound receptors  
CC and proteins, along with the cDNA sequences encoding them. The novel  
CC proteins of the invention may have cytostatic activities through the  
CC stimulation of chondrocytes. The nucleic acids of the invention may be  
CC useful for the manufacture of a medicament for diagnosing or treating a  
CC tumour in a mammal. In addition, they may be useful for measuring or  
CC detecting the expression of a tumour associated gene. The present  
CC sequence is a human PRO protein of the invention.

XX Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;

QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT---EEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEPILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSNKMVSMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFQEAactsPLAKHTTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIYVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 150 IRIIQERNGLVPDCLTDGSDVSDLEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1486

ADH58442

ID ADH58442 standard; protein; 367 AA.

XX ADH58442;

XX

DT 25-MAR-2004 (first entry)

XX Novel human secreted and transmembrane protein PRO189.

DE human; PRO; membrane bound protein; membrane bound receptor;

XX

KW





[illegible]

PR 18-JUL-2002; 2002US-00197942.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX WPI; 2004-096593/10.  
DR N-PSDB; ADI13514.  
XX  
PT Fifty seven nucleic acids encoding PRO polypeptides, useful for  
PT stimulating Tumor Necrosis Factor alpha or chondrocyte proliferation,  
PT particularly for treating e.g. lung or breast tumors.  
XX  
PS Claim 1; Fig 6; 301pp; English.  
XX  
CC This invention relates to novel nucleic acids encoding human PRO secreted  
CC and transmembrane proteins. Extracellular proteins play important roles  
CC in the formation, differentiation and maintenance of multicellular  
CC organisms. The fate of many individual cells (for example proliferation,  
CC migration or differentiation) is typically governed by information  
CC received from other cells and the immediate environment. The information  
CC is often transmitted by secreted polypeptides (for example mitogenic  
CC factors, survival factors, cytotoxic factors, differentiation factors,  
CC neuropeptides and hormones) which are received and interpreted by diverse  
CC cell receptors or membrane bound proteins. These membrane bound proteins  
CC and receptors may be of use as pharmaceutical and diagnostic agents, such  
CC as in the blocking of receptor-ligand interactions. The current invention  
CC provides the amino acid sequences of novel human membrane bound receptors  
CC and proteins, along with the cDNA sequences encoding them. The novel  
CC proteins of the invention may have cytostatic activities through the  
CC stimulation of chondrocytes. The nucleic acids of the invention may be  
CC useful for the manufacture of a medicament for diagnosing or treating a  
CC tumour in a mammal. In addition, they may be useful for measuring or  
CC detecting the expression of a tumour associated gene. The present  
CC sequence is the amino acid sequence of a human PRO protein of the  
CC invention.  
XX  
SQ Sequence 367 AA;  
  
Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNMVSMVTLGLHPWIANIDDTQY-----LAA 430  
Db 101 ----EDQFOEACTSPLAKHTSQAI-----LQPVLAEDFTIFKAMMVQKNIEMQLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLPLGAVDDGEHSQNEKI 484  
Db 150 IRIIQERNGVLPDCLTDGSDVVSdleHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNVIEGTK 494  
Db 200 KRKKQLSEAK 209  
  
RESULT 1490  
ADK00771  
ID ADK00771 standard; protein; 367 AA.  
XX  
AC ADK00771;  
XX  
DT 06-MAY-2004 (first entry)

XX Human PRO polypeptide #3.  
DE  
XX  
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN US2003186373-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 16-SEP-2002; 2002US-00245013.  
XX  
PR 15-SEP-2000; 2000US-0232887P.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-041199/04.  
DR N-PSDB; ADK00770.  
XX  
PT Isolated nucleic acid molecule useful in molecular biology, including  
PT uses as hybridization probes, in chromosome and gene mapping, and in  
PT generation of anti-sense, comprises nucleotide sequence that encodes PRO  
PT polypeptide.  
XX  
PS Claim 11; SEQ ID NO 6; 301pp; English.  
XX  
CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for inducing endothelial cell  
CC tube formation and for treating sports-related joint problems, articular  
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
CC represents a human PRO polypeptide of the invention.  
XX  
SQ Sequence 367 AA;  
  
Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEINTYKAHLDLEEYRN 322  
Db 28 PILDVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100



Qy 383 VSAVEKQVTRHLEDVFSKRNSSNKMVSVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEAECTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
Qy 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 150 IRIQERNGLVPDCLTDGSDVVSDEHEEMKILREVLRS-----KEEYDQEEER 199  
Qy 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1491  
ADL08512  
ID ADL08512 standard; protein; 367 AA.  
XX  
AC ADL08512;  
DT 06-MAY-2004 (first entry)  
XX  
DE Human secreted/transmembrane polypeptide PRO189.  
XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW endothelial cell tube formation; chondrocyte cell differentiation;  
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;  
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;  
KW liver tumour; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2003186372-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 09-SEP-2002; 2002US-00238196.  
XX  
PR 11-FEB-2000; 2000WO-US003565.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 18-JUL-2002; 2002US-00197942.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2004-041198/04.  
DR N-PSDB; ADL08511.  
XX  
PT New isolated nucleic acid molecule for use in molecular biology, as  
PT hybridization probe, in chromosome and gene mapping, and in generation of  
PT anti-sense ribonucleic acid and deoxyribonucleic acid.  
XX  
PS Claim 11; SEQ ID NO 6; 301pp; English.  
XX

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of

CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006  
CC polypeptides are useful for inhibiting the proliferation of human  
CC microvascular endothelial cells. PRO polypeptides are useful for  
CC detecting the presence of tumour in a mammal, including tumours of lung,  
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,  
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and  
CC PRO34274 polypeptides are useful for inducing endothelial cell tube  
CC formation. PRO or the antibody are useful in the preparation of a  
CC medicament for treating a condition responsive to PRO polypeptide. The  
CC oligonucleotide probes are useful for isolating genomic and cDNA  
CC nucleotide sequences, for measuring or detecting the expression of an  
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a  
CC hybridisation probe, in chromosome and gene mapping, in the generation of  
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and  
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The  
CC present sequence represents a PRO protein.  
XX  
SQ Sequence 367 AA;

Query Match 3.2%; Score 83.5; DB 8; Length 367;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
Matches 55; Conservative 23; Mismatches 77; Indels 95; Gaps 10;  
QY 272 PMADLVALLGSLVDSSGHILVPGIYDEV-----VPLT-----EEEINTYKAHLDLEEYRN 322  
Db 28 PILDFVEQKCEVNCCKGGHVITPGSPPEVILVACVPLVDFDDEESKLTYTEIH---QEYK- 83  
QY 323 SSRVEKFLFDTKKEIIMHLMWRYPSPSLIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMN 382  
Db 84 -ELVEKLL-----EGYLKEIGIN----- 100  
QY 383 VSAVEKQVTRHLEDVFSKRNSSNKMVSVMTLGLHPWIANIDDTQY-----LAA 430  
Db 101 -----EDQFQEAECTSPLAKTHTSQAI-----LQPVLAEDFTIFKAMVQKNIEMLQA 149  
QY 431 KRAIRTVFGTEPDMIRDGSTI-----PIAKMFQEIIVHKSVVLIPLGAVDDGHSQNEKI 484  
Db 150 IRIQERNGLVPDCLTDGSDVVSDEHEEMKILREVLRS-----KEEYDQEEER 199  
QY 485 NRWNYIEGTK 494  
Db 200 KRKKQLSEAK 209

RESULT 1492  
ABU24455  
ID ABU24455 standard; protein; 408 AA.  
XX  
AC ABU24455;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by prokaryotic essential gene #9982.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Clostridium botulinum.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA28325.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 52379; 1766pp; English.  
XX

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway;  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 408 AA;

Query Match 3.2%; Score 83.5; DB 6; Length 408;  
Best Local Similarity 19.2%; Pred. No. 1.7e+02;  
Matches 92; Conservative 63; Mismatches 152; Indels 173; Gaps 25;

QY 34 LLEKVFQYI--DLHQDEFVQTLKEWVAIESDSVQVPFRQELFRMMVAADTLQRLGAR 91  
DB 4 VLERFLGYIKVDTSSE-----ESDTV-PTTKTQLEFAKKL---GEELKAIGLK 48  
QY 92 VASVDMGPOQLPDGQSLPIPPVILAEIGS--DPTKGTVCFYGHLDVQPADRGDWLTDPY 149  
DB 49 DVSVDEN-----GYVMATLESNIDKKVPTIGFIAHMDTSPDLSGTN--INPR 93  
QY 150 VLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALE-QDLPVNIKPIIEGMEEAGSVALEE 208  
DB 94 IVEKYDGQDIVLNKEKN---IVLKINEPPEILEYKGQDIVVTDGNTLLGADDKAGIA--- 147  
QY 209 LVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGT-----RGSYFMVEVKCR 256  
DB 148 -----EITAMEYLI-----NHPEIKHGTIKVGFTPBDEVGKGADHFDVK---- 187  
QY 257 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD 316  
DB 188 -----KFG-----ADLAYTL-----DGGG-----IGELECETFNA---- 212  
QY 317 LEEYRNSSRVEKFLDFTKEEILMHLWRYPVSLSIHGIEGAFDEPG-----TKTVIPGRVI 370  
DB 213 -----AKAKVI-----IEGRNVHPSAKNKMVTNAVL---VA 240

QY 371 GKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAA 430  
DB 241 NKF-INMLPENEV---PERTEGYEGFFHLLSVKSEV---ETAELNYIIRDFDRKKFEER 292  
QY 431 KRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVVLIPLGAVDDGHSQNEKINRWNYI 490  
DB 293 KEQIKEV-----GKKINEEYNKEIVCV---KVEDQYNNMKEKIDEVKYV 333

RESULT 1493

ADN20153

ID ADN20153 standard; protein; 428 AA.

XX

AC ADN20153;

XX 02-DEC-2004 (first entry)

DE Bacterial polypeptide #2806.

XX Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

PN 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 2806; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan









Best Local Similarity 18.0%; Pred. No. 1.9e+02;  
Matches 55; Conservative 59; Mismatches 140; Indels 51; Gaps 10;  
QY 12 LLAVALLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVOTLKEWVAIESDSVQVPRFR 71  
Db 144 ITALHTALVNGGVFVY-VPKNVVVEHPVQYVVLHDDENASFYNHVIIVTEESAE----- 196  
QY 72 QELFRMMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPPVILAEELGSDPTKGTV----- 127  
Db 197 -----VTYVENYLSNAG-----EGNQLNIISEVIAGANSNITYGSVDYMD 237  
QY 128 -CFYGHLL---DVQPADRGDW----LTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 238 KGFTGHIIRRGITEADASINWALGLMNEGSQIIDTNTNLFGRSTSSLSKSVVVG TG----- 293  
QY 180 FRALEQDLPVNIKFIIEGMEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQKPAI 239  
Db 294 ----EQKINLTskivQYgKETDGYILKHGMKEHASSVFNIGYIKHGKGTKSIANQESRV 349  
QY 240 ---TYGTRGNSYFMVEVKCRD-QDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGI 295  
Db 350 LMLSEHARGDANPILLIDEDDVQAGHAASVGRVDPDQLYYLS- RGISQREAEERLVHGF 408  
QY 296 YDEVV 300  
Db 409 LDPVV 413

RESULT 1497  
ABP66024  
ID ABP66024 standard; protein; 444 AA.  
XX  
AC ABP66024;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:768.  
XX  
KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;  
KW antidiarrheic; antibacterial; inhibitor of Salmonella; detection;  
KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;  
KW rotavirus; food composition; pharmaceutical composition.  
XX  
OS Bifidobacterium longum.  
XX  
PN EP1227152-A1.  
XX  
PD 31-JUL-2002.  
XX  
PF 30-JAN-2001; 2001EP-00102050.  
XX  
PR 30-JAN-2001; 2001EP-00102050.  
XX  
PA (NEST ) SOC PROD NESTLE SA.  
XX  
DR WPI; 2002-668397/72.  
XX  
PT Novel polynucleotide comprising Bifidobacterium genome sequence useful as  
PT a probe or primer for detecting and/or identifying Bifidobacterium longum  
PT in a biological sample.  
XX  
PS Claim 3; SEQ ID NO 768; 80pp; English.  
XX  
CC The present invention describes a polynucleotide (I) comprising a  
CC sequence of a Bifidobacterium genome selected from the nucleotide  
CC sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at  
CC least 90% identity or which hybridises with the sequences given in  
CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a  
CC fusion protein, comprising a sequence selected from 1097 sequences given  
CC in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a  
CC heterologous polypeptide. (I) has antidiarrheic and antibacterial  
CC activities, and can be used as an inhibitor of Salmonella. (I) (which is  
CC a probe) is useful for the detection and/or identification of

CC Bifidobacterium longum in a biological sample. A carrier containing the  
CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be  
CC used for preventing and/or treating diarrhoea brought about by pathogenic  
CC bacteria and/or rotavirus. The carrier is a food composition selected  
CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented  
CC products, ice-creams, fermented cereal based products, milk based  
CC powders, infant formula, pet food or a pharmaceutical composition  
CC selected from tablets, liquid bacterial suspensions, dried oral  
CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.  
CC (I) is useful in DNA arrays or chips to carry out analysis of the  
CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent  
CC Bifidobacterium related nucleotide sequences given in the Sequence  
CC Listing from the present invention but not mentioned further within the  
CC specification. N.B. The sequence data for this patent is not represented  
CC in the printed specification but is based on sequence information  
CC supplied by the European Patent Office  
XX  
SQ Sequence 444 AA;

Query Match 3.2%; Score 83.5; DB 5; Length 444;  
Best Local Similarity 27.1%; Pred. No. 1.9e+02;  
Matches 51; Conservative 25; Mismatches 61; Indels 51; Gaps 12;  
QY 84 TLQRLG-ARVASVDMG-PQQLPDGQSLPIPPPVILAEELGSDPTKGTVCFYGHLDVQPA--D 139  
Db 93 TVRRHGDTVVASTDGFKPSR-----VILA-----GHLDTVFPVIDN 127  
QY 140 RGDGWL T--DPYVLTEV-----DGKLYGRGATDNKG--PVLAWINAVSAFRALEQDLPV 189  
Db 128 FPPKWLEPGDSLIREEIAHAHPEDRVLWGRGATDMKASDAVMYLAATLDGRTPETPKV 187  
QY 190 NIKFIIIEGMEE--AGSVALEELVEKEKDRFFSGVDYIIVISD--NLWI-----SQRKPAI 239  
Db 188 DLTYVFYDHEEVVAEKNGLRKVEAHPD--WTTGDFAIIGEPTNSGIEGCGNGTIRPDVW 245  
QY 240 TYGTRGNS 247  
Db 246 THGVAHS 253

RESULT 1498  
ADS29606  
ID ADS29606 standard; protein; 445 AA.  
XX  
AC ADS29606;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #18639.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.





Db 139 GSDELNFIAEALAKFVATECEDFHLPEGRQRELGTFFSPVKQTSLSGSLIKWTKGFS 198  
QY 179 AFRALQDLVNIKFIEGMEEAGSVALEELVEKDRFFSGVDYIVISDNLWISQRKPA 238  
Db 199 IEEAVGQDV---VGALNKALERVG-----LDMRIA 226  
QY 239 ITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMADLVALLGSLVDSS-----G 288  
Db 227 LVNDTVGT-----LAGGRYYPDVVAAVILGTGTNAAYVERATAIPKW 269  
QY 289 HILVPGIYDEVVPLTEEBEINTYKAIHLDLEEYRNSRVEKFLPDTKEEILMHLWRYPSLS 348  
Db 270 HGLLPKSGEMVINM---EWGNFRSSHLPTEFDHTLDFES--LNPGEQILEKI----- 317  
QY 349 IHG-----JEGAFDEPGTKTVIPGRVICKFSIRLVPHM-----NVSAVEKQVTR 392  
Db 318 ISGMYLGEILRRVLLKMAEDAAFFGDTVPFSKLRIPIIR-TPHMSAMHNDTSPDLKIVGS 376  
QY 393 HLEDVFSKRNSNM---VVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGS 449  
Db 377 KIKDILEVPTTSLKMRKVVIS-----LCNIATR--GARLSAAGIYGILKKLGRDIT 426  
QY 450 TIPIAKMFQEIYVHKSVVLIPLGAVDDG--EH 478  
Db 427 K-----DEEVQKSVI-----AMDGGLFEH 445

RESULT 1500

ABO61640  
ID ABO61640 standard; protein; 464 AA.

XX ABO61640;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 8157.

DE Recombinant expression vector; transcription regulatory element;  
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

XX N-PSDB; ACH95191.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for

XX preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 8157; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
XX pneumoniae polypeptide. Also described are: a recombinant expression  
XX vector comprising the nucleic acid, operably linked to a transcription  
XX regulatory element; and a cell comprising the recombinant expression  
XX vector. The nucleic acid is useful for preparing a vaccine composition  
XX against Klebsiella pneumoniae. This is the amino acid sequence of a  
XX Klebsiella pneumoniae polypeptide of the invention

XX Sequence 464 AA;

Query Match  
Best Local Similarity 3.2%; Score 83.5; DB 7; Length 464;  
Matches 68; Conservative 45; Mismatches 133; Indels 105; Gaps 14;  
QY 51 QTLKEWVAIESVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSLP- 109  
Db 70 ETLLAWLALLOCGARVLPNPQ-----LPAVLLQAL--LPALTMQHQLVNLGVDVLP 119  
QY 110 -IPPVILAEELGSDPTKGTVCFYGH-----LDVQ 136  
Db 120 NLPMLTLQLVEGE--HAVCWHGDRLVSMTLTSGSIGLPKAAVHSASAHLSAAGVLALM 176  
QY 137 PADRGDGLTDPVVLTEVDGK-----LYG-RGATDNKGPVLAWINA-----VSAF 180  
Db 177 PFAAGDDWLLS-LPLFHVSGQGIWVRWLLAGARLTVRDKQPLAQMLHGCTHASLVPTQLW 235  
QY 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGV----- 221  
Db 236 RLLNDDAAVSLKAVLLGGASI-PVELTERARKQGIIRSCGYGLTEFASTVCAKEADGAAD 294  
QY 222 -----DYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFG-----GIL 269  
Db 295 VGEALPGREVKIVAGEIWLRRASSMAAGYWRDQQLSLTN-----NEGWFATRDREGAL 346  
QY 270 HEPMADLVALLGSLVDSGSHILVPGIYDEVVPLTEEBEINTYKAIHLDLEEY 320  
Db 347 HNGRLTVVGRLDNLFSSGGEIGIQPEEVERVI-LAHPQVQQVFIIVPLDDAEY 396

Search completed: February 8, 2005, 23:31:56  
Job time : 364 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 8, 2005, 23:21:12 ; Search time 484 Seconds  
(without alignments)  
1223.511 Million cell updates/sec

Title: US-10-036-342-57  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2623	100.0	507	26	US-10-035-719-57	Sequence 57, Appl
4	2623	100.0	507	26	US-10-035-855-57	Sequence 57, Appl
5	2623	100.0	507	26	US-10-035-958-57	Sequence 57, Appl
6	2623	100.0	507	26	US-10-035-977-57	Sequence 57, Appl
7	2623	100.0	507	26	US-10-036-041-57	Sequence 57, Appl
8	2623	100.0	507	26	US-10-036-063-57	Sequence 57, Appl
9	2623	100.0	507	26	US-10-036-150-57	Sequence 57, Appl
10	2623	100.0	507	26	US-10-036-160-57	Sequence 57, Appl
11	2623	100.0	507	26	US-10-036-214-57	Sequence 57, Appl
12	2623	100.0	507	26	US-10-036-342-57	Sequence 57, Appl
13	2623	100.0	507	28	US-10-226-486-57	Sequence 57, Appl
14	2623	100.0	507	28	US-10-275-107-68	Sequence 68, Appl
15	2623	100.0	507	34	US-10-884-091-57	Sequence 57, Appl
16	2612.5	99.6	508	1	PCT-US02-08124-497	Sequence 497, App
17	2612.5	99.6	508	1	PCT-US02-08276-371	Sequence 371, App
18	2612.5	99.6	508	1	PCT-US02-08277-785	Sequence 785, App
19	2612.5	99.6	508	1	PCT-US02-09785-650	Sequence 650, App
20	2612.5	99.6	508	21	US-09-731-872-242	Sequence 242, App
21	2612.5	99.6	508	23	US-09-876-997-242	Sequence 242, App
22	2612.5	99.6	508	24	US-09-948-783-139	Sequence 139, App
23	2612.5	99.6	508	27	US-10-100-683-5905	Sequence 5905, Ap
24	2612.5	99.6	508	30	US-10-405-027-3067	Sequence 3067, Ap
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26	2612.5	99.6	508	30	US-10-405-027-4314	Sequence 4314, Ap
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47	1743	66.5	358	28	US-10-258-898A-6866	Sequence 6866, Ap
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49	1736	66.2	342	18	US-09-488-725A-3294	Sequence 3294, Ap
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61	1363	52.0	475	28	US-10-286-897-3027	Sequence 3027, Ap
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65	1358	51.8	475	28	US-10-220-381-18	Sequence 18, Appl
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71	1356	51.7	475	35	US-10-917-503-12214	Sequence 12214, A	144	506.5	19.3	440	28	US-10-282-122A-48298	Sequence 48298, A
72	1356	51.7	475	37	US-60-636-723-217	Sequence 217, App	145	470	17.9	95	23	US-09-834-366-13891	Sequence 13891, A
73	1355	51.7	476	1	PCT-US00-05882-1397	Sequence 1397, Ap	146	470	17.9	95	37	US-60-197-873-13891	Sequence 13891, A
74	1355	51.7	476	1	PCT-US01-01310-103	Sequence 103, App	147	441	16.8	458	30	US-10-415-182A-5666	Sequence 5666, Ap
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76	1355	51.7	476	22	US-09-764-901-12	Sequence 12, Appl	149	438.5	16.7	457	30	US-10-472-928-104	Sequence 104, App
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82	1194.5	45.5	462	22	US-09-791-537-28598	Sequence 28598, A	155	411	15.7	83	23	US-09-834-366-13893	Sequence 13893, A
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89	1139.5	43.4	415	22	US-09-791-537-28600	Sequence 28600, A	162	395.5	15.1	345	37	US-60-096-409-14559	Sequence 14559, A
90	1139.5	43.4	415	37	US-60-173-464-21196	Sequence 21196, A	163	395	15.1	463	21	US-09-739-449-11805	Sequence 11805, A
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93	1136.5	43.3	417	37	US-60-167-217-790	Sequence 790, App	166	377.5	14.4	460	1	PCT-US02-36123-2902	Sequence 2902, Ap
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97	1047	39.9	363	37	US-60-636-723-218	Sequence 218, App	170	329	12.5	141	20	US-09-646-673A-91	Sequence 91, Appl
98	1047	39.9	363	37	US-60-636-723-220	Sequence 220, App	171	329	12.5	141	20	US-09-646-673A-168	Sequence 168, App
99	1045	39.8	400	37	US-60-636-723-225	Sequence 225, App	172	329	12.5	141	27	US-10-131-410-91	Sequence 91, Appl
100	1044	39.8	481	29	US-10-326-956-871	Sequence 871, App	173	329	12.5	141	27	US-10-131-410-168	Sequence 168, App
101	1021.5	38.9	357	37	US-60-565-632-8730	Sequence 8730, Ap	174	321	12.2	157	1	PCT-US01-08631-32012	Sequence 32012, A
102	1021.5	38.9	357	37	US-60-579-062-8730	Sequence 8730, Ap	175	319.5	12.2	137	18	US-09-417-507-43388	Sequence 43388, A
103	1010	38.5	391	1	PCT-US02-29560-273	Sequence 273, App	176	318	12.1	134	22	US-09-757-032-901	Sequence 901, App
104	1010	38.5	391	1	PCT-US02-29560A-273	Sequence 273, App	177	302.5	11.5	457	21	US-09-738-626-6496	Sequence 6496, Ap
105	1010	38.5	391	28	US-10-245-882-273	Sequence 273, App	178	302.5	11.5	457	34	US-10-805-394-6496	Sequence 6496, Ap
106	1010	38.5	391	37	US-60-636-723-221	Sequence 221, App	179	292.5	11.2	250	27	US-10-179-131-8587	Sequence 8587, Ap
107	1007.5	38.4	385	28	US-10-218-140-5272	Sequence 5272, Ap	180	284	10.8	368	37	US-60-345-785-4	Sequence 4, Appli
108	1000	38.1	348	1	PCT-US01-08631-46235	Sequence 46235, A	181	281	10.7	103	33	US-10-767-795-100556	Sequence 100556,
109	990	37.7	492	27	US-10-179-131-5701	Sequence 5701, Ap	182	267.5	10.2	114	1	PCT-US01-14827-13634	Sequence 13634, A
110	990	37.7	492	32	US-10-603-113-14755	Sequence 14755, A	183	261	10.0	103	23	US-09-834-366-17009	Sequence 17009, A
111	990	37.7	492	37	US-60-096-409-14755	Sequence 14755, A	184	261	10.0	103	32	US-10-664-025-4417	Sequence 4417, Ap
112	914.5	34.9	231	37	US-60-212-656-428	Sequence 428, App	185	261	10.0	103	37	US-60-147-499-4417	Sequence 4417, Ap
113	914.5	34.9	231	37	US-60-230-435-1051	Sequence 1051, Ap	186	261	10.0	103	37	US-60-197-873-17009	Sequence 17009, A
114	914.5	34.9	237	37	US-60-212-664-408	Sequence 408, App	187	253.5	9.7	100	1	PCT-US01-08631-32013	Sequence 32013, A
115	914.5	34.9	237	37	US-60-216-770-61	Sequence 61, Appl	188	252.5	9.6	116	23	US-09-834-366-13782	Sequence 13782, A
116	882	33.6	311	20	US-09-629-469A-11268	Sequence 11268, A	189	252.5	9.6	116	37	US-60-197-873-13782	Sequence 13782, A
117	882	33.6	311	35	US-10-917-503-11268	Sequence 11268, A	190	248	9.5	98	33	US-10-793-479-5701	Sequence 5701, Ap
118	882	33.6	311	37	US-60-636-723-223	Sequence 223, App	191	248	9.5	98	33	US-10-793-479-5702	Sequence 5702, Ap
119	798	30.4	171	27	US-10-170-205E-32001	Sequence 32001, A	192	242.5	9.2	267	20	US-09-606-740A-358	Sequence 358, App
120	766	29.2	171	33	US-10-760-320A-4757	Sequence 4757, Ap	193	242.5	9.2	267	30	US-10-454-437-192	Sequence 192, App
121	766	29.2	171	33	US-10-760-620A-4757	Sequence 4757, Ap	194	242.5	9.2	267	30	US-10-454-437A-192	Sequence 192, App
122	729	27.8	286	1	PCT-US01-01310-78	Sequence 78, Appl	195	233	8.9	231	30	US-10-454-437-194	Sequence 194, App
123	729	27.8	286	26	US-10-073-885-78	Sequence 78, Appl	196	233	8.9	231	30	US-10-454-437A-194	Sequence 194, App
124	705	26.9	276	37	US-60-636-723-226	Sequence 226, App	197	230	8.8	375	37	US-60-579-902-6520	Sequence 6520, Ap
125	694	26.5	279	37	US-60-636-723-222	Sequence 222, App	198	225.5	8.6	406	30	US-10-431-652-5309	Sequence 5309, Ap
126	618.5	23.6	133	1	PCT-US00-35017A-1427	Sequence 1427, Ap	199	219	8.3	375	37	US-60-606-098-9302	Sequence 9302, Ap
127	618.5	23.6	133	28	US-10-296-115-1427	Sequence 1427, Ap	200	215	8.2	370	30	US-10-447-013-30	Sequence 30, Appl
128	607.5	23.2	148	32	US-10-664-025-3957	Sequence 3957, Ap	201	211.5	8.1	379	22	US-09-791-537-123468	Sequence 123468,
129	607.5	23.2	148	37	US-60-147-499-3957	Sequence 3957, Ap	202	211	8.0	431	18	US-09-450-969-4689	Sequence 4689, Ap
130	601.5	22.9	286	1	PCT-US01-08656-10918	Sequence 10918, A	203	211	8.0	431	26	US-10-092-411A-4338	Sequence 4338, Ap
131	601.5	22.9	286	28	US-10-273-573-10918	Sequence 10918, A	204	211	8.0	431	33	US-10-724-972A-4689	Sequence 4689, Ap
132	580.5	22.1	119	28	US-10-276-781-1808	Sequence 1808, Ap	205	211	8.0	431	35	US-10-902-441-4338	Sequence 4338, Ap
133	568.5	21.7	408	1	PCT-US01-08631-46236	Sequence 46236, A	206	210	8.0	376	30	US-10-446-203-9125	Sequence 9125, Ap
134	532	20.3	148	23	US-09-834-366-13780	Sequence 13780, A	207	209.5	8.0	376	1	PCT-US02-36123-1620	Sequence 1620, Ap
135	532	20.3	148	37	US-60-197-873-13780	Sequence 13780, A	208	209.5	8.0	376	31	US-10-501-282-1620	Sequence 1620, Ap
136	526.5	20.1	140	23	US-09-834-366-13776	Sequence 13776, A	209	209	8.0	376	16	US-09-252-691-10092	Sequence 10092, A
137	526.5	20.1	140	37	US-60-197-873-13776	Sequence 13776, A	210	209	8.0	376	16	US-09-252-691C-10092	Sequence 10092, A
138	525.5	20.0	467	27	US-10-156-761-10612	Sequence 10612, A	211	209	8.0	376	30	US-10-417-886-10092	Sequence 10092, A
139	514.5	19.6	526	18	US-09-417-507-31767	Sequence 31767, A	212	206.5	7.9	463	1	PCT-US02-09107B-52178	Sequence 52178, A
140	510	19.4	458	19	US-09-540-209B-9027	Sequence 9027, Ap	213	206.5	7.9	463	28	US-10-282-122A-52178	Sequence 52178, A
141	507	19.3	170	20	US-09-629-469A-12849	Sequence 12849, A	214	201	7.7	465	1	PCT-US02-09107B-51968	Sequence 51968, A
142	507	19.3	170	35	US-10-917-503-12849	Sequence 12849, A	215	201	7.7	465	28	US-10-282-122A-51968	Sequence 51968, A

216	199	7.6	378	23	US-09-897-516-6787	Sequence 6787, Ap	289	161	6.1	469	1	PCT-US02-09107B-71650	Sequence 71650, A
217	199	7.6	378	23	US-09-897-516A-6793	Sequence 6793, Ap	290	161	6.1	469	28	US-10-282-122A-71650	Sequence 71650, A
218	199	7.6	378	37	US-60-215-161-6787	Sequence 6787, Ap	291	160	6.1	471	18	US-09-450-969-6038	Sequence 6038, Ap
219	197.5	7.5	470	1	PCT-US02-09107B-60517	Sequence 60517, A	292	160	6.1	471	33	US-10-724-972A-6038	Sequence 6038, Ap
220	197.5	7.5	470	28	US-10-282-122A-60517	Sequence 60517, A	293	159	6.1	385	37	US-60-579-902-5947	Sequence 5947, Ap
221	195.5	7.5	632	29	US-10-366-683-17148	Sequence 17148, A	294	158.5	6.0	466	1	PCT-US02-03987-13537	Sequence 13537, A
222	195.5	7.5	632	30	US-10-419-128-17148	Sequence 17148, A	295	158.5	6.0	466	23	US-09-815-242-13537	Sequence 13537, A
223	192	7.3	383	22	US-09-791-537-120603	Sequence 120603, A	296	158.5	6.0	466	26	US-10-072-851-13537	Sequence 13537, A
224	188.5	7.2	386	32	US-10-603-114-8238	Sequence 8238, Ap	297	158	6.0	402	32	US-10-603-108-2685	Sequence 2685, Ap
225	188	7.2	471	1	PCT-US02-03987-10682	Sequence 10682, A	298	158	6.0	402	37	US-60-128-476-4655	Sequence 4655, Ap
226	188	7.2	471	1	PCT-US02-09107B-57092	Sequence 57092, A	299	157.5	6.0	466	22	US-09-769-744A-32	Sequence 32, Appl
227	188	7.2	471	23	US-09-815-242-10682	Sequence 10682, A	300	157.5	6.0	466	30	US-10-472-928-1136	Sequence 1136, Ap
228	188	7.2	471	26	US-10-072-851-10682	Sequence 10682, A	301	157.5	6.0	466	32	US-10-640-833-5296	Sequence 5296, Ap
229	188	7.2	471	28	US-10-282-122A-57092	Sequence 57092, A	302	157.5	6.0	470	32	US-10-617-320-3616	Sequence 3616, Ap
230	187	7.1	426	29	US-10-369-493-23113	Sequence 23113, A	303	156.5	6.0	433	28	US-10-219-999-36414	Sequence 36414, A
231	187	7.1	426	37	US-60-360-039-23113	Sequence 23113, A	304	156.5	6.0	433	30	US-10-425-114-47964	Sequence 47964, A
232	187	7.1	440	30	US-10-417-884-4071	Sequence 4071, Ap	305	156.5	6.0	433	30	US-10-425-114A-47964	Sequence 47964, A
233	187	7.1	440	30	US-10-417-884A-4071	Sequence 4071, Ap	306	156.5	6.0	433	37	US-60-324-109-22307	Sequence 22307, A
234	186.5	7.1	453	1	PCT-US02-09107B-53370	Sequence 53370, A	307	156.5	6.0	438	30	US-10-424-599-247689	Sequence 247689, A
235	186.5	7.1	453	28	US-10-282-122A-53370	Sequence 53370, A	308	156.5	6.0	446	33	US-10-739-930-9772	Sequence 9772, Ap
236	185.5	7.1	467	37	US-60-546-745-31	Sequence 31, Appl	309	156	5.9	385	37	US-60-606-098-6925	Sequence 6925, Ap
237	183	7.0	362	29	US-10-369-493-7208	Sequence 7208, Ap	310	156	5.9	410	22	US-09-791-537-85008	Sequence 85008, A
238	183	7.0	362	37	US-60-360-039-7208	Sequence 7208, Ap	311	156	5.9	410	29	US-10-369-493-21465	Sequence 21465, A
239	182	6.9	438	22	US-09-791-537-103857	Sequence 103857, A	312	156	5.9	410	37	US-60-360-039-21465	Sequence 21465, A
240	181	6.9	309	1	PCT-US02-36123-1618	Sequence 1618, Ap	313	155.5	5.9	466	1	PCT-US02-03987-13394	Sequence 13394, A
241	181	6.9	309	31	US-10-501-282-1618	Sequence 1618, Ap	314	155.5	5.9	466	1	PCT-US02-09107B-73856	Sequence 73856, A
242	178	6.8	378	21	US-09-739-449-12653	Sequence 12653, A	315	155.5	5.9	466	23	US-09-815-242-13394	Sequence 13394, A
243	178	6.8	378	23	US-09-803-110-12653	Sequence 12653, A	316	155.5	5.9	466	26	US-10-072-851-13394	Sequence 13394, A
244	176	6.7	318	34	US-10-894-438-2	Sequence 2, Appli	317	155.5	5.9	466	28	US-10-282-122A-73856	Sequence 73856, A
245	176	6.7	432	1	PCT-US02-22979-24	Sequence 24, Appl	318	155	5.9	398	21	US-09-739-449-10735	Sequence 10735, A
246	176	6.7	432	33	US-10-758-979-24	Sequence 24, Appl	319	155	5.9	398	23	US-09-803-110-10735	Sequence 10735, A
247	175	6.7	402	30	US-10-434-665-5335	Sequence 5335, Ap	320	155	5.9	465	1	PCT-US02-09107B-45796	Sequence 45796, A
248	175	6.7	447	30	US-10-425-115-252533	Sequence 252533, A	321	155	5.9	465	28	US-10-282-122A-45796	Sequence 45796, A
249	174	6.6	394	29	US-10-375-039-44	Sequence 44, Appl	322	153	5.8	451	19	US-09-513-996A-63541	Sequence 63541, A
250	174	6.6	439	28	US-10-264-213-221	Sequence 221, App	323	153	5.8	475	24	US-09-935-625-21921	Sequence 21921, A
251	173	6.6	183	20	US-09-675-784A-8486	Sequence 8486, Ap	324	153	5.8	497	24	US-09-935-625-21920	Sequence 21920, A
252	172.5	6.6	382	23	US-09-897-516-5747	Sequence 5747, Ap	325	152	5.8	446	19	US-09-513-996A-3362	Sequence 3362, Ap
253	172.5	6.6	382	23	US-09-897-516A-5753	Sequence 5753, Ap	326	152	5.8	447	19	US-09-595-329A-2008	Sequence 2008, Ap
254	172.5	6.6	382	37	US-60-215-161-5747	Sequence 5747, Ap	327	151.5	5.8	527	24	US-09-935-625-22510	Sequence 22510, A
255	172	6.6	331	28	US-10-288-930-78	Sequence 78, Appl	328	151	5.8	388	11	US-08-761-184-1517	Sequence 1517, Ap
256	172	6.6	355	30	US-10-447-013-28	Sequence 28, Appl	329	151	5.8	388	12	US-08-821-931-1517	Sequence 1517, Ap
257	172	6.6	377	22	US-09-791-537-26670	Sequence 26670, A	330	151	5.8	388	13	US-08-993-002A-7594	Sequence 7594, Ap
258	172	6.6	425	30	US-10-434-665-3861	Sequence 3861, Ap	331	151	5.8	388	29	US-10-335-977-7594	Sequence 7594, Ap
259	172	6.6	463	22	US-09-791-537-72747	Sequence 72747, A	332	151	5.8	391	11	US-08-761-184-1349	Sequence 1349, Ap
260	172	6.6	465	28	US-10-264-213-220	Sequence 220, App	333	151	5.8	391	12	US-08-821-931-1349	Sequence 1349, Ap
261	171.5	6.5	450	22	US-09-791-537-51450	Sequence 51450, A	334	151	5.8	391	13	US-08-993-002A-7595	Sequence 7595, Ap
262	171	6.5	418	18	US-09-450-969-4531	Sequence 4531, Ap	335	151	5.8	391	29	US-10-335-977-7595	Sequence 7595, Ap
263	171	6.5	418	26	US-10-092-411A-3552	Sequence 3552, Ap	336	151	5.8	469	1	PCT-US02-09107B-44103	Sequence 44103, A
264	171	6.5	418	33	US-10-724-972A-4531	Sequence 4531, Ap	337	151	5.8	469	22	US-09-791-537-54256	Sequence 54256, A
265	171	6.5	418	35	US-10-902-441-3552	Sequence 3552, Ap	338	151	5.8	469	28	US-10-282-122A-44103	Sequence 44103, A
266	171	6.5	468	30	US-10-415-182A-2586	Sequence 2586, Ap	339	150.5	5.7	419	29	US-10-369-493-19543	Sequence 19543, A
267	170.5	6.5	412	12	US-08-827-356-4332	Sequence 4332, Ap	340	150.5	5.7	419	37	US-60-360-039-19543	Sequence 19543, A
268	170.5	6.5	412	20	US-09-611-529-3959	Sequence 3959, Ap	341	150.5	5.7	446	24	US-09-935-625-22511	Sequence 22511, A
269	170.5	6.5	412	25	US-09-950-084-3959	Sequence 3959, Ap	342	150	5.7	388	30	US-10-447-013-4	Sequence 4, Appli
270	168.5	6.4	372	1	PCT-US03-13699-995	Sequence 995, App	343	150	5.7	388	30	US-10-447-013-29	Sequence 29, Appl
271	166	6.3	469	1	PCT-US02-09107B-74544	Sequence 74544, A	344	150	5.7	823	27	US-10-179-131-9963	Sequence 9963, Ap
272	166	6.3	469	28	US-10-282-122A-74544	Sequence 74544, A	345	149	5.7	396	32	US-10-603-114-8308	Sequence 8308, Ap
273	166	6.3	486	30	US-10-415-182A-2588	Sequence 2588, Ap	346	149	5.7	440	19	US-09-513-996A-3363	Sequence 3363, Ap
274	165.5	6.3	446	30	US-10-424-599-211102	Sequence 211102, A	347	149	5.7	441	19	US-09-595-329A-2009	Sequence 2009, Ap
275	165	6.3	400	22	US-09-791-537-96232	Sequence 96232, A	348	149	5.7	457	28	US-10-219-999-55751	Sequence 55751, A
276	165	6.3	469	1	PCT-US02-09107B-71186	Sequence 71186, A	349	149	5.7	457	28	US-10-219-999-59130	Sequence 59130, A
277	165	6.3	469	28	US-10-282-122A-71186	Sequence 71186, A	350	149	5.7	457	30	US-10-425-115-322596	Sequence 322596, A
278	164.5	6.3	470	1	PCT-US02-09107B-72074	Sequence 72074, A	351	149	5.7	457	37	US-60-324-109-20191	Sequence 20191, A
279	164.5	6.3	470	28	US-10-282-122A-72074	Sequence 72074, A	352	149	5.7	469	1	PCT-US02-03987-12290	Sequence 12290, A
280	164	6.3	467	1	PCT-US02-36123-3412	Sequence 3412, Ap	353	149	5.7	469	23	US-09-815-242-12290	Sequence 12290, A
281	164	6.3	467	31	US-10-501-282-3412	Sequence 3412, Ap	354	149	5.7	469	26	US-10-072-851-12290	Sequence 12290, A
282	164	6.3	489	1	PCT-US02-36123-3414	Sequence 3414, Ap	355	149	5.7	474	30	US-10-425-114-66262	Sequence 66262, A
283	164	6.3	489	31	US-10-501-282-3414	Sequence 3414, Ap	356	149	5.7	474	30	US-10-425-114-72430	Sequence 72430, A
284	163.5	6.2	467	22	US-09-791-537-71958	Sequence 71958, A	357	149	5.7	474	30	US-10-425-114A-66262	Sequence 66262, A
285	162.5	6.2	450	30	US-10-417-884-6534	Sequence 6534, Ap	358	149	5.7	474	30	US-10-425-114A-72430	Sequence 72430, A
286	162.5	6.2	450	30	US-10-417-884A-6534	Sequence 6534, Ap	359	148.5	5.7	430	19	US-09-513-996A-63542	Sequence 63542, A
287	162.5	6.2	472	22	US-09-791-537-63765	Sequence 63765, A	360	148.5	5.7	430	24	US-09-935-625-21922	Sequence 21922, A
288	161	6.1	457	33	US-10-767-701-45996	Sequence 45996, A	361	148.5	5.7	430	24	US-09-935-625-22512	Sequence 22512, A



362	147.5	5.6	352	28	US-10-219-999-47743	Sequence 47743, A	435	136	5.2	190	26	US-10-072-851-5877	Sequence 5877, Ap
363	147.5	5.6	352	30	US-10-425-114-57922	Sequence 57922, A	436	134.5	5.1	341	19	US-09-513-996A-54830	Sequence 54830, A
364	147.5	5.6	352	30	US-10-425-114A-57922	Sequence 57922, A	437	134	5.1	391	29	US-10-369-493-11006	Sequence 11006, A
365	147.5	5.6	352	37	US-60-324-109-29352	Sequence 29352, A	438	134	5.1	391	37	US-60-360-039-11006	Sequence 11006, A
366	147	5.6	448	22	US-09-791-537-12371	Sequence 12371, A	439	133.5	5.1	434	29	US-10-366-683-21048	Sequence 21048, A
367	146	5.6	422	1	PCT-US04-37204-6390	Sequence 6390, Ap	440	133.5	5.1	434	30	US-10-419-128-21048	Sequence 21048, A
368	144	5.5	380	22	US-09-791-537-30388	Sequence 30388, A	441	133	5.1	65	18	US-09-417-507-35759	Sequence 35759, A
369	143.5	5.5	407	22	US-09-791-537-63910	Sequence 63910, A	442	133	5.1	366	1	PCT-US03-28227-3939	Sequence 3939, Ap
370	142.5	5.4	374	21	US-09-739-449-12738	Sequence 12738, A	443	132.5	5.1	463	1	PCT-US04-37204-7229	Sequence 7229, Ap
371	142.5	5.4	374	23	US-09-803-110-12738	Sequence 12738, A	444	132	5.0	383	1	PCT-US03-26488-69	Sequence 69, Appl
372	142	5.4	455	22	US-09-791-537-104729	Sequence 104729, A	445	132	5.0	383	22	US-09-791-537-128676	Sequence 128676, A
373	141.5	5.4	450	19	US-09-513-996A-3311	Sequence 3311, Ap	446	132	5.0	468	26	US-10-015-127-11248	Sequence 11248, A
374	141.5	5.4	451	19	US-09-595-329A-1946	Sequence 1946, Ap	447	132	5.0	473	28	US-10-275-107-69	Sequence 69, Appl
375	141	5.4	408	1	PCT-US04-03417-54	Sequence 54, Appl	448	132	5.0	473	30	US-10-433-757-4	Sequence 4, Appli
376	141	5.4	408	9	US-08-555-857-4	Sequence 4, Appli	449	131.5	5.0	351	31	US-10-506-454-128	Sequence 128, App
377	141	5.4	408	12	US-08-827-864-4	Sequence 4, Appli	450	131.5	5.0	351	37	US-60-361-742-128	Sequence 128, App
378	141	5.4	408	22	US-09-791-537-64771	Sequence 64771, A	451	130	5.0	342	1	PCT-US03-28227-3943	Sequence 3943, Ap
379	141	5.4	408	27	US-10-109-860-4	Sequence 4, Appli	452	130	5.0	400	20	US-09-614-150-25302	Sequence 25302, A
380	141	5.4	408	27	US-10-109-860B-4	Sequence 4, Appli	453	130	5.0	400	20	US-09-614-150A-25302	Sequence 25302, A
381	141	5.4	408	27	US-10-170-205E-6004	Sequence 6004, Ap	454	130	5.0	400	22	US-09-791-537-128760	Sequence 128760, A
382	141	5.4	408	28	US-10-219-051B-5651	Sequence 5651, Ap	455	130	5.0	400	37	US-60-173-464-20938	Sequence 20938, A
383	141	5.4	408	33	US-10-733-969A-14	Sequence 14, Appl	456	130	5.0	400	37	US-60-191-637-25418	Sequence 25418, A
384	141	5.4	408	33	US-10-772-636-54	Sequence 54, Appl	457	130	5.0	400	37	US-60-191-681-20027	Sequence 20027, A
385	141	5.4	408	35	US-10-990-328-14889	Sequence 14889, A	458	130	5.0	443	30	US-10-472-928-4512	Sequence 4512, Ap
386	141	5.4	408	37	US-60-498-106-16	Sequence 16, Appl	459	129	4.9	361	27	US-10-170-205E-24268	Sequence 24268, A
387	141	5.4	421	35	US-10-940-774-10991	Sequence 10991, A	460	129	4.9	361	37	US-60-452-680-15076	Sequence 15076, A
388	141	5.4	522	37	US-60-230-435-1093	Sequence 1093, Ap	461	128.5	4.9	258	30	US-10-434-665-4891	Sequence 4891, Ap
389	140.5	5.4	401	19	US-09-513-996A-54829	Sequence 54829, A	462	128.5	4.9	502	37	US-60-345-785-2	Sequence 2, Appli
390	140.5	5.4	406	22	US-09-791-537-80222	Sequence 80222, A	463	127.5	4.9	361	1	PCT-US02-32850-22	Sequence 22, Appl
391	140.5	5.4	441	1	PCT-US03-28227-3936	Sequence 3936, Ap	464	127.5	4.9	361	1	PCT-US02-32850A-22	Sequence 22, Appl
392	140.5	5.4	443	30	US-10-449-902-37025	Sequence 37025, A	465	127.5	4.9	361	26	US-10-014-896-4	Sequence 4, Appli
393	140.5	5.4	443	30	US-10-449-902-54462	Sequence 54462, A	466	127.5	4.9	361	35	US-10-919-124-4	Sequence 4, Appli
394	140.5	5.4	753	21	US-09-708-427-27430	Sequence 27430, A	467	127	4.8	372	1	PCT-US03-28227-3941	Sequence 3941, Ap
395	139.5	5.3	443	32	US-10-640-833-4278	Sequence 4278, Ap	468	127	4.8	378	1	PCT-US03-28227-3940	Sequence 3940, Ap
396	139.5	5.3	446	32	US-10-617-320-4675	Sequence 4675, Ap	469	126.5	4.8	167	33	US-10-767-795-60754	Sequence 60754, A
397	139	5.3	474	22	US-09-791-537-71057	Sequence 71057, A	470	126.5	4.8	339	19	US-09-513-996A-54831	Sequence 54831, A
398	138.5	5.3	341	19	US-09-513-996A-3364	Sequence 3364, Ap	471	126.5	4.8	359	37	US-60-167-217-14769	Sequence 14769, A
399	138.5	5.3	342	19	US-09-595-329A-2010	Sequence 2010, Ap	472	126.5	4.8	359	37	US-60-173-464-12011	Sequence 12011, A
400	138.5	5.3	362	12	US-08-827-356-5163	Sequence 5163, Ap	473	126.5	4.8	448	22	US-09-791-537-96235	Sequence 96235, A
401	138.5	5.3	362	20	US-09-611-529-5609	Sequence 5609, Ap	474	126	4.8	256	30	US-10-437-963-158066	Sequence 158066, A
402	138.5	5.3	362	25	US-09-950-084-5609	Sequence 5609, Ap	475	126	4.8	373	1	PCT-US03-38573-39	Sequence 39, Appl
403	138	5.3	576775	12	US-08-895-611D-2	Sequence 2, Appli	476	126	4.8	449	1	PCT-US02-03987-5375	Sequence 5375, Ap
404	138	5.3	576775	12	US-08-895-611D-2	Sequence 2, Appli	477	126	4.8	449	23	US-09-815-242-5375	Sequence 5375, Ap
405	138	5.3	576775	18	US-09-458-180-2	Sequence 2, Appli	478	126	4.8	449	26	US-10-072-851-5375	Sequence 5375, Ap
406	138	5.3	576775	23	US-09-895-611D-2	Sequence 2, Appli	479	126	4.8	449	37	US-60-242-578-773	Sequence 773, App
407	137.5	5.2	387	16	US-09-252-691C-8791	Sequence 8791, Ap	480	126	4.8	449	37	US-60-253-625-2117	Sequence 2117, Ap
408	137.5	5.2	387	16	US-09-252-691C-8791	Sequence 8791, Ap	481	126	4.8	449	37	US-60-257-931-2906	Sequence 2906, Ap
409	137.5	5.2	387	30	US-10-417-886-8791	Sequence 8791, Ap	482	126	4.8	449	37	US-60-269-308-3926	Sequence 3926, Ap
410	137.5	5.2	393	29	US-10-366-683-22875	Sequence 22875, A	483	125.5	4.8	236	37	US-60-213-845-350	Sequence 350, App
411	137.5	5.2	393	30	US-10-419-128-22875	Sequence 22875, A	484	125.5	4.8	359	20	US-09-614-150-14688	Sequence 14688, A
412	137	5.2	215	1	PCT-US02-03987-13061	Sequence 13061, A	485	125.5	4.8	359	20	US-09-614-150A-14688	Sequence 14688, A
413	137	5.2	215	23	US-09-815-242-13061	Sequence 13061, A	486	125.5	4.8	359	22	US-09-791-537-128757	Sequence 128757, A
414	137	5.2	215	26	US-10-072-851-13061	Sequence 13061, A	487	125.5	4.8	359	37	US-60-191-637-14729	Sequence 14729, A
415	137	5.2	370	16	US-09-270-849B-195190	Sequence 195190, A	488	125.5	4.8	359	37	US-60-191-681-11609	Sequence 11609, A
416	137	5.2	408	20	US-09-614-150-25308	Sequence 25308, A	489	125.5	4.8	430	18	US-09-450-969-4600	Sequence 4600, Ap
417	137	5.2	408	20	US-09-614-150A-25308	Sequence 25308, A	490	125.5	4.8	430	26	US-10-092-411A-4302	Sequence 4302, Ap
418	137	5.2	408	22	US-09-791-537-128759	Sequence 128759, A	491	125.5	4.8	430	33	US-10-724-972A-4600	Sequence 4600, Ap
419	137	5.2	408	37	US-60-173-464-20944	Sequence 20944, A	492	125.5	4.8	430	35	US-10-902-441-4302	Sequence 4302, Ap
420	137	5.2	408	37	US-60-191-637-25424	Sequence 25424, A	493	125.5	4.8	432	1	PCT-US03-04450-52	Sequence 52, Appl
421	137	5.2	408	37	US-60-191-681-20033	Sequence 20033, A	494	125.5	4.8	432	29	US-10-365-742-52	Sequence 52, Appl
422	137	5.2	429	19	US-09-513-996A-3312	Sequence 3312, Ap	495	125	4.8	39	21	US-09-724-391-118	Sequence 118, App
423	137	5.2	430	19	US-09-595-329A-1947	Sequence 1947, Ap	496	125	4.8	373	1	PCT-US03-02500-52	Sequence 52, Appl
424	137	5.2	487	30	US-10-437-963-158067	Sequence 158067, A	497	125	4.8	373	27	US-10-109-860-2	Sequence 2, Appli
425	137	5.2	576	1	PCT-US02-09107B-68213	Sequence 68213, A	498	125	4.8	373	27	US-10-109-860B-2	Sequence 2, Appli
426	137	5.2	576	28	US-10-282-122A-68213	Sequence 68213, A	499	125	4.8	373	27	US-10-170-205E-5896	Sequence 5896, Ap
427	137	5.2	814	37	US-60-167-217-14782	Sequence 14782, A	500	125	4.8	373	31	US-10-502-459-52	Sequence 52, Appl
428	136.5	5.2	446	26	US-10-092-411A-5125	Sequence 5125, Ap	501	124.5	4.7	401	20	US-09-614-150-14709	Sequence 14709, A
429	136.5	5.2	446	35	US-10-902-441-5125	Sequence 5125, Ap	502	124.5	4.7	401	20	US-09-614-150A-14709	Sequence 14709, A
430	136.5	5.2	457	30	US-10-437-963-117985	Sequence 117985, A	503	124.5	4.7	401	22	US-09-791-537-128761	Sequence 128761, A
431	136.5	5.2	502	26	US-10-014-896-2	Sequence 2, Appli	504	124.5	4.7	401	37	US-60-173-464-12029	Sequence 12029, A
432	136.5	5.2	502	35	US-10-919-124-2	Sequence 2, Appli	505	124.5	4.7	401	37	US-60-191-637-14750	Sequence 14750, A
433	136	5.2	190	1	PCT-US02-03987-5877	Sequence 5877, Ap	506	124.5	4.7	401	37	US-60-191-681-11627	Sequence 11627, A
434	136	5.2	190	23	US-09-815-242-5877	Sequence 5877, Ap	507	124.5	4.7	446	30	US-10-424-599-239368	Sequence 239368, A



508	124	4.7	381	31	US-10-506-454-1579	Sequence 1579, Ap	581	113.5	4.3	226	22	US-09-760-480-186	Sequence 186, App
509	124	4.7	381	37	US-60-361-742-1581	Sequence 1581, Ap	582	113.5	4.3	226	28	US-10-216-428-186	Sequence 186, App
510	123.5	4.7	367	1	PCT-US03-28227-3942	Sequence 3942, Ap	583	113.5	4.3	226	28	US-10-238-706-16	Sequence 16, Appli
511	123.5	4.7	441	30	US-10-446-203-12164	Sequence 12164, A	584	113.5	4.3	409	32	US-10-645-723-5	Sequence 5, Appli
512	123	4.7	273	30	US-10-425-115-290485	Sequence 290485,	585	113.5	4.3	409	32	US-10-645-723-6	Sequence 6, Appli
513	122.5	4.7	440	27	US-10-156-761-9438	Sequence 9438, Ap	586	113.5	4.3	409	32	US-10-645-723A-5	Sequence 5, Appli
514	122.5	4.7	481	37	US-60-391-781-1059	Sequence 1059, Ap	587	113.5	4.3	409	32	US-10-645-723A-6	Sequence 6, Appli
515	122.5	4.7	481	37	US-60-638-099-16690	Sequence 16690, A	588	113	4.3	36	30	US-10-405-027-4315	Sequence 4315, Ap
516	122.5	4.7	481	37	US-60-638-099-42761	Sequence 42761, A	589	113	4.3	36	30	US-10-405-027-4316	Sequence 4316, Ap
517	122.5	4.7	481	37	US-60-638-099-47439	Sequence 47439, A	590	113	4.3	385	22	US-09-791-537-53515	Sequence 53515, A
518	122.5	4.7	492	37	US-60-638-099-1613	Sequence 1613, Ap	591	113	4.3	409	14	US-09-023-809-1	Sequence 1, Appli
519	122.5	4.7	1332	22	US-09-791-537-144544	Sequence 144544,	592	113	4.3	409	14	US-09-023-809-1	Sequence 1, Appli
520	122	4.7	2291	20	US-09-614-150-12420	Sequence 12420, A	593	113	4.3	410	1	PCT-US03-30770-5	Sequence 5, Appli
521	122	4.7	2291	20	US-09-614-150A-12420	Sequence 12420, A	594	113	4.3	410	1	PCT-US03-30770-6	Sequence 6, Appli
522	122	4.7	2291	37	US-60-167-217-12454	Sequence 12454, A	595	113	4.3	410	1	PCT-US98-01635-7	Sequence 7, Appli
523	122	4.7	2291	37	US-60-173-464-10089	Sequence 10089, A	596	113	4.3	410	22	US-09-791-537-39128	Sequence 39128, A
524	122	4.7	2291	37	US-60-191-637-12455	Sequence 12455, A	597	113	4.3	410	22	US-09-791-537-127307	Sequence 127307,
525	122	4.7	2291	37	US-60-191-681-9758	Sequence 9758, Ap	598	113	4.3	410	32	US-10-674-666-5	Sequence 5, Appli
526	121	4.6	616	12	US-08-827-356-4618	Sequence 4618, Ap	599	113	4.3	410	32	US-10-674-666-6	Sequence 6, Appli
527	121	4.6	616	20	US-09-611-529-7196	Sequence 7196, Ap	600	113	4.3	410	33	US-10-757-843-1	Sequence 1, Appli
528	121	4.6	616	25	US-09-950-084-7196	Sequence 7196, Ap	601	113	4.3	441	21	US-09-738-626-6613	Sequence 6613, Ap
529	120.5	4.6	481	37	US-60-391-781-1485	Sequence 1485, Ap	602	113	4.3	441	34	US-10-805-394-6613	Sequence 6613, Ap
530	120	4.6	441	27	US-10-156-761-14162	Sequence 14162, A	603	112.5	4.3	337	22	US-09-791-537-9242	Sequence 9242, Ap
531	119.5	4.6	361	1	PCT-US03-30720-888	Sequence 888, App	604	112.5	4.3	481	37	US-60-638-099-22195	Sequence 22195, A
532	119.5	4.6	361	26	US-10-094-749-2952	Sequence 2952, Ap	605	112.5	4.3	1176	22	US-09-791-537-120463	Sequence 120463,
533	119.5	4.6	361	28	US-10-295-027-201	Sequence 201, App	606	112.5	4.3	1176	32	US-10-679-063-20934	Sequence 20934, A
534	119.5	4.6	445	26	US-10-015-127-12737	Sequence 12737, A	607	112	4.3	166	28	US-10-218-140-218	Sequence 218, App
535	119	4.5	214	18	US-09-417-507-34050	Sequence 34050, A	608	112	4.3	409	14	US-09-023-809-2	Sequence 2, Appli
536	118.5	4.5	443	22	US-09-716-964A-184	Sequence 28973, A	609	112	4.3	409	14	US-09-023-809-2	Sequence 2, Appli
537	118.5	4.5	1433	21	US-09-716-964B-184	Sequence 184, App	610	112	4.3	409	32	US-10-645-723-7	Sequence 7, Appli
538	118.5	4.5	1433	21	US-09-716-964B-184	Sequence 184, App	611	112	4.3	409	32	US-10-645-723-8	Sequence 8, Appli
539	118.5	4.5	1433	32	US-10-670-817-184	Sequence 184, App	612	112	4.3	409	32	US-10-645-723-9	Sequence 9, Appli
540	118.5	4.5	1433	32	US-10-670-844-184	Sequence 184, App	613	112	4.3	409	32	US-10-645-723-10	Sequence 10, Appli
541	118.5	4.5	1433	32	US-10-671-106-184	Sequence 184, App	614	112	4.3	409	32	US-10-645-723A-7	Sequence 7, Appli
542	118.5	4.5	1433	32	US-10-671-134-184	Sequence 184, App	615	112	4.3	409	32	US-10-645-723A-8	Sequence 8, Appli
543	118.5	4.5	1433	32	US-10-671-207-184	Sequence 184, App	616	112	4.3	409	32	US-10-645-723A-9	Sequence 9, Appli
544	118.5	4.5	1433	32	US-10-671-403-184	Sequence 184, App	617	112	4.3	409	32	US-10-645-723A-10	Sequence 10, Appli
545	118.5	4.5	1433	32	US-10-671-412-184	Sequence 184, App	618	112	4.3	410	29	US-10-343-175-10	Sequence 10, Appli
546	118.5	4.5	1433	32	US-10-671-419-184	Sequence 184, App	619	112	4.3	410	33	US-10-757-843-2	Sequence 2, Appli
547	118.5	4.5	1433	32	US-10-671-859-184	Sequence 184, App	620	112	4.3	446	30	US-10-449-902-31166	Sequence 31166, A
548	118.5	4.5	1433	32	US-10-672-638-184	Sequence 184, App	621	112	4.3	446	30	US-10-449-902-47743	Sequence 47743, A
549	118.5	4.5	1433	32	US-10-673-098-184	Sequence 184, App	622	112	4.3	467	30	US-10-425-114-47811	Sequence 47811, A
550	118.5	4.5	1433	32	US-10-673-119-184	Sequence 184, App	623	112	4.3	467	30	US-10-425-114A-47811	Sequence 47811, A
551	118.5	4.5	1433	32	US-10-673-120-184	Sequence 184, App	624	112	4.3	1328	22	US-09-791-537-144539	Sequence 144539,
552	118.5	4.5	1433	32	US-10-673-127-184	Sequence 184, App	625	111.5	4.3	597	20	US-09-673-840A-322	Sequence 322, App
553	118	4.5	336	1	PCT-US03-28227-3937	Sequence 3937, Ap	626	111.5	4.3	597	20	US-09-674-266A-288	Sequence 288, App
554	117.5	4.5	362	22	US-09-791-537-131648	Sequence 131648,	627	111.5	4.3	616	1	PCT-US00-05918-663	Sequence 663, App
555	117	4.5	1846	1	PCT-US03-40978-1194	Sequence 1194, Ap	628	111.5	4.3	616	24	US-09-925-302-663	Sequence 663, App
556	117	4.5	1846	33	US-10-741-600-1194	Sequence 1194, Ap	629	111.5	4.3	630	20	US-09-611-502-3516	Sequence 3516, Ap
557	117	4.5	1846	35	US-10-932-349-2166	Sequence 2166, Ap	630	111.5	4.3	765	20	US-09-673-840A-420	Sequence 420, App
558	117	4.5	1846	37	US-60-500-337-2166	Sequence 2166, Ap	631	111.5	4.3	765	20	US-09-674-266A-628	Sequence 628, App
559	116.5	4.4	231	27	US-10-170-205B-5895	Sequence 5895, Ap	632	111.5	4.3	770	1	PCT-US01-16450-1991	Sequence 1991, Ap
560	116.5	4.4	343	1	PCT-US03-02500-51	Sequence 51, Appli	633	111.5	4.3	770	1	PCT-US01-16450A-1991	Sequence 1991, Ap
561	116.5	4.4	343	1	PCT-US03-28227-3944	Sequence 3944, Ap	634	111.5	4.3	770	28	US-10-264-237-1991	Sequence 1991, Ap
562	116.5	4.4	343	31	US-10-502-459-51	Sequence 51, Appli	635	111.5	4.3	1163	28	US-10-267-502-431	Sequence 431, App
563	116	4.4	329	1	PCT-US02-09107B-58022	Sequence 58022, A	636	111.5	4.3	1447	18	US-09-488-725A-2449	Sequence 2449, App
564	116	4.4	329	28	US-10-282-122A-58022	Sequence 58022, A	637	111.5	4.3	1447	28	US-10-258-898A-2449	Sequence 2449, Ap
565	116	4.4	334	30	US-10-417-884-6586	Sequence 6586, Ap	638	111.5	4.3	1447	28	US-10-286-897-2449	Sequence 2449, Ap
566	116	4.4	334	30	US-10-417-884A-6586	Sequence 6586, Ap	639	111.5	4.3	1466	18	US-09-488-725A-2448	Sequence 2448, Ap
567	116	4.4	475	21	US-09-708-427-63657	Sequence 63657, A	640	111.5	4.3	1466	28	US-10-258-898A-2448	Sequence 2448, Ap
568	115	4.4	461	28	US-10-219-999-32380	Sequence 32380, A	641	111.5	4.3	1466	28	US-10-286-897-2448	Sequence 2448, Ap
569	115	4.4	461	30	US-10-425-114-42127	Sequence 42127, A	642	111.5	4.3	1798	1	PCT-US02-19773-96	Sequence 96, Appli
570	115	4.4	461	30	US-10-425-114A-42127	Sequence 42127, A	643	111.5	4.3	1798	27	US-10-176-847-96	Sequence 96, Appli
571	115	4.4	461	37	US-60-324-109-17378	Sequence 17378, A	644	111.5	4.3	1811	1	PCT-US01-08631-39390	Sequence 39390, A
572	115	4.4	463	28	US-10-219-999-54490	Sequence 54490, A	645	111.5	4.3	1812	1	PCT-US01-14827-12208	Sequence 12208, A
573	115	4.4	463	30	US-10-425-114-62643	Sequence 62643, A	646	111.5	4.3	2048	35	US-10-941-087-264	Sequence 264, App
574	115	4.4	463	30	US-10-425-114A-62643	Sequence 62643, A	647	111.5	4.3	2048	37	US-60-570-505-478	Sequence 478, App
575	115	4.4	514	30	US-10-425-115-235840	Sequence 235840,	648	111.5	4.3	2048	37	US-60-576-801-384	Sequence 384, App
576	114.5	4.4	636	1	PCT-US02-09107B-69766	Sequence 69766, A	649	111.5	4.3	2048	37	US-60-592-189-43	Sequence 43, Appli
577	114.5	4.4	636	28	US-10-282-122A-69766	Sequence 69766, A	650	111.5	4.3	2048	37	US-60-625-562-183	Sequence 183, App
578	114	4.3	265	30	US-10-434-665-6459	Sequence 6459, Ap	651	111.5	4.3	2048	37	US-60-636-720-453	Sequence 453, App
579	114	4.3	803	32	US-10-603-114-4623	Sequence 4623, Ap	652	111.5	4.3	2057	1	PCT-US04-24001-830	Sequence 830, App
580	113.5	4.3	116	23	US-09-865-590A-18458	Sequence 18458, A	653	111.5	4.3	2057	33	US-10-719-993-830	Sequence 830, App

654	111.5	4.3	2057	35	US-10-912-745-260	Sequence 260, App	727	110	4.2	1104	37	US-60-500-337-2155	Sequence 2155, Ap
655	111.5	4.3	2057	35	US-10-912-745A-260	Sequence 260, App	728	110	4.2	1279	1	PCT-US03-40978-1191	Sequence 1191, Ap
656	111.5	4.3	2057	35	US-10-941-087-266	Sequence 266, App	729	110	4.2	1279	33	US-10-741-600-1191	Sequence 1191, Ap
657	111.5	4.3	2057	37	US-60-502-656-120	Sequence 120, App	730	110	4.2	1279	35	US-10-932-349-2163	Sequence 2163, Ap
658	111.5	4.3	2057	37	US-60-502-656A-120	Sequence 120, App	731	110	4.2	1279	37	US-60-500-337-2163	Sequence 2163, Ap
659	111.5	4.3	2057	37	US-60-512-690-389	Sequence 389, App	732	110	4.2	1821	37	US-60-248-798-212	Sequence 212, App
660	111.5	4.3	2057	37	US-60-519-832-389	Sequence 389, App	733	110	4.2	1845	1	PCT-US03-40978-1193	Sequence 1193, Ap
661	111.5	4.3	2057	37	US-60-530-410-163	Sequence 163, App	734	110	4.2	1845	1	PCT-US03-40978-1196	Sequence 1196, Ap
662	111.5	4.3	2057	37	US-60-552-390-389	Sequence 389, App	735	110	4.2	1845	33	US-10-741-600-1193	Sequence 1196, Ap
663	111.5	4.3	2057	37	US-60-570-505-480	Sequence 480, App	736	110	4.2	1845	33	US-10-741-600-1196	Sequence 1196, Ap
664	111.5	4.3	2057	37	US-60-576-801-386	Sequence 386, App	737	110	4.2	1845	35	US-10-932-349-2165	Sequence 2165, Ap
665	111.5	4.3	2057	37	US-60-592-189-45	Sequence 45, Appl	738	110	4.2	1845	35	US-10-932-349-2168	Sequence 2168, Ap
666	111.5	4.3	2057	37	US-60-625-562-185	Sequence 185, App	739	110	4.2	1845	37	US-60-500-337-2165	Sequence 2168, Ap
667	111.5	4.3	2057	37	US-60-636-720-455	Sequence 455, App	740	110	4.2	1845	37	US-60-500-337-2168	Sequence 2168, Ap
668	111.5	4.3	2060	27	US-10-144-779-539	Sequence 539, App	741	110	4.2	1914	1	PCT-US03-40978-1185	Sequence 1185, Ap
669	111.5	4.3	2061	1	PCT-US02-02781-181	Sequence 181, App	742	110	4.2	1914	1	PCT-US04-19485-11	Sequence 11, Appl
670	111.5	4.3	2061	1	PCT-US02-13392-1	Sequence 1, Appli	743	110	4.2	1914	22	US-09-791-537-35039	Sequence 35039, A
671	111.5	4.3	2061	1	PCT-US03-37143-232	Sequence 232, App	744	110	4.2	1914	22	US-10-741-600-1185	Sequence 1185, Ap
672	111.5	4.3	2061	26	US-10-060-036-181	Sequence 181, App	745	110	4.2	1914	33	US-10-756-149-5420	Sequence 5420, Ap
673	111.5	4.3	2061	26	US-10-087-192-486	Sequence 486, App	746	110	4.2	1914	33	US-10-932-349-2157	Sequence 2157, Ap
674	111.5	4.3	2061	27	US-10-170-205E-21130	Sequence 21130, A	747	110	4.2	1914	35	US-10-932-349-2157	Sequence 2157, Ap
675	111.5	4.3	2061	30	US-10-476-203-1	Sequence 1, Appli	748	110	4.2	1917	27	US-10-170-205E-26915	Sequence 26915, A
676	111.5	4.3	2061	35	US-10-941-087-265	Sequence 265, App	749	110	4.2	1917	37	US-60-453-050-10531	Sequence 10531, A
677	111.5	4.3	2061	37	US-60-452-680-23381	Sequence 23381, A	750	110	4.2	1917	37	US-60-453-135-10531	Sequence 10531, A
678	111.5	4.3	2061	37	US-60-461-762-555	Sequence 555, App	751	110	4.2	1917	37	US-60-466-412-10531	Sequence 10531, A
679	111.5	4.3	2061	37	US-60-470-166-1384	Sequence 1384, Ap	752	109.5	4.2	486	33	US-10-767-701-46096	Sequence 46096, A
680	111.5	4.3	2061	37	US-60-570-505-479	Sequence 479, App	753	109	4.2	279	1	PCT-US02-36123-1616	Sequence 1616, Ap
681	111.5	4.3	2061	37	US-60-576-801-385	Sequence 385, App	754	109	4.2	279	31	US-10-501-282-1616	Sequence 1616, Ap
682	111.5	4.3	2061	37	US-60-584-405-179	Sequence 179, App	755	109	4.2	290	29	US-10-366-683-19355	Sequence 19355, A
683	111.5	4.3	2061	37	US-60-592-189-44	Sequence 44, Appl	756	109	4.2	290	30	US-10-419-128-19355	Sequence 19355, A
684	111.5	4.3	2061	37	US-60-636-720-454	Sequence 184, App	757	109	4.2	414	1	PCT-US02-36123-5366	Sequence 5366, Ap
685	111.5	4.3	2061	37	US-09-606-740A-372	Sequence 454, App	758	109	4.2	414	31	US-10-501-282-5366	Sequence 5366, Ap
686	111	4.2	422	20	US-10-454-437-202	Sequence 202, App	759	108.5	4.1	95	23	US-09-867-550-42	Sequence 42, Appl
687	111	4.2	422	30	US-10-454-437A-202	Sequence 202, App	760	108.5	4.1	230	21	US-09-708-427-54389	Sequence 54389, A
688	111	4.2	422	30	US-10-454-437A-202	Sequence 202, App	761	108.5	4.1	1162	30	US-10-427-741-10	Sequence 10, Appl
689	111	4.2	1231	29	US-10-369-493-3503	Sequence 3503, Ap	762	108.5	4.1	1162	32	US-10-633-423-10	Sequence 10, Appl
690	111	4.2	1231	37	US-60-360-039-3503	Sequence 3503, Ap	763	108.5	4.1	1496	18	US-09-488-725A-2450	Sequence 2450, Ap
691	110.5	4.2	164	16	US-09-270-849B-179865	Sequence 179865, A	764	108.5	4.1	1496	28	US-10-258-898A-2450	Sequence 2450, Ap
692	110.5	4.2	401	20	US-09-614-150-13974	Sequence 13974, A	765	108.5	4.1	1496	28	US-10-286-897-2450	Sequence 2450, Ap
693	110.5	4.2	401	20	US-09-614-150A-13974	Sequence 13974, A	766	108	4.1	188	30	US-10-425-115-333475	Sequence 333475, A
694	110.5	4.2	401	37	US-60-173-464-11405	Sequence 11405, A	767	108	4.1	246	30	US-10-454-437-206	Sequence 206, App
695	110.5	4.2	401	37	US-60-191-637-14015	Sequence 14015, A	768	108	4.1	246	30	US-10-454-437A-206	Sequence 206, App
696	110.5	4.2	401	37	US-60-191-681-11036	Sequence 11036, A	769	108	4.1	741	18	US-09-417-507-30085	Sequence 30085, A
697	110.5	4.2	439	28	US-10-219-999-33394	Sequence 33394, A	770	108	4.1	991	22	US-09-791-537-30998	Sequence 30998, A
698	110.5	4.2	439	30	US-10-425-115-267724	Sequence 267724, A	771	107.5	4.1	379	30	US-10-417-884-5519	Sequence 5519, Ap
699	110.5	4.2	1478	28	US-10-219-051B-12365	Sequence 12365, A	772	107.5	4.1	379	30	US-10-417-884-5519	Sequence 5519, Ap
700	110.5	4.2	1478	28	US-10-240-154-10	Sequence 10, Appl	773	107	4.1	552	29	US-10-380-731-647	Sequence 647, App
701	110.5	4.2	1487	32	US-10-669-143-49	Sequence 49, Appl	774	107	4.1	552	30	US-10-405-027-5684	Sequence 5684, Ap
702	110.5	4.2	1488	28	US-10-219-051B-967	Sequence 967, App	775	107	4.1	552	30	US-10-405-027-5685	Sequence 5685, Ap
703	110.5	4.2	1488	28	US-10-219-051B-971	Sequence 971, App	776	106.5	4.1	225	33	US-10-767-795-117439	Sequence 117439, A
704	110.5	4.2	1488	28	US-10-219-051B-975	Sequence 975, App	777	106.5	4.1	321	1	PCT-US02-09107B-60897	Sequence 60897, A
705	110.5	4.2	1488	28	US-10-219-051B-979	Sequence 979, App	778	106.5	4.1	321	28	US-10-282-122A-60897	Sequence 60897, A
706	110	4.2	409	1	PCT-US03-30770-7	Sequence 7, Appli	779	106.5	4.1	553	25	US-09-958-460-4	Sequence 4, Appli
707	110	4.2	409	1	PCT-US03-30770-8	Sequence 8, Appli	780	106.5	4.1	553	25	US-09-958-460-4	Sequence 4, Appli
708	110	4.2	409	1	PCT-US03-30770-9	Sequence 9, Appli	781	106.5	4.1	553	34	US-10-898-142-4	Sequence 5, Appli
709	110	4.2	409	1	PCT-US03-30770-10	Sequence 10, Appl	782	106.5	4.1	565	31	US-10-506-454-531	Sequence 531, App
710	110	4.2	409	32	US-10-674-666-7	Sequence 7, Appli	783	106.5	4.1	565	37	US-60-361-742-531	Sequence 531, App
711	110	4.2	409	32	US-10-674-666-8	Sequence 8, Appli	784	106.5	4.1	1464	18	US-09-488-725A-6020	Sequence 6020, Ap
712	110	4.2	409	32	US-10-674-666-9	Sequence 9, Appli	785	106.5	4.1	1464	18	US-09-488-725A-6021	Sequence 6021, Ap
713	110	4.2	409	32	US-10-674-666-10	Sequence 10, Appl	786	106.5	4.1	1464	18	US-09-488-725A-6022	Sequence 6022, Ap
714	110	4.2	441	30	US-10-437-963-143921	Sequence 143921, A	787	106.5	4.1	1464	28	US-10-258-898A-6020	Sequence 6021, Ap
715	110	4.2	615	35	US-10-940-774-11320	Sequence 11320, A	788	106.5	4.1	1464	28	US-10-258-898A-6021	Sequence 6021, Ap
716	110	4.2	650	1	PCT-US02-09107B-76703	Sequence 76703, A	789	106.5	4.1	1464	28	US-10-258-898A-6022	Sequence 6022, Ap
717	110	4.2	650	22	US-09-791-537-60573	Sequence 60573, A	790	106.5	4.1	1464	28	US-10-286-897-6020	Sequence 6020, Ap
718	110	4.2	650	28	US-10-282-122A-76703	Sequence 76703, A	791	106.5	4.1	1464	28	US-10-286-897-6021	Sequence 6021, Ap
719	110	4.2	784	1	PCT-US03-40978-1189	Sequence 1189, Ap	792	106.5	4.1	1464	28	US-10-286-897-6022	Sequence 6022, Ap
720	110	4.2	784	33	US-10-741-600-1189	Sequence 1189, Ap	793	105.5	4.0	403	1	PCT-US02-03987-10282	Sequence 10282, A
721	110	4.2	784	35	US-10-932-349-2161	Sequence 2161, Ap	794	105.5	4.0	403	22	US-09-791-537-85005	Sequence 85005, A
722	110	4.2	784	37	US-60-500-337-2161	Sequence 2161, Ap	795	105.5	4.0	403	23	US-09-815-242-10282	Sequence 10282, A
723	110	4.2	991	37	US-60-556-903-278	Sequence 278, App	796	105.5	4.0	403	26	US-10-072-851-10282	Sequence 10282, A
724	110	4.2	1104	1	PCT-US03-40978-1183	Sequence 1183, Ap	797	105.5	4.0	498	19	US-09-540-209B-6264	Sequence 6264, Ap
725	110	4.2	1104	33	US-10-741-600-1183	Sequence 1183, Ap	798	105.5	4.0	583	1	PCT-US01-08631-39393	Sequence 39393, A
726	110	4.2	1104	35	US-10-932-349-2155	Sequence 2155, Ap	799	105.5	4.0	762	37	US-60-638-099-12107	Sequence 12107, A



800	105.5	4.0	1430	1	PCT-US01-08631-39391	Sequence 39391, A	873	102.5	3.9	762	37	US-60-638-099-19689	Sequence 19689, A
801	105.5	4.0	1430	1	PCT-US01-14827-12209	Sequence 12209, A	874	102.5	3.9	864	30	US-10-437-963-153309	Sequence 153309, A
802	105	4.0	552	1	PCT-US03-40701-8	Sequence 8, Appli	875	102.5	3.9	887	29	US-10-369-493-19640	Sequence 19640, A
803	105	4.0	641	32	US-10-679-063-8383	Sequence 8383, Ap	876	102.5	3.9	887	37	US-60-360-039-19640	Sequence 19640, A
804	105	4.0	1950	1	PCT-US04-14421-154	Sequence 154, App	877	102.5	3.9	1118	30	US-10-410-681-36	Sequence 36, Appl
805	105	4.0	1950	34	US-10-603-512-154	Sequence 154, App	878	102.5	3.9	1445	16	US-09-266-556-18	Sequence 18, Appl
806	104.5	4.0	383	32	US-10-603-114-7526	Sequence 7526, Ap	879	102.5	3.9	1446	20	US-09-611-529-4235	Sequence 4235, Ap
807	104.5	4.0	762	37	US-60-638-099-25483	Sequence 25483, A	880	102.5	3.9	1446	25	US-09-950-084-4235	Sequence 4235, Ap
808	104.5	4.0	851	1	PCT-US03-40618-7099	Sequence 7099, Ap	881	102	3.9	370	19	US-09-540-209B-9968	Sequence 9968, Ap
809	104.5	4.0	851	33	US-10-741-849-7099	Sequence 7099, Ap	882	102	3.9	381	37	US-60-638-099-32077	Sequence 32077, A
810	104.5	4.0	851	37	US-60-434-832-7099	Sequence 7099, Ap	883	102	3.9	383	21	US-09-708-427-31509	Sequence 31509, A
811	104.5	4.0	1115	21	US-09-708-427-4736	Sequence 4736, Ap	884	102	3.9	1738	1	PCT-US02-24459-100	Sequence 100, App
812	104.5	4.0	1145	21	US-09-708-427-4735	Sequence 4735, Ap	885	102	3.9	1738	28	US-10-210-130-100	Sequence 100, App
813	104.5	4.0	1218	21	US-09-708-427-4734	Sequence 4734, Ap	886	101.5	3.9	169	33	US-10-767-701-40542	Sequence 40542, A
814	104.5	4.0	1372	1	PCT-US01-08631-44913	Sequence 44913, A	887	101.5	3.9	629	22	US-09-791-537-3506	Sequence 3506, Ap
815	104.5	4.0	1378	1	PCT-US01-08631-54037	Sequence 54037, A	888	101.5	3.9	851	27	US-10-179-131-10162	Sequence 10162, A
816	104.5	4.0	1379	1	PCT-US01-08631-40616	Sequence 40616, A	889	101.5	3.9	1058	27	US-10-155-881-27878	Sequence 27878, A
817	104.5	4.0	1400	1	PCT-US01-08631-39510	Sequence 39510, A	890	101.5	3.9	1058	30	US-10-437-963-129864	Sequence 129864, A
818	104.5	4.0	1788	1	PCT-US01-08631-37108	Sequence 37108, A	891	101	3.9	353	30	US-10-431-652-5230	Sequence 5230, Ap
819	104.5	4.0	2048	30	US-10-408-765-1102	Sequence 1102, Ap	892	101	3.9	656	27	US-10-132-134-30	Sequence 30, Appl
820	104.5	4.0	2048	30	US-10-408-765A-1102	Sequence 1102, Ap	893	101	3.9	1087	30	US-10-449-902-45269	Sequence 45269, A
821	104.5	4.0	2048	37	US-60-389-987-1102	Sequence 1102, Ap	894	101	3.9	1403	30	US-10-437-963-137174	Sequence 137174, A
822	104.5	4.0	2048	37	US-60-412-418-1102	Sequence 1102, Ap	895	101	3.9	2116	33	US-10-732-923-20537	Sequence 20537, A
823	104.5	4.0	2563	1	PCT-US01-08631-45126	Sequence 45126, A	896	100.5	3.8	399	1	PCT-US02-09107B-61271	Sequence 61271, A
824	104	4.0	340	20	US-09-614-150-14721	Sequence 14721, A	897	100.5	3.8	399	28	US-10-282-122A-61271	Sequence 61271, A
825	104	4.0	340	20	US-09-614-150A-14721	Sequence 14721, A	898	100.5	3.8	417	21	US-09-724-676-49124	Sequence 49124, A
826	104	4.0	340	37	US-60-167-217-14800	Sequence 14800, A	899	100.5	3.8	417	21	US-09-724-676-49138	Sequence 49138, A
827	104	4.0	340	37	US-60-173-464-12035	Sequence 12035, A	900	100.5	3.8	417	21	US-09-724-676A-49124	Sequence 49124, A
828	104	4.0	340	37	US-60-191-637-14762	Sequence 14762, A	901	100.5	3.8	417	21	US-09-724-676A-49138	Sequence 49138, A
829	104	4.0	340	37	US-60-191-681-11633	Sequence 11633, A	902	100.5	3.8	548	33	US-10-767-701-44071	Sequence 44071, A
830	104	4.0	366	30	US-10-425-115-328817	Sequence 328817, A	903	100.5	3.8	623	30	US-10-472-928-3180	Sequence 3180, Ap
831	104	4.0	458	1	PCT-US02-32727-2506	Sequence 2506, Ap	904	100.5	3.8	623	30	US-10-474-776-352	Sequence 352, App
832	104	4.0	458	25	US-09-978-825-2506	Sequence 2506, Ap	905	100.5	3.8	648	29	US-10-369-493-20334	Sequence 20334, A
833	104	4.0	458	26	US-10-057-498-2506	Sequence 2506, Ap	906	100.5	3.8	648	37	US-60-360-039-20334	Sequence 20334, A
834	104	4.0	475	37	US-60-638-099-25148	Sequence 25148, A	907	100.5	3.8	656	29	US-10-369-493-1268	Sequence 1268, Ap
835	104	4.0	1155	1	PCT-US02-09107B-47116	Sequence 47116, A	908	100.5	3.8	656	37	US-60-360-039-1268	Sequence 1268, Ap
836	104	4.0	1155	28	US-10-282-122A-47116	Sequence 47116, A	909	100.5	3.8	731	33	US-10-732-923-23166	Sequence 23166, A
837	103.5	3.9	79	37	US-60-195-044-179	Sequence 179, App	910	100.5	3.8	731	37	US-60-592-978-13042	Sequence 13042, A
838	103.5	3.9	260	25	US-09-957-806A-16	Sequence 16, Appl	911	100.5	3.8	826	1	PCT-US01-03832-41	Sequence 41, Appl
839	103.5	3.9	546	34	US-10-821-234-902	Sequence 902, App	912	100.5	3.8	826	1	PCT-US03-04515-43	Sequence 43, Appl
840	103.5	3.9	578	30	US-10-469-204-162	Sequence 162, App	913	100.5	3.8	826	26	US-10-092-985-41	Sequence 41, Appl
841	103.5	3.9	805	30	US-10-485-517-297	Sequence 297, App	914	100.5	3.8	826	29	US-10-312-309-41	Sequence 41, Appl
842	103.5	3.9	932	1	PCT-US02-09107B-52510	Sequence 52510, A	915	100.5	3.8	826	35	US-10-927-620-41	Sequence 41, Appl
843	103.5	3.9	932	28	US-10-282-122A-52510	Sequence 52510, A	916	100.5	3.8	861	1	PCT-US04-07434-10	Sequence 10, Appl
844	103.5	3.9	1435	1	PCT-US99-01547-8	Sequence 8, Appli	917	100.5	3.8	872	1	PCT-US04-07434-82	Sequence 82, Appl
845	103.5	3.9	1435	16	US-09-235-245-8	Sequence 8, Appli	918	100.5	3.8	873	1	PCT-US04-07434-18	Sequence 18, Appl
846	103.5	3.9	1435	26	US-10-048-071-8	Sequence 8, Appli	919	100.5	3.8	877	1	PCT-US04-07434-76	Sequence 76, Appl
847	103.5	3.9	1435	28	US-10-282-287-8	Sequence 8, Appli	920	100.5	3.8	878	1	PCT-US04-07434-30	Sequence 30, Appl
848	103.5	3.9	1436	1	PCT-US02-03987-5566	Sequence 5566, Ap	921	100.5	3.8	889	1	PCT-US04-07434-142	Sequence 142, App
849	103.5	3.9	1436	23	US-09-815-242-5566	Sequence 5566, Ap	922	100.5	3.8	892	1	PCT-US04-07434-28	Sequence 28, Appl
850	103.5	3.9	1436	26	US-10-072-851-5566	Sequence 5566, Ap	923	100.5	3.8	894	1	PCT-US04-07434-130	Sequence 130, App
851	103.5	3.9	1436	37	US-60-242-578-895	Sequence 895, App	924	100.5	3.8	917	1	PCT-US04-07434-94	Sequence 94, Appl
852	103.5	3.9	1436	37	US-60-253-625-2239	Sequence 2239, Ap	925	100.5	3.8	934	1	PCT-US04-07434-138	Sequence 138, App
853	103.5	3.9	1436	37	US-60-257-931-3120	Sequence 3120, Ap	926	100.5	3.8	957	1	PCT-US04-07434-36	Sequence 36, Appl
854	103.5	3.9	1436	37	US-60-269-308-4142	Sequence 4142, Ap	927	100.5	3.8	968	1	PCT-US04-07434-110	Sequence 110, App
855	103.5	3.9	1438	1	PCT-US02-09107B-43797	Sequence 43797, A	928	100.5	3.8	973	1	PCT-US04-07434-98	Sequence 98, Appl
856	103.5	3.9	1438	28	US-10-282-122A-43797	Sequence 43797, A	929	100.5	3.8	992	1	PCT-US04-07434-42	Sequence 42, Appl
857	103.5	3.9	1438	34	US-10-857-625-641	Sequence 641, App	930	100.5	3.8	1003	1	PCT-US04-07434-126	Sequence 126, App
858	103.5	3.9	1438	37	US-60-474-768-641	Sequence 641, App	931	100.5	3.8	1008	1	PCT-US04-07434-114	Sequence 114, App
859	103.5	3.9	1442	1	PCT-US02-03987-12321	Sequence 12321, A	932	100.5	3.8	1013	1	PCT-US04-07434-106	Sequence 106, App
860	103.5	3.9	1442	23	US-09-815-242-12321	Sequence 12321, A	933	100.5	3.8	1040	1	PCT-US04-07434-88	Sequence 88, Appl
861	103.5	3.9	1442	26	US-10-072-851-12321	Sequence 12321, A	934	100.5	3.8	1048	1	PCT-US04-07434-122	Sequence 122, App
862	103	3.9	330	1	PCT-US02-09107B-56974	Sequence 56974, A	935	100.5	3.8	1100	1	PCT-US04-07434-48	Sequence 48, Appl
863	103	3.9	330	28	US-10-282-122A-56974	Sequence 56974, A	936	100.5	3.8	1127	1	PCT-US04-07434-134	Sequence 134, App
864	103	3.9	385	30	US-10-434-665-4952	Sequence 4952, Ap	937	100.5	3.8	1206	1	PCT-US04-07434-102	Sequence 102, App
865	103	3.9	444	32	US-10-679-063-6404	Sequence 6404, Ap	938	100.5	3.8	1241	1	PCT-US04-07434-118	Sequence 118, App
866	103	3.9	444	37	US-60-556-841-4887	Sequence 4887, Ap	939	100.5	3.8	1454	22	US-09-791-537-143886	Sequence 143886, A
867	103	3.9	470	30	US-10-425-115-355541	Sequence 355541, A	940	100.5	3.8	1473	26	US-10-037-417-112	Sequence 112, App
868	103	3.9	470	30	US-10-438-246-5797	Sequence 5797, Ap	941	100.5	3.8	1473	26	US-10-037-417-112	Sequence 112, App
869	103	3.9	809	32	US-10-603-114-6686	Sequence 6686, Ap	942	100.5	3.8	7465	37	US-60-556-841-7521	Sequence 7521, Ap
870	103	3.9	897	22	US-09-791-537-48740	Sequence 48740, A	943	100	3.8	273	21	US-09-708-427-18990	Sequence 18990, A
871	103	3.9	991	27	US-10-179-131-5951	Sequence 5951, A	944	100	3.8	282	21	US-09-708-427-18989	Sequence 18989, A
872	102.5	3.9	162	26	US-10-015-127-12167	Sequence 12167, A	945	100	3.8	462	21	US-09-708-427-18988	Sequence 18988, A



946	100	3.8	471	32	US-10-603-114-5705	Sequence 5705, Ap	1019	99	3.8	1913	22	US-09-791-537-120457	Sequence 120457,
947	100	3.8	528	22	US-09-760-443-1332	Sequence 1332, Ap	1020	98.5	3.8	440	27	US-10-170-205E-35414	Sequence 35414, A
948	100	3.8	528	28	US-10-212-054-1332	Sequence 1332, Ap	1021	98.5	3.8	440	37	US-60-452-680-20798	Sequence 20798, A
949	100	3.8	528	28	US-10-238-659-556	Sequence 556, App	1022	98.5	3.8	440	37	US-60-461-762-417	Sequence 417, App
950	100	3.8	612	30	US-10-449-902-36770	Sequence 36770, A	1023	98.5	3.8	440	37	US-60-470-166-1088	Sequence 1088, Ap
951	100	3.8	612	30	US-10-449-902-50163	Sequence 50163, A	1024	98.5	3.8	506	27	US-10-170-205E-35037	Sequence 35037, A
952	100	3.8	612	30	US-10-449-902-54750	Sequence 54750, A	1025	98.5	3.8	506	37	US-60-452-680-20797	Sequence 20797, A
953	100	3.8	613	22	US-09-791-537-109700	Sequence 109700,	1026	98.5	3.8	506	37	US-60-461-762-416	Sequence 416, App
954	100	3.8	809	30	US-10-437-963-149905	Sequence 149905,	1027	98.5	3.8	506	37	US-60-470-166-1087	Sequence 1087, Ap
955	100	3.8	1028	32	US-10-679-063-14068	Sequence 14068, A	1028	98.5	3.8	573	1	PCT-US02-36123-5274	Sequence 5274, Ap
956	100	3.8	1028	37	US-60-638-099-21262	Sequence 21262, A	1029	98.5	3.8	573	31	US-10-501-282-5274	Sequence 5274, Ap
957	100	3.8	1769	1	PCT-US04-24001-831	Sequence 831, App	1030	98.5	3.8	580	1	PCT-US02-36123-5276	Sequence 5276, Ap
958	100	3.8	1769	33	US-10-719-993-831	Sequence 831, App	1031	98.5	3.8	580	31	US-10-501-282-5276	Sequence 5276, Ap
959	100	3.8	1769	35	US-10-912-745-259	Sequence 259, App	1032	98.5	3.8	603	1	PCT-US02-36123-5278	Sequence 5278, Ap
960	100	3.8	1769	35	US-10-912-745A-259	Sequence 259, App	1033	98.5	3.8	603	31	US-10-501-282-5278	Sequence 5278, Ap
961	100	3.8	1769	35	US-10-941-087-263	Sequence 263, App	1034	98.5	3.8	609	1	PCT-US02-36123-5280	Sequence 5280, Ap
962	100	3.8	1769	37	US-60-502-656-119	Sequence 119, App	1035	98.5	3.8	609	31	US-10-501-282-5280	Sequence 5280, Ap
963	100	3.8	1769	37	US-60-502-656A-119	Sequence 119, App	1036	98.5	3.8	697	30	US-10-425-115-255466	Sequence 255466,
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965	100	3.8	1769	37	US-60-519-832-388	Sequence 388, App	1038	98.5	3.8	829	29	US-10-369-493-4177	Sequence 4177, Ap
966	100	3.8	1769	37	US-60-530-410-162	Sequence 162, App	1039	98.5	3.8	829	37	US-60-360-039-4177	Sequence 4177, Ap
967	100	3.8	1769	37	US-60-552-390-388	Sequence 388, App	1040	98.5	3.8	873	22	US-09-791-537-25715	Sequence 25715, A
968	100	3.8	1769	37	US-60-570-505-477	Sequence 477, App	1041	98.5	3.8	1923	1	PCT-US01-08656-8541	Sequence 8541, Ap
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971	100	3.8	1769	37	US-60-636-720-523	Sequence 523, App	1044	98.5	3.8	3114	28	US-10-273-573-8546	Sequence 8546, Ap
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973	99.5	3.8	370	22	US-09-791-537-93365	Sequence 93365, A	1046	98.5	3.8	3418	14	US-09-084-471A-13	Sequence 13, Appli
974	99.5	3.8	437	33	US-10-732-923-18655	Sequence 18655, A	1047	98.5	3.8	3418	14	US-09-084-471C-9	Sequence 9, Appli
975	99.5	3.8	437	37	US-60-581-351-6078	Sequence 6078, Ap	1048	98.5	3.8	3418	14	US-09-084-471C-13	Sequence 13, Appli
976	99.5	3.8	437	37	US-60-592-978-21237	Sequence 21237, A	1049	98.5	3.8	3418	14	US-09-084-471D-9	Sequence 9, Appli
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979	99.5	3.8	622	1	PCT-US03-28227-4361	Sequence 4361, Ap	1052	98.5	3.8	4167	28	US-10-273-573-8545	Sequence 8545, Ap
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981	99.5	3.8	653	37	US-60-360-039-21645	Sequence 21645, A	1054	98	3.7	475	37	US-60-638-099-19321	Sequence 19321, A
982	99.5	3.8	807	1	PCT-US01-08631-45311	Sequence 45311, A	1055	98	3.7	477	34	US-10-812-829-629	Sequence 629, App
983	99.5	3.8	1190	22	US-09-791-537-73287	Sequence 73287, A	1056	98	3.7	477	37	US-60-581-351-12786	Sequence 12786, A
984	99	3.8	319	19	US-09-513-996A-63543	Sequence 63543, A	1057	98	3.7	477	37	US-60-638-099-16807	Sequence 16807, A
985	99	3.8	511	27	US-11-001-793-7970	Sequence 7970, Ap	1058	98	3.7	502	37	US-60-382-898-383	Sequence 383, App
986	99	3.8	511	36	US-10-100-683-7970	Sequence 7970, Ap	1059	98	3.7	895	30	US-10-446-203-12499	Sequence 12499, A
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988	99	3.8	587	32	US-10-679-063-21950	Sequence 21950, A	1061	98	3.7	1703	1	PCT-US02-17443-168	Sequence 168, App
989	99	3.8	1031	30	US-10-410-681-40	Sequence 40, Appl	1062	98	3.7	1703	27	US-10-160-619-168	Sequence 168, App
990	99	3.8	1275	1	PCT-US03-17408-167	Sequence 167, App	1063	98	3.7	2111	37	US-60-638-099-32812	Sequence 32812, A
991	99	3.8	1275	22	US-09-791-537-33117	Sequence 33117, A	1064	97.5	3.7	390	21	US-09-739-449-10005	Sequence 10005, A
992	99	3.8	1275	30	US-10-452-024-167	Sequence 167, App	1065	97.5	3.7	390	23	US-09-803-110-10005	Sequence 10005, A
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994	99	3.8	1276	1	PCT-US03-17408-164	Sequence 164, App	1067	97.5	3.7	402	22	US-09-791-537-79658	Sequence 79658, A
995	99	3.8	1276	1	PCT-US03-17408-168	Sequence 168, App	1068	97.5	3.7	402	28	US-10-282-122A-58973	Sequence 58973, A
996	99	3.8	1276	1	PCT-US97-15394-66	Sequence 66, Appl	1069	97.5	3.7	402	37	US-60-581-351-9620	Sequence 9620, Ap
997	99	3.8	1276	11	US-08-704-159-66	Sequence 66, Appl	1070	97.5	3.7	462	29	US-10-366-683-28292	Sequence 28292, A
998	99	3.8	1276	19	US-09-547-188-8	Sequence 8, Appli	1071	97.5	3.7	462	30	US-10-419-128-28292	Sequence 28292, A
999	99	3.8	1276	22	US-09-791-537-13527	Sequence 13527, A	1072	97.5	3.7	482	37	US-60-638-099-17620	Sequence 17620, A
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1007	99	3.8	1276	30	US-10-452-024-168	Sequence 168, App	1080	97.5	3.7	587	21	US-09-724-676A-71950	Sequence 71947, A
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1015	99	3.8	1286	28	US-10-205-516A-22	Sequence 22, Appl	1088	97.5	3.7	656	21	US-09-724-676A-71954	Sequence 71954, A
1016	99	3.8	1610	1	PCT-US04-10077-15	Sequence 15, Appl	1089	97.5	3.7	656	21	US-09-724-676A-71954	Sequence 71954, A
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1093	97.5	3.7	674	29	US-10-352-843-11	Sequence 11, Appl	1166	96	3.7	485	37	US-60-360-039-17171	Sequence 17171, A
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1099	97.5	3.7	852	21	US-09-724-676-71948	Sequence 71951, A	1172	96	3.7	896	24	US-09-923-563A-1	Sequence 1, Appli
1100	97.5	3.7	863	21	US-09-724-676-71948	Sequence 71948, A	1173	96	3.7	1209	30	US-10-425-115-270046	Sequence 270046, A
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1102	97.5	3.7	896	21	US-09-724-676-71953	Sequence 71953, A	1175	96	3.7	1267	25	US-09-978-825-15633	Sequence 15633, A
1103	97.5	3.7	896	21	US-09-724-676A-71953	Sequence 71953, A	1176	96	3.7	1267	26	US-10-057-498-15633	Sequence 15633, A
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1105	97.5	3.7	952	19	US-09-573-655A-1879	Sequence 1758, Ap	1178	96	3.7	1448	1	PCT-US02-03987-15396	Sequence 15396, A
1106	97.5	3.7	952	19	US-09-573-655B-1758	Sequence 1879, Ap	1179	96	3.7	1448	26	US-10-032-585-7452	Sequence 7452, Ap
1107	97.5	3.7	952	19	US-09-573-655B-1879	Sequence 1879, Ap	1180	96	3.7	1448	26	US-10-072-851-15396	Sequence 15396, A
1108	97.5	3.7	981	30	US-10-431-652-4484	Sequence 4484, Ap	1181	96	3.7	1448	37	US-60-314-050-7452	Sequence 7452, Ap
1109	97.5	3.7	2000	29	US-10-326-956-853	Sequence 853, App	1182	96	3.7	1699	34	US-10-842-313-8	Sequence 8, Appli
1110	97.5	3.7	2672	32	US-10-679-063-25458	Sequence 25458, A	1183	96	3.7	1699	37	US-60-469-894-8	Sequence 8, Appli
1111	97	3.7	371	30	US-10-408-765-1330	Sequence 1330, Ap	1184	96	3.7	1707	1	PCT-US03-09921-17	Sequence 17, Appl
1112	97	3.7	371	30	US-10-408-765A-1330	Sequence 1330, Ap	1185	96	3.7	1707	27	US-10-167-631A-2	Sequence 2, Appli
1113	97	3.7	371	37	US-60-389-987-1330	Sequence 1330, Ap	1186	96	3.7	1707	30	US-10-467-685-10	Sequence 10, Appl
1114	97	3.7	371	37	US-60-412-418-1330	Sequence 1330, Ap	1187	96	3.7	1707	31	US-10-509-853-17	Sequence 17, Appl
1115	97	3.7	396	26	US-10-015-127-10960	Sequence 10960, A	1188	96	3.7	1709	34	US-10-842-313-2	Sequence 2, Appli
1116	97	3.7	611	32	US-10-679-063-9379	Sequence 9379, Ap	1189	96	3.7	1709	37	US-60-469-894-2	Sequence 2, Appli
1117	97	3.7	727	37	US-60-581-351-11826	Sequence 11826, A	1190	96	3.7	1711	34	US-10-842-313-10	Sequence 10, Appl
1118	97	3.7	730	30	US-10-437-963-164068	Sequence 164068, A	1191	96	3.7	1711	37	US-60-469-894-10	Sequence 10, Appl
1119	97	3.7	773	33	US-10-732-923-23195	Sequence 23195, A	1192	96	3.7	1721	34	US-10-842-313-4	Sequence 4, Appli
1120	97	3.7	773	37	US-60-592-978-9459	Sequence 9459, Ap	1193	96	3.7	1721	34	US-10-842-313-6	Sequence 6, Appli
1121	97	3.7	3034	23	US-09-897-516-4393	Sequence 4393, Ap	1194	96	3.7	1721	37	US-60-469-894-4	Sequence 4, Appli
1122	97	3.7	3034	23	US-09-897-516A-4399	Sequence 4399, Ap	1195	96	3.7	1721	37	US-60-469-894-6	Sequence 6, Appli
1123	97	3.7	3034	37	US-60-215-161-4393	Sequence 4393, Ap	1196	96	3.7	1734	34	US-10-842-313-12	Sequence 12, Appl
1124	97	3.7	4746	29	US-10-369-493-433	Sequence 433, App	1197	96	3.7	1734	37	US-60-469-894-12	Sequence 12, Appl
1125	97	3.7	4746	37	US-60-360-039-433	Sequence 433, App	1198	96	3.7	1990	27	US-10-144-779-402	Sequence 402, App
1126	96.5	3.7	421	1	PCT-US02-09107B-51099	Sequence 51099, A	1199	95.5	3.6	325	22	US-09-791-537-105551	Sequence 105551, A
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1128	96.5	3.7	498	37	US-60-571-854-76	Sequence 76, Appl	1201	95.5	3.6	479	32	US-10-679-063-21523	Sequence 21523, A
1129	96.5	3.7	560	30	US-10-415-302-2	Sequence 2, Appli	1202	95.5	3.6	479	37	US-60-592-978-3592	Sequence 3592, Ap
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1131	96.5	3.7	560	30	US-10-415-302-16	Sequence 16, Appl	1204	95.5	3.6	506	1	PCT-US02-38407-32	Sequence 32, Appl
1132	96.5	3.7	761	1	PCT-US04-21492-146	Sequence 146, App	1205	95.5	3.6	506	29	US-10-308-448-32	Sequence 32, Appl
1133	96.5	3.7	761	1	PCT-US04-21492A-146	Sequence 146, App	1206	95.5	3.6	508	29	US-10-369-493-8410	Sequence 8410, Ap
1134	96.5	3.7	1622	1	PCT-US02-09107B-63833	Sequence 63833, A	1207	95.5	3.6	508	37	US-60-360-039-8410	Sequence 8410, Ap
1135	96.5	3.7	1622	26	US-10-080-170-154	Sequence 154, App	1208	95.5	3.6	565	37	US-60-638-099-44691	Sequence 44691, A
1136	96.5	3.7	1622	28	US-10-282-122A-63833	Sequence 63833, A	1209	95.5	3.6	727	24	US-09-935-625-26480	Sequence 26480, A
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1138	96.5	3.7	4551	17	US-09-320-878-1	Sequence 1, Appli	1211	95.5	3.6	758	18	US-09-468-646B-31	Sequence 31, Appl
1139	96.5	3.7	4551	22	US-09-793-708-1	Sequence 1, Appli	1212	95.5	3.6	758	18	US-09-468-646C-31	Sequence 31, Appl
1140	96.5	3.7	4551	27	US-10-160-539-1	Sequence 1, Appli	1213	95.5	3.6	766	24	US-09-935-625-26479	Sequence 26479, A
1141	96.5	3.7	4551	27	US-10-160-539A-1	Sequence 1, Appli	1214	95.5	3.6	809	22	US-09-791-537-7538	Sequence 7538, Ap
1142	96.5	3.7	4551	28	US-10-201-365-2	Sequence 2, Appli	1215	95.5	3.6	812	24	US-09-935-625-26478	Sequence 26478, A
1143	96.5	3.7	4551	30	US-10-468-828-1	Sequence 1, Appli	1216	95.5	3.6	866	26	US-10-078-725-135	Sequence 135, App
1144	96.5	3.7	4613	23	US-09-836-821-31	Sequence 31, Appl	1217	95.5	3.6	866	37	US-60-270-153-135	Sequence 135, App
1145	96.5	3.7	4613	23	US-09-860-846-31	Sequence 31, Appl	1218	95.5	3.6	944	21	US-09-708-427-30680	Sequence 30680, A
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1152	96.5	3.7	11877	23	US-09-860-846-6	Sequence 6, Appli	1225	95.5	3.6	1043	37	US-60-243-468-1341	Sequence 1341, Ap
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1157	96	3.7	313	32	US-10-679-063-5549	Sequence 5549, Ap	1230	95.5	3.6	1620	1	PCT-US01-08656-10983	Sequence 10983, A
1158	96	3.7	313	37	US-60-556-841-3451	Sequence 3451, Ap	1231	95.5	3.6	1620	28	US-10-273-573-10983	Sequence 10983, A
1159	96	3.7	327	32	US-10-679-063-18802	Sequence 18802, A	1232	95.5	3.6	1733	37	US-60-638-099-39140	Sequence 39140, A
1160	96	3.7	334	22	US-09-791-537-2750	Sequence 2750, Ap	1233	95.5	3.6	1733	37	US-60-638-099-42756	Sequence 42756, A
1161	96	3.7	338	37	US-60-258-275-465	Sequence 465, App	1234	95	3.6	405	33	US-10-767-795-79038	Sequence 79038, A
1162	96	3.7	381	37	US-60-638-099-44508	Sequence 44508, A	1235	95	3.6	408	14	US-09-023-809-3	Sequence 3, Appli
1163	96	3.7	477	37	US-60-581-351-12707	Sequence 12707, A	1236	95	3.6	408	14	US-09-023-809-3	Sequence 3, Appli
1164	96	3.7	477	37	US-60-638-099-19172	Sequence 19172, A	1237	95	3.6	409	1	PCT-US01-14116-1	Sequence 1, Appli



1238	95	3.6	409	1	PCT-US01-14116-3	Sequence 3, Appli	1311	94.5	3.6	566	22	US-09-791-537-120473	Sequence 120473,
1239	95	3.6	409	1	PCT-US01-14116-4	Sequence 4, Appli	1312	94.5	3.6	568	21	US-09-708-427-2600	Sequence 2600, Ap
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1242	95	3.6	409	1	PCT-US03-30770-3	Sequence 3, Appli	1315	94.5	3.6	662	29	US-10-369-493-22747	Sequence 22747, A
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1246	95	3.6	409	32	US-10-645-723-3	Sequence 3, Appli	1319	94.5	3.6	787	28	US-10-282-122A-64434	Sequence 64434, A
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1273	95	3.6	851	33	US-10-760-620A-4110	Sequence 4110, Ap	1346	94	3.6	431	21	US-09-708-427-7380	Sequence 7380, Ap
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1279	95	3.6	876	37	US-60-474-768-697	Sequence 697, App	1352	94	3.6	639	26	US-10-072-851-15475	Sequence 15475, A
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1283	95	3.6	1256	37	US-60-096-409-18057	Sequence 18057, A	1356	94	3.6	733	22	US-09-791-537-131115	Sequence 131115,
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1289	95	3.6	2110	37	US-60-638-099-23613	Sequence 23613, A	1362	94	3.6	823	26	US-10-092-411A-4081	Sequence 4081, Ap
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1291	95	3.6	2249	37	US-60-229-514-52	Sequence 52, Appl	1364	94	3.6	823	35	US-10-902-441-4081	Sequence 4081, Ap
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1293	94.5	3.6	172	26	US-10-092-411A-3427	Sequence 3427, Ap	1366	94	3.6	876	22	US-09-791-537-25350	Sequence 25350, A
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1299	94.5	3.6	371	29	US-10-335-977-6819	Sequence 6819, Ap	1372	94	3.6	1028	33	US-10-732-923-13674	Sequence 13674, A
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1301	94.5	3.6	402	12	US-08-892-020-204	Sequence 204, App	1374	94	3.6	1053	18	US-09-465-110A-3	Sequence 3, Appli
1302	94.5	3.6	402	13	US-08-993-002A-6820	Sequence 6820, App	1375	94	3.6	1053	22	US-09-791-537-118398	Sequence 118398,
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1306	94.5	3.6	402	29	US-10-335-977-6820	Sequence 6820, Ap	1379	94	3.6	1331	22	US-09-791-537-144550	Sequence 144550,
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1308	94.5	3.6	424	21	US-09-708-427-2601	Sequence 2601, Ap	1381	94	3.6	1347	37	US-60-212-656-478	Sequence 478, App
1309	94.5	3.6	474	30	US-10-424-599-254116	Sequence 254116,	1382	94	3.6	1371	37	US-60-230-435-1399	Sequence 1399, Ap
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1384	94	3.6	1546	37	US-60-360-039-543	Sequence 543, App	1457	93	3.5	255	26	US-10-031-915-47	Sequence 47, Appl
1385	93.5	3.6	307	21	US-09-708-427-31511	Sequence 31511, A	1458	93	3.5	255	33	US-10-732-923-1544	Sequence 1544, Ap
1386	93.5	3.6	313	21	US-09-708-427-31510	Sequence 31510, A	1459	93	3.5	255	35	US-10-959-539-47	Sequence 47, Appl
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1388	93.5	3.6	431	1	PCT-US03-40701-11	Sequence 11, Appl	1461	93	3.5	373	37	US-60-096-409-19382	Sequence 19382, A
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1392	93.5	3.6	535	18	US-09-450-969-3956	Sequence 3956, Ap	1465	93	3.5	484	22	US-09-791-537-114236	Sequence 114236, A
1393	93.5	3.6	535	26	US-10-092-411A-3338	Sequence 3338, Ap	1466	93	3.5	487	27	US-10-156-761-11764	Sequence 11764, A
1394	93.5	3.6	535	33	US-10-724-972A-3956	Sequence 3956, Ap	1467	93	3.5	515	1	PCT-US03-28227-2871	Sequence 2871, Ap
1395	93.5	3.6	535	35	US-10-902-441-3338	Sequence 3338, Ap	1468	93	3.5	554	22	US-09-791-537-37361	Sequence 37361, A
1396	93.5	3.6	574	37	US-60-638-099-27684	Sequence 27684, A	1469	93	3.5	588	1	PCT-US02-09107B-67147	Sequence 67147, A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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6	432.5	16.5	457	7	US-11-028-169-4829	Sequence 4829, Ap
7	432.5	16.5	457	7	US-11-028-204-4829	Sequence 4829, Ap
8	432.5	16.5	457	7	US-11-027-877-4829	Sequence 4829, Ap
9	432.5	16.5	457	7	US-11-027-879-4829	Sequence 4829, Ap
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111	89	3.4	353	7	US-11-031-175-10913	Sequence 10913, A	184	81.5	3.1	2138	7	US-11-028-149-5274	Sequence 5274, Ap
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143	84.5	3.2	332	7	US-11-028-197-4063	Sequence 4063, Ap	216	81	3.1	1203	7	US-11-028-291-3634	Sequence 3634, Ap
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157	83.5	3.2	1063	6	US-10-450-763-43038	Sequence 43038, A	230	80.5	3.1	464	7	US-11-028-099-3968	Sequence 3968, Ap
158	83	3.2	407	7	US-11-031-175-15171	Sequence 15171, A	231	80.5	3.1	464	7	US-11-028-197-3968	Sequence 3968, Ap
159	82.5	3.1	461	6	US-10-450-763-32866	Sequence 32866, A	232	80.5	3.1	464	7	US-11-027-844-3968	Sequence 3968, Ap
160	82.5	3.1	1366	6	US-10-489-448-1092	Sequence 1092, Ap	233	80.5	3.1	464	7	US-11-028-050-3968	Sequence 3968, Ap
161	82	3.1	311	6	US-10-450-763-31532	Sequence 31532, A	234	80.5	3.1	464	7	US-11-027-877-3968	Sequence 3968, Ap
162	82	3.1	337	6	US-10-450-763-42053	Sequence 42053, A	235	80.5	3.1	464	7	US-11-028-457-3968	Sequence 3968, Ap
163	82	3.1	337	6	US-10-450-763-43255	Sequence 43255, A	236	80.5	3.1	464	7	US-11-027-891-3968	Sequence 3968, Ap
164	82	3.1	337	6	US-10-450-763-45791	Sequence 45791, A	237	80.5	3.1	464	7	US-11-028-291-3968	Sequence 3968, Ap
165	82	3.1	543	6	US-10-450-763-40661	Sequence 40661, A	238	80.5	3.1	655	6	US-10-450-763-41563	Sequence 41563, A
166	82	3.1	629	6	US-10-450-763-49213	Sequence 49213, A	239	80.5	3.1	707	7	US-11-031-175-16063	Sequence 16063, A
167	82	3.1	881	6	US-10-450-763-35639	Sequence 35639, A	240	80.5	3.1	845	1	PCT-US04-09510-605	Sequence 605, App
168	82	3.1	881	6	US-10-450-763-50617	Sequence 50617, A	241	80	3.0	1797	6	US-10-450-763-44239	Sequence 44239, A
169	82	3.1	1158	6	US-10-450-763-52710	Sequence 52710, A	242	80	3.0	338	6	US-10-450-763-38489	Sequence 38489, A
170	81.5	3.1	238	6	US-10-450-763-49622	Sequence 49622, A	243	80	3.0	552	6	US-10-494-853-1	Sequence 1, Appli
171	81.5	3.1	335	7	US-11-031-175-12406	Sequence 12406, A	244	80	3.0	587	7	US-11-027-399-4237	Sequence 4237, Ap
										587	7	US-11-027-843-4237	Sequence 4237, Ap

245	80	3.0	587	7	US-11-027-878-4237	Sequence 4237, Ap	318	79	3.0	1554	6	US-10-450-763-37647	Sequence 37647, A
246	80	3.0	587	7	US-11-028-169-4237	Sequence 4237, Ap	319	79	3.0	1584	6	US-10-450-763-37649	Sequence 37649, A
247	80	3.0	587	7	US-11-028-204-4237	Sequence 4237, Ap	320	79	3.0	1627	6	US-10-450-763-36476	Sequence 36476, A
248	80	3.0	587	7	US-11-027-877-4237	Sequence 4237, Ap	321	79	3.0	1634	5	US-09-896-923B-74	Sequence 74, Appl
249	80	3.0	587	7	US-11-027-879-4237	Sequence 4237, Ap	322	79	3.0	1735	7	US-11-031-175-14547	Sequence 14547, A
250	80	3.0	587	7	US-11-028-149-4237	Sequence 4237, Ap	323	78.5	3.0	446	7	US-11-027-399-4349	Sequence 4349, Ap
251	80	3.0	587	7	US-11-027-802-4237	Sequence 4237, Ap	324	78.5	3.0	446	7	US-11-027-843-4349	Sequence 4349, Ap
252	80	3.0	587	7	US-11-027-890-4237	Sequence 4237, Ap	325	78.5	3.0	446	7	US-11-027-878-4349	Sequence 4349, Ap
253	80	3.0	587	7	US-11-027-892-4237	Sequence 4237, Ap	326	78.5	3.0	446	7	US-11-028-169-4349	Sequence 4349, Ap
254	80	3.0	587	7	US-11-028-099-4237	Sequence 4237, Ap	327	78.5	3.0	446	7	US-11-028-204-4349	Sequence 4349, Ap
255	80	3.0	587	7	US-11-028-197-4237	Sequence 4237, Ap	328	78.5	3.0	446	7	US-11-027-877-4349	Sequence 4349, Ap
256	80	3.0	587	7	US-11-027-844-4237	Sequence 4237, Ap	329	78.5	3.0	446	7	US-11-027-879-4349	Sequence 4349, Ap
257	80	3.0	587	7	US-11-028-050-4237	Sequence 4237, Ap	330	78.5	3.0	446	7	US-11-027-879-4349	Sequence 4349, Ap
258	80	3.0	587	7	US-11-028-457-4237	Sequence 4237, Ap	331	78.5	3.0	446	7	US-11-028-149-4349	Sequence 4349, Ap
259	80	3.0	587	7	US-11-027-891-4237	Sequence 4237, Ap	332	78.5	3.0	446	7	US-11-027-802-4349	Sequence 4349, Ap
260	80	3.0	587	7	US-11-028-291-4237	Sequence 4237, Ap	333	78.5	3.0	446	7	US-11-027-892-4349	Sequence 4349, Ap
261	80	3.0	815	6	US-10-450-763-35517	Sequence 35517, A	334	78.5	3.0	446	7	US-11-028-099-4349	Sequence 4349, Ap
262	80	3.0	815	6	US-10-450-763-36119	Sequence 36119, A	335	78.5	3.0	446	7	US-11-028-197-4349	Sequence 4349, Ap
263	80	3.0	815	6	US-10-450-763-38514	Sequence 38514, A	336	78.5	3.0	446	7	US-11-027-844-4349	Sequence 4349, Ap
264	80	3.0	913	6	US-10-450-763-32820	Sequence 32820, A	337	78.5	3.0	446	7	US-11-028-050-4349	Sequence 4349, Ap
265	80	3.0	1204	7	US-11-027-399-4083	Sequence 4083, Ap	338	78.5	3.0	446	7	US-11-028-457-4349	Sequence 4349, Ap
266	80	3.0	1204	7	US-11-027-843-4083	Sequence 4083, Ap	339	78.5	3.0	446	7	US-11-027-891-4349	Sequence 4349, Ap
267	80	3.0	1204	7	US-11-027-878-4083	Sequence 4083, Ap	340	78.5	3.0	446	7	US-11-027-891-4349	Sequence 4349, Ap
268	80	3.0	1204	7	US-11-028-169-4083	Sequence 4083, Ap	341	78.5	3.0	551	6	US-10-450-763-39720	Sequence 39720, A
269	80	3.0	1204	7	US-11-028-204-4083	Sequence 4083, Ap	342	78.5	3.0	564	1	PCT-US04-42360-2585	Sequence 2585, Ap
270	80	3.0	1204	7	US-11-027-877-4083	Sequence 4083, Ap	343	78.5	3.0	583	6	US-10-450-763-40632	Sequence 40632, A
271	80	3.0	1204	7	US-11-027-879-4083	Sequence 4083, Ap	344	78.5	3.0	627	6	US-10-450-763-34421	Sequence 34421, A
272	80	3.0	1204	7	US-11-028-149-4083	Sequence 4083, Ap	345	78.5	3.0	668	7	US-11-031-175-14244	Sequence 14244, A
273	80	3.0	1204	7	US-11-027-802-4083	Sequence 4083, Ap	346	78.5	3.0	699	7	US-11-021-951-23	Sequence 23, Appl
274	80	3.0	1204	7	US-11-027-890-4083	Sequence 4083, Ap	347	78.5	3.0	757	7	US-11-031-206-184	Sequence 184, App
275	80	3.0	1204	7	US-11-027-892-4083	Sequence 4083, Ap	348	78.5	3.0	810	6	US-10-450-763-58214	Sequence 58214, A
276	80	3.0	1204	7	US-11-028-099-4083	Sequence 4083, Ap	349	78.5	3.0	840	1	PCT-US04-09510-606	Sequence 606, App
277	80	3.0	1204	7	US-11-028-197-4083	Sequence 4083, Ap	350	78.5	3.0	1058	6	US-10-450-763-49403	Sequence 49403, A
278	80	3.0	1204	7	US-11-027-844-4083	Sequence 4083, Ap	351	78.5	3.0	1092	7	US-11-023-584-4	Sequence 4, Appli
279	80	3.0	1204	7	US-11-028-050-4083	Sequence 4083, Ap	352	78.5	3.0	1213	6	US-10-450-763-52167	Sequence 52167, A
280	80	3.0	1204	7	US-11-028-457-4083	Sequence 4083, Ap	353	78.5	3.0	4292	6	US-10-450-763-47419	Sequence 47419, A
281	80	3.0	1204	7	US-11-027-891-4083	Sequence 4083, Ap	354	78	3.0	272	7	US-11-027-399-3866	Sequence 3866, Ap
282	80	3.0	1204	7	US-11-028-291-4083	Sequence 4083, Ap	355	78	3.0	272	7	US-11-027-843-3866	Sequence 3866, Ap
283	80	3.0	1330	6	US-10-450-763-54792	Sequence 54792, A	356	78	3.0	272	7	US-11-027-878-3866	Sequence 3866, Ap
284	79.5	3.0	470	6	US-10-450-763-37655	Sequence 37655, A	357	78	3.0	272	7	US-11-028-169-3866	Sequence 3866, Ap
285	79.5	3.0	470	6	US-10-450-763-56863	Sequence 56863, A	358	78	3.0	272	7	US-11-028-204-3866	Sequence 3866, Ap
286	79.5	3.0	511	7	US-11-031-175-10893	Sequence 10893, A	359	78	3.0	272	7	US-11-027-877-3866	Sequence 3866, Ap
287	79.5	3.0	578	6	US-10-450-763-59033	Sequence 59033, A	360	78	3.0	272	7	US-11-027-879-3866	Sequence 3866, Ap
288	79.5	3.0	863	1	PCT-US05-01273-37	Sequence 37, Appl	361	78	3.0	272	7	US-11-028-149-3866	Sequence 3866, Ap
289	79.5	3.0	863	7	US-11-036-871-37	Sequence 37, Appl	362	78	3.0	272	7	US-11-027-802-3866	Sequence 3866, Ap
290	79.5	3.0	1230	1	PCT-US04-42360-1948	Sequence 1948, Ap	363	78	3.0	272	7	US-11-027-890-3866	Sequence 3866, Ap
291	79	3.0	372	6	US-10-450-763-34165	Sequence 34165, A	364	78	3.0	272	7	US-11-027-892-3866	Sequence 3866, Ap
292	79	3.0	372	6	US-10-450-763-44435	Sequence 44435, A	365	78	3.0	272	7	US-11-028-099-3866	Sequence 3866, Ap
293	79	3.0	478	7	US-11-031-175-14070	Sequence 14070, A	366	78	3.0	272	7	US-11-028-197-3866	Sequence 3866, Ap
294	79	3.0	545	1	PCT-US04-44033-17	Sequence 17, Appl	367	78	3.0	272	7	US-11-027-844-3866	Sequence 3866, Ap
295	79	3.0	583	7	US-11-027-399-3571	Sequence 3571, Ap	368	78	3.0	272	7	US-11-028-050-3866	Sequence 3866, Ap
296	79	3.0	583	7	US-11-027-843-3571	Sequence 3571, Ap	369	78	3.0	272	7	US-11-028-457-3866	Sequence 3866, Ap
297	79	3.0	583	7	US-11-027-878-3571	Sequence 3571, Ap	370	78	3.0	272	7	US-11-027-891-3866	Sequence 3866, Ap
298	79	3.0	583	7	US-11-028-169-3571	Sequence 3571, Ap	371	78	3.0	272	7	US-11-028-291-3866	Sequence 3866, Ap
299	79	3.0	583	7	US-11-028-204-3571	Sequence 3571, Ap	372	78	3.0	345	7	US-11-027-399-4544	Sequence 4544, Ap
300	79	3.0	583	7	US-11-027-877-3571	Sequence 3571, Ap	373	78	3.0	345	7	US-11-027-843-4544	Sequence 4544, Ap
301	79	3.0	583	7	US-11-027-879-3571	Sequence 3571, Ap	374	78	3.0	345	7	US-11-027-878-4544	Sequence 4544, Ap
302	79	3.0	583	7	US-11-028-149-3571	Sequence 3571, Ap	375	78	3.0	345	7	US-11-028-169-4544	Sequence 4544, Ap
303	79	3.0	583	7	US-11-027-802-3571	Sequence 3571, Ap	376	78	3.0	345	7	US-11-028-204-4544	Sequence 4544, Ap
304	79	3.0	583	7	US-11-027-890-3571	Sequence 3571, Ap	377	78	3.0	345	7	US-11-027-877-4544	Sequence 4544, Ap
305	79	3.0	583	7	US-11-027-892-3571	Sequence 3571, Ap	378	78	3.0	345	7	US-11-027-879-4544	Sequence 4544, Ap
306	79	3.0	583	7	US-11-028-099-3571	Sequence 3571, Ap	379	78	3.0	345	7	US-11-028-149-4544	Sequence 4544, Ap
307	79	3.0	583	7	US-11-028-197-3571	Sequence 3571, Ap	380	78	3.0	345	7	US-11-027-802-4544	Sequence 4544, Ap
308	79	3.0	583	7	US-11-027-844-3571	Sequence 3571, Ap	381	78	3.0	345	7	US-11-027-890-4544	Sequence 4544, Ap
309	79	3.0	583	7	US-11-028-050-3571	Sequence 3571, Ap	382	78	3.0	345	7	US-11-027-892-4544	Sequence 4544, Ap
310	79	3.0	583	7	US-11-028-457-3571	Sequence 3571, Ap	383	78	3.0	345	7	US-11-028-099-4544	Sequence 4544, Ap
311	79	3.0	583	7	US-11-027-891-3571	Sequence 3571, Ap	384	78	3.0	345	7	US-11-028-197-4544	Sequence 4544, Ap
312	79	3.0	583	7	US-11-028-291-3571	Sequence 3571, Ap	385	78	3.0	345	7	US-11-027-844-4544	Sequence 4544, Ap
313	79	3.0	891	6	US-10-489-448-1070	Sequence 1070, Ap	386	78	3.0	345	7	US-11-028-050-4544	Sequence 4544, Ap
314	79	3.0	992	6	US-10-450-763-36268	Sequence 36268, A	387	78	3.0	345	7	US-11-028-457-4544	Sequence 4544, Ap
315	79	3.0	1063	6	US-10-450-763-31717	Sequence 31717, A	388	78	3.0	345	7	US-11-027-891-4544	Sequence 4544, Ap
316	79	3.0	1526	6	US-10-450-763-36475	Sequence 36475, A	389	78	3.0	345	7	US-11-028-291-4544	Sequence 4544, Ap
317	79	3.0	1526	6	US-10-450-763-37648	Sequence 37648, A	390	78	3.0	678	6	US-10-450-763-60021	Sequence 60021, A



391	78	3.0	843	6	US-10-450-763-59255	Sequence 59255, A	464	76	2.9	398	7	US-11-027-890-3408	Sequence 3408, Ap
392	78	3.0	883	7	US-11-027-399-2900	Sequence 2900, Ap	465	76	2.9	398	7	US-11-027-892-3408	Sequence 3408, Ap
393	78	3.0	883	7	US-11-027-843-2900	Sequence 2900, Ap	466	76	2.9	398	7	US-11-028-099-3408	Sequence 3408, Ap
394	78	3.0	883	7	US-11-027-878-2900	Sequence 2900, Ap	467	76	2.9	398	7	US-11-028-197-3408	Sequence 3408, Ap
395	78	3.0	883	7	US-11-028-169-2900	Sequence 2900, Ap	468	76	2.9	398	7	US-11-027-844-3408	Sequence 3408, Ap
396	78	3.0	883	7	US-11-028-204-2900	Sequence 2900, Ap	469	76	2.9	398	7	US-11-028-050-3408	Sequence 3408, Ap
397	78	3.0	883	7	US-11-027-877-2900	Sequence 2900, Ap	470	76	2.9	398	7	US-11-028-457-3408	Sequence 3408, Ap
398	78	3.0	883	7	US-11-027-879-2900	Sequence 2900, Ap	471	76	2.9	398	7	US-11-027-891-3408	Sequence 3408, Ap
399	78	3.0	883	7	US-11-028-149-2900	Sequence 2900, Ap	472	76	2.9	398	7	US-11-028-291-3408	Sequence 3408, Ap
400	78	3.0	883	7	US-11-027-802-2900	Sequence 2900, Ap	473	76	2.9	632	6	US-10-450-763-37661	Sequence 37661, A
401	78	3.0	883	7	US-11-027-890-2900	Sequence 2900, Ap	474	76	2.9	658	7	US-11-027-399-4743	Sequence 4743, Ap
402	78	3.0	883	7	US-11-027-892-2900	Sequence 2900, Ap	475	76	2.9	658	7	US-11-027-843-4743	Sequence 4743, Ap
403	78	3.0	883	7	US-11-028-099-2900	Sequence 2900, Ap	476	76	2.9	658	7	US-11-027-878-4743	Sequence 4743, Ap
404	78	3.0	883	7	US-11-028-197-2900	Sequence 2900, Ap	477	76	2.9	658	7	US-11-028-169-4743	Sequence 4743, Ap
405	78	3.0	883	7	US-11-027-844-2900	Sequence 2900, Ap	478	76	2.9	658	7	US-11-028-204-4743	Sequence 4743, Ap
406	78	3.0	883	7	US-11-028-050-2900	Sequence 2900, Ap	479	76	2.9	658	7	US-11-027-877-4743	Sequence 4743, Ap
407	78	3.0	883	7	US-11-028-457-2900	Sequence 2900, Ap	480	76	2.9	658	7	US-11-027-879-4743	Sequence 4743, Ap
408	78	3.0	883	7	US-11-028-291-2900	Sequence 2900, Ap	481	76	2.9	658	7	US-11-028-149-4743	Sequence 4743, Ap
409	78	3.0	883	7	US-11-027-891-2900	Sequence 2900, Ap	482	76	2.9	658	7	US-11-027-802-4743	Sequence 4743, Ap
410	78	3.0	2324	7	US-11-031-175-9732	Sequence 9732, Ap	483	76	2.9	658	7	US-11-027-890-4743	Sequence 4743, Ap
411	78	3.0	3150	6	US-10-450-763-50773	Sequence 50773, A	484	76	2.9	658	7	US-11-027-892-4743	Sequence 4743, Ap
412	77.5	3.0	315	7	US-11-031-175-11852	Sequence 11852, A	485	76	2.9	658	7	US-11-028-099-4743	Sequence 4743, Ap
413	77.5	3.0	376	6	US-10-450-763-39711	Sequence 39711, A	486	76	2.9	658	7	US-11-028-197-4743	Sequence 4743, Ap
414	77.5	3.0	804	6	US-10-450-763-45931	Sequence 45931, A	487	76	2.9	658	7	US-11-027-844-4743	Sequence 4743, Ap
415	77.5	3.0	946	6	US-10-450-763-48296	Sequence 48296, A	488	76	2.9	658	7	US-11-028-050-4743	Sequence 4743, Ap
416	77.5	3.0	1663	6	US-10-450-763-41525	Sequence 41525, A	489	76	2.9	658	7	US-11-028-457-4743	Sequence 4743, Ap
417	77.5	3.0	7429	1	PCT-US04-29630-5	Sequence 5, Appli	490	76	2.9	658	7	US-11-027-891-4743	Sequence 4743, Ap
418	77	2.9	205	7	US-11-025-607-287	Sequence 287, App	491	76	2.9	658	7	US-11-028-291-4743	Sequence 4743, Ap
419	77	2.9	206	1	PCT-US04-09510-706	Sequence 706, App	492	76	2.9	749	1	PCT-US04-42360-1694	Sequence 1694, Ap
420	77	2.9	301	6	US-10-450-763-44438	Sequence 44438, A	493	76	2.9	776	5	US-09-896-923B-2	Sequence 2, Appli
421	77	2.9	484	1	PCT-US04-42360-626	Sequence 626, App	494	76	2.9	873	6	US-10-496-011-6	Sequence 6, Appli
422	77	2.9	517	7	US-11-031-175-10229	Sequence 10229, A	495	76	2.9	971	6	US-10-450-763-43387	Sequence 43387, A
423	77	2.9	558	1	PCT-US04-42360-1547	Sequence 1547, Ap	496	76	2.9	1057	6	US-10-450-763-40193	Sequence 40193, A
424	77	2.9	558	1	PCT-US04-42360-1570	Sequence 1570, Ap	497	76	2.9	1089	7	US-11-031-175-14239	Sequence 14239, A
425	77	2.9	4561	6	US-10-450-763-60562	Sequence 60562, A	498	76	2.9	1214	6	US-10-450-763-32314	Sequence 32314, A
426	77	2.9	9222	6	US-10-450-763-51423	Sequence 51423, A	499	76	2.9	1300	5	US-09-896-923B-3	Sequence 3, Appli
427	76.5	2.9	314	7	US-11-027-399-3992	Sequence 3992, Ap	500	76	2.9	1807	1	PCT-US04-42360-730	Sequence 730, App
428	76.5	2.9	314	7	US-11-027-843-3992	Sequence 3992, Ap	501	75.5	2.9	187	6	US-10-450-763-56634	Sequence 56634, A
429	76.5	2.9	314	7	US-11-027-878-3992	Sequence 3992, Ap	502	75.5	2.9	476	1	PCT-US04-42360-873	Sequence 873, App
430	76.5	2.9	314	7	US-11-028-169-3992	Sequence 3992, Ap	503	75.5	2.9	532	6	US-10-450-763-40639	Sequence 40639, A
431	76.5	2.9	314	7	US-11-028-204-3992	Sequence 3992, Ap	504	75.5	2.9	556	6	US-10-450-763-46284	Sequence 46284, A
432	76.5	2.9	314	7	US-11-027-877-3992	Sequence 3992, Ap	505	75.5	2.9	699	7	US-11-025-607-12	Sequence 12, Appli
433	76.5	2.9	314	7	US-11-027-879-3992	Sequence 3992, Ap	506	75.5	2.9	747	7	US-11-031-175-16170	Sequence 16170, A
434	76.5	2.9	314	7	US-11-028-149-3992	Sequence 3992, Ap	507	75.5	2.9	1305	6	US-10-450-763-56203	Sequence 56203, A
435	76.5	2.9	314	7	US-11-027-802-3992	Sequence 3992, Ap	508	75.5	2.9	1371	6	US-10-450-763-51575	Sequence 51575, A
436	76.5	2.9	314	7	US-11-027-890-3992	Sequence 3992, Ap	509	75.5	2.9	1497	6	US-10-450-763-50512	Sequence 50512, A
437	76.5	2.9	314	7	US-11-027-892-3992	Sequence 3992, Ap	510	75	2.9	251	6	US-10-450-763-43511	Sequence 43511, A
438	76.5	2.9	314	7	US-11-028-099-3992	Sequence 3992, Ap	511	75	2.9	304	6	US-10-450-763-50145	Sequence 50145, A
439	76.5	2.9	314	7	US-11-028-197-3992	Sequence 3992, Ap	512	75	2.9	304	6	US-10-450-763-50145	Sequence 50145, A
440	76.5	2.9	314	7	US-11-027-844-3992	Sequence 3992, Ap	513	75	2.9	408	6	US-10-450-763-38949	Sequence 38949, A
441	76.5	2.9	314	7	US-11-028-050-3992	Sequence 3992, Ap	514	75	2.9	438	6	US-10-489-448-1777	Sequence 1777, Ap
442	76.5	2.9	314	7	US-11-028-457-3992	Sequence 3992, Ap	515	75	2.9	553	6	US-10-450-763-55392	Sequence 55392, A
443	76.5	2.9	314	7	US-11-027-891-3992	Sequence 3992, Ap	516	75	2.9	566	7	US-11-033-545-452	Sequence 452, App
444	76.5	2.9	314	7	US-11-028-291-3992	Sequence 3992, Ap	517	75	2.9	571	6	US-10-450-763-54739	Sequence 54739, A
445	76.5	2.9	353	1	PCT-US03-15712-88	Sequence 88, Appl	518	75	2.9	571	6	US-10-450-763-59393	Sequence 59393, A
446	76.5	2.9	572	6	US-10-450-763-47905	Sequence 47905, A	519	75	2.9	745	7	US-11-031-175-10275	Sequence 10275, A
447	76.5	2.9	583	6	US-10-348-074A-46	Sequence 46, Appl	520	75	2.9	755	6	US-10-450-763-40882	Sequence 40882, A
448	76.5	2.9	857	7	US-11-031-175-12312	Sequence 12312, A	521	75	2.9	767	6	US-10-450-763-41893	Sequence 41893, A
449	76.5	2.9	865	6	US-10-450-763-59252	Sequence 59252, A	522	75	2.9	820	7	US-11-027-399-4219	Sequence 4219, Ap
450	76.5	2.9	959	1	PCT-US04-42360-157	Sequence 157, App	523	75	2.9	820	7	US-11-027-843-4219	Sequence 4219, Ap
451	76.5	2.9	1553	6	US-10-450-763-32559	Sequence 32559, A	524	75	2.9	820	7	US-11-027-879-4219	Sequence 4219, Ap
452	76.5	2.9	2301	1	PCT-US04-31504-30	Sequence 30, Appl	525	75	2.9	820	7	US-11-027-878-4219	Sequence 4219, Ap
453	76	2.9	228	6	US-10-450-763-42434	Sequence 42434, A	526	75	2.9	820	7	US-11-028-169-4219	Sequence 4219, Ap
454	76	2.9	398	7	US-11-027-399-3408	Sequence 3408, Ap	527	75	2.9	820	7	US-11-027-877-4219	Sequence 4219, Ap
455	76	2.9	398	7	US-11-027-843-3408	Sequence 3408, Ap	528	75	2.9	820	7	US-11-027-879-4219	Sequence 4219, Ap
456	76	2.9	398	7	US-11-027-878-3408	Sequence 3408, Ap	529	75	2.9	820	7	US-11-028-149-4219	Sequence 4219, Ap
457	76	2.9	398	7	US-11-028-169-3408	Sequence 3408, Ap	530	75	2.9	820	7	US-11-027-802-4219	Sequence 4219, Ap
458	76	2.9	398	7	US-11-028-204-3408	Sequence 3408, Ap	531	75	2.9	820	7	US-11-027-890-4219	Sequence 4219, Ap
459	76	2.9	398	7	US-11-027-877-3408	Sequence 3408, Ap	532	75	2.9	820	7	US-11-027-892-4219	Sequence 4219, Ap
460	76	2.9	398	7	US-11-027-879-3408	Sequence 3408, Ap	533	75	2.9	820	7	US-11-028-099-4219	Sequence 4219, Ap
461	76	2.9	398	7	US-11-027-879-3408	Sequence 3408, Ap	534	75	2.9	820	7	US-11-028-197-4219	Sequence 4219, Ap
462	76	2.9	398	7	US-11-028-149-3408	Sequence 3408, Ap	535	75	2.9	820	7	US-11-027-844-4219	Sequence 4219, Ap
463	76	2.9	398	7	US-11-027-802-3408	Sequence 3408, Ap	536	75	2.9	820	7	US-11-028-050-4219	Sequence 4219, Ap



537	75	2.9	820	7	US-11-028-457-4219	Sequence 4219, Ap	610	73.5	2.8	407	7	US-11-028-169-3040	Sequence 3040, Ap
538	75	2.9	820	7	US-11-027-891-4219	Sequence 4219, Ap	611	73.5	2.8	407	7	US-11-028-204-3040	Sequence 3040, Ap
539	75	2.9	820	7	US-11-028-291-4219	Sequence 4219, Ap	612	73.5	2.8	407	7	US-11-027-877-3040	Sequence 3040, Ap
540	75	2.9	848	7	US-11-031-175-14707	Sequence 14707, A	613	73.5	2.8	407	7	US-11-027-877-3040	Sequence 3040, Ap
541	75	2.9	965	6	US-10-450-763-45805	Sequence 45805, A	614	73.5	2.8	407	7	US-11-028-149-3040	Sequence 3040, Ap
542	75	2.9	1211	7	US-11-033-545-555	Sequence 555, App	615	73.5	2.8	407	7	US-11-027-802-3040	Sequence 3040, Ap
543	75	2.9	1798	6	US-10-450-763-40292	Sequence 40292, A	616	73.5	2.8	407	7	US-11-027-890-3040	Sequence 3040, Ap
544	74.5	2.8	209	6	US-10-450-763-50530	Sequence 50530, A	617	73.5	2.8	407	7	US-11-027-892-3040	Sequence 3040, Ap
545	74.5	2.8	326	7	US-11-031-175-15158	Sequence 15158, A	618	73.5	2.8	407	7	US-11-028-099-3040	Sequence 3040, Ap
546	74.5	2.8	386	6	US-10-450-763-48894	Sequence 48894, A	619	73.5	2.8	407	7	US-11-028-197-3040	Sequence 3040, Ap
547	74.5	2.8	432	7	US-11-031-175-12060	Sequence 12060, A	620	73.5	2.8	407	7	US-11-027-844-3040	Sequence 3040, Ap
548	74.5	2.8	434	6	US-10-491-545A-36	Sequence 36, Appl	621	73.5	2.8	407	7	US-11-028-050-3040	Sequence 3040, Ap
549	74.5	2.8	467	6	US-10-450-763-34692	Sequence 34692, A	622	73.5	2.8	407	7	US-11-028-457-3040	Sequence 3040, Ap
550	74.5	2.8	554	7	US-11-031-175-15061	Sequence 15061, A	623	73.5	2.8	407	7	US-11-027-891-3040	Sequence 3040, Ap
551	74.5	2.8	570	6	US-10-450-763-43025	Sequence 43025, A	624	73.5	2.8	407	7	US-11-028-291-3040	Sequence 3040, Ap
552	74.5	2.8	583	6	US-10-450-763-59217	Sequence 59217, A	625	73.5	2.8	446	7	US-11-031-175-12791	Sequence 12791, A
553	74.5	2.8	623	7	US-11-031-175-10027	Sequence 10027, A	626	73.5	2.8	596	6	US-10-489-448-1874	Sequence 1874, Ap
554	74.5	2.8	764	6	US-10-450-763-54635	Sequence 54635, A	627	73.5	2.8	714	6	US-10-450-763-45506	Sequence 45506, A
555	74.5	2.8	801	6	US-10-450-763-57554	Sequence 57554, A	628	73.5	2.8	714	6	US-10-450-763-46006	Sequence 46006, A
556	74.5	2.8	943	7	US-11-031-175-10641	Sequence 10641, A	629	73.5	2.8	858	6	US-10-489-448-1475	Sequence 1475, Ap
557	74.5	2.8	1965	6	US-10-450-763-46292	Sequence 46292, A	630	73.5	2.8	1193	6	US-10-450-763-48448	Sequence 48448, A
558	74.5	2.8	2303	1	PCT-US04-31504-32	Sequence 32, Appl	631	73.5	2.8	1302	7	US-11-031-175-14853	Sequence 14853, A
559	74.5	2.8	4687	1	PCT-US04-42360-1642	Sequence 1642, Ap	632	73.5	2.8	1765	6	US-10-450-763-52990	Sequence 52990, A
560	74.5	2.8	4854	6	US-10-450-763-36386	Sequence 36386, A	633	73.5	2.8	1944	6	US-10-450-763-42376	Sequence 42376, A
561	74.5	2.8	4866	5	US-09-424-783-2	Sequence 2, Appl	634	73.5	2.8	2114	6	US-10-450-763-39435	Sequence 39435, A
562	74.5	2.8	4899	6	US-10-450-763-42673	Sequence 42673, A	635	73.5	2.8	2214	7	US-11-031-175-15988	Sequence 15988, A
563	74.5	2.8	4934	6	US-10-450-763-53705	Sequence 53705, A	636	73.5	2.8	2356	6	US-10-450-763-39431	Sequence 39431, A
564	74	2.8	236	6	US-10-450-763-59651	Sequence 59651, A	637	73.5	2.8	2640	6	US-10-450-763-56084	Sequence 56084, A
565	74	2.8	243	7	US-11-031-175-15036	Sequence 15036, A	638	73	2.8	180	6	US-10-450-763-40846	Sequence 40846, A
566	74	2.8	246	7	US-11-031-175-15999	Sequence 15999, A	639	73	2.8	239	7	US-11-031-175-13167	Sequence 13167, A
567	74	2.8	328	7	US-11-027-399-4551	Sequence 4551, Ap	640	73	2.8	379	7	US-11-031-175-12816	Sequence 12816, A
568	74	2.8	328	7	US-11-027-843-4551	Sequence 4551, Ap	641	73	2.8	606	6	US-10-450-763-41795	Sequence 41795, A
569	74	2.8	328	7	US-11-027-878-4551	Sequence 4551, Ap	642	73	2.8	606	6	US-10-450-763-57566	Sequence 57566, A
570	74	2.8	328	7	US-11-028-169-4551	Sequence 4551, Ap	643	73	2.8	668	6	US-10-450-763-44082	Sequence 44082, A
571	74	2.8	328	7	US-11-028-204-4551	Sequence 4551, Ap	644	73	2.8	692	6	US-10-450-763-40291	Sequence 40291, A
572	74	2.8	328	7	US-11-027-877-4551	Sequence 4551, Ap	645	73	2.8	711	6	US-10-450-763-60666	Sequence 60666, A
573	74	2.8	328	7	US-11-027-879-4551	Sequence 4551, Ap	646	73	2.8	750	7	US-11-027-399-4010	Sequence 4010, Ap
574	74	2.8	328	7	US-11-028-149-4551	Sequence 4551, Ap	647	73	2.8	750	7	US-11-027-843-4010	Sequence 4010, Ap
575	74	2.8	328	7	US-11-027-802-4551	Sequence 4551, Ap	648	73	2.8	750	7	US-11-027-878-4010	Sequence 4010, Ap
576	74	2.8	328	7	US-11-027-890-4551	Sequence 4551, Ap	649	73	2.8	750	7	US-11-028-169-4010	Sequence 4010, Ap
577	74	2.8	328	7	US-11-027-892-4551	Sequence 4551, Ap	650	73	2.8	750	7	US-11-028-204-4010	Sequence 4010, Ap
578	74	2.8	328	7	US-11-028-099-4551	Sequence 4551, Ap	651	73	2.8	750	7	US-11-027-877-4010	Sequence 4010, Ap
579	74	2.8	328	7	US-11-028-197-4551	Sequence 4551, Ap	652	73	2.8	750	7	US-11-027-879-4010	Sequence 4010, Ap
580	74	2.8	328	7	US-11-027-844-4551	Sequence 4551, Ap	653	73	2.8	750	7	US-11-028-149-4010	Sequence 4010, Ap
581	74	2.8	328	7	US-11-028-050-4551	Sequence 4551, Ap	654	73	2.8	750	7	US-11-027-802-4010	Sequence 4010, Ap
582	74	2.8	328	7	US-11-028-457-4551	Sequence 4551, Ap	655	73	2.8	750	7	US-11-027-890-4010	Sequence 4010, Ap
583	74	2.8	328	7	US-11-027-891-4551	Sequence 4551, Ap	656	73	2.8	750	7	US-11-027-892-4010	Sequence 4010, Ap
584	74	2.8	328	7	US-11-028-291-4551	Sequence 4551, Ap	657	73	2.8	750	7	US-11-028-099-4010	Sequence 4010, Ap
585	74	2.8	420	7	US-11-021-825-121	Sequence 121, App	658	73	2.8	750	7	US-11-028-197-4010	Sequence 4010, Ap
586	74	2.8	432	7	US-11-031-175-15774	Sequence 15774, A	659	73	2.8	750	7	US-11-027-844-4010	Sequence 4010, Ap
587	74	2.8	490	7	US-11-031-175-10306	Sequence 10306, A	660	73	2.8	750	7	US-11-028-050-4010	Sequence 4010, Ap
588	74	2.8	533	1	PCT-US04-23166A-782	Sequence 782, App	661	73	2.8	750	7	US-11-028-457-4010	Sequence 4010, Ap
589	74	2.8	541	6	US-10-283-686A-5	Sequence 5, Appl	662	73	2.8	750	7	US-11-027-891-4010	Sequence 4010, Ap
590	74	2.8	615	6	US-10-450-763-37724	Sequence 37724, A	663	73	2.8	750	7	US-11-028-291-4010	Sequence 4010, Ap
591	74	2.8	628	6	US-10-450-763-54913	Sequence 54913, A	664	73	2.8	1224	7	US-11-031-175-16312	Sequence 16312, A
592	74	2.8	719	6	US-10-450-763-44358	Sequence 44358, A	665	73	2.8	2517	7	US-11-031-175-15380	Sequence 15380, A
593	74	2.8	960	6	US-10-450-763-56562	Sequence 56562, A	666	73	2.8	4591	6	US-10-450-763-53336	Sequence 53336, A
594	74	2.8	1001	1	PCT-US04-09510-930	Sequence 930, App	667	72.5	2.8	281	6	US-10-450-763-48893	Sequence 48893, A
595	74	2.8	1014	6	US-10-450-763-37215	Sequence 37215, A	668	72.5	2.8	340	7	US-11-031-175-14524	Sequence 14524, A
596	74	2.8	1014	6	US-10-450-763-47843	Sequence 47843, A	669	72.5	2.8	348	6	US-10-489-448-3421	Sequence 3421, Ap
597	74	2.8	1014	6	US-10-450-763-53512	Sequence 53512, A	670	72.5	2.8	416	6	US-10-450-763-44356	Sequence 44356, A
598	74	2.8	1211	7	US-11-033-545-401	Sequence 401, App	671	72.5	2.8	440	6	US-10-450-763-48147	Sequence 48147, A
599	74	2.8	1302	6	US-10-450-763-44456	Sequence 44456, A	672	72.5	2.8	447	7	US-11-031-175-14948	Sequence 14948, A
600	74	2.8	1523	5	US-09-896-923B-72	Sequence 72, Appl	673	72.5	2.8	474	6	US-10-450-763-60112	Sequence 60112, A
601	74	2.8	1747	7	US-11-031-175-14765	Sequence 14765, A	674	72.5	2.8	506	6	US-10-450-763-46098	Sequence 46098, A
602	74	2.8	1814	6	US-10-450-763-43064	Sequence 43064, A	675	72.5	2.8	580	6	US-10-450-763-50379	Sequence 50379, A
603	74	2.8	3419	1	PCT-US04-42360-180	Sequence 180, App	676	72.5	2.8	638	6	US-10-450-763-56551	Sequence 56551, A
604	73.5	2.8	258	6	US-10-450-763-34973	Sequence 34973, A	677	72.5	2.8	641	6	US-10-450-763-40146	Sequence 40146, A
605	73.5	2.8	313	7	US-11-031-175-14967	Sequence 14967, A	678	72.5	2.8	653	6	US-10-450-763-41591	Sequence 41591, A
606	73.5	2.8	389	7	US-11-031-175-12890	Sequence 12890, A	679	72.5	2.8	707	6	US-10-450-763-48234	Sequence 48234, A
607	73.5	2.8	407	7	US-11-027-399-3040	Sequence 3040, Ap	680	72.5	2.8	709	6	US-10-519-238-3	Sequence 3, Appl
608	73.5	2.8	407	7	US-11-027-843-3040	Sequence 3040, Ap	681	72.5	2.8	792	6	US-10-450-763-33418	Sequence 33418, A
609	73.5	2.8	407	7	US-11-027-878-3040	Sequence 3040, Ap	682	72.5	2.8	850	6	US-10-679-102-31	Sequence 31, Appl

683	72.5	2.8	851	6	US-10-450-763-57843	Sequence 57843, A	756	71.5	2.7	481	7	US-11-027-877-2945	Sequence 2945, Ap
684	72.5	2.8	893	6	US-10-450-763-30617	Sequence 30617, A	757	71.5	2.7	481	7	US-11-027-879-2945	Sequence 2945, Ap
685	72.5	2.8	893	6	US-10-450-763-30970	Sequence 30970, A	758	71.5	2.7	481	7	US-11-028-149-2945	Sequence 2945, Ap
686	72.5	2.8	915	1	PCT-US04-42360-2173	Sequence 2173, Ap	759	71.5	2.7	481	7	US-11-027-802-2945	Sequence 2945, Ap
687	72.5	2.8	915	1	PCT-US04-42360-2229	Sequence 2229, Ap	760	71.5	2.7	481	7	US-11-027-890-2945	Sequence 2945, Ap
688	72.5	2.8	999	1	PCT-US04-09510-829	Sequence 829, App	761	71.5	2.7	481	7	US-11-027-892-2945	Sequence 2945, Ap
689	72.5	2.8	1118	6	US-10-450-763-46682	Sequence 46682, A	762	71.5	2.7	481	7	US-11-028-099-2945	Sequence 2945, Ap
690	72.5	2.8	1182	7	US-11-031-175-9855	Sequence 9855, Ap	763	71.5	2.7	481	7	US-11-028-197-2945	Sequence 2945, Ap
691	72.5	2.8	1195	6	US-10-450-763-57901	Sequence 57901, A	764	71.5	2.7	481	7	US-11-027-844-2945	Sequence 2945, Ap
692	72.5	2.8	1698	7	US-11-031-175-12813	Sequence 12813, A	765	71.5	2.7	481	7	US-11-028-050-2945	Sequence 2945, Ap
693	72.5	2.8	2447	6	US-10-450-763-52739	Sequence 52739, A	766	71.5	2.7	481	7	US-11-028-457-2945	Sequence 2945, Ap
694	72	2.7	195	7	US-11-027-399-5169	Sequence 5169, Ap	767	71.5	2.7	481	7	US-11-027-891-2945	Sequence 2945, Ap
695	72	2.7	195	7	US-11-027-843-5169	Sequence 5169, Ap	768	71.5	2.7	481	7	US-11-028-291-2945	Sequence 2945, Ap
696	72	2.7	195	7	US-11-027-878-5169	Sequence 5169, Ap	769	71.5	2.7	484	6	US-10-450-763-46567	Sequence 46567, A
697	72	2.7	195	7	US-11-028-169-5169	Sequence 5169, Ap	770	71.5	2.7	488	6	US-10-518-868-9	Sequence 9, Appli
698	72	2.7	195	7	US-11-028-204-5169	Sequence 5169, Ap	771	71.5	2.7	488	6	US-10-518-868-16	Sequence 16, Appli
699	72	2.7	195	7	US-11-027-877-5169	Sequence 5169, Ap	772	71.5	2.7	488	6	US-10-518-868-4	Sequence 4, Appli
700	72	2.7	195	7	US-11-028-149-5169	Sequence 5169, Ap	773	71.5	2.7	516	6	US-10-489-448-1191	Sequence 1191, Ap
701	72	2.7	195	7	US-11-027-802-5169	Sequence 5169, Ap	774	71.5	2.7	520	6	US-10-450-763-37444	Sequence 37444, A
702	72	2.7	195	7	US-11-027-890-5169	Sequence 5169, Ap	775	71.5	2.7	529	6	US-10-518-868-7	Sequence 7, Appli
703	72	2.7	195	7	US-11-027-892-5169	Sequence 5169, Ap	776	71.5	2.7	529	6	US-10-518-868-17	Sequence 17, Appli
704	72	2.7	195	7	US-11-028-099-5169	Sequence 5169, Ap	777	71.5	2.7	544	6	US-10-450-763-37948	Sequence 37948, A
705	72	2.7	195	7	US-11-028-197-5169	Sequence 5169, Ap	778	71.5	2.7	557	1	PCT-US04-17965-2166	Sequence 2166, Ap
706	72	2.7	195	7	US-11-028-197-5169	Sequence 5169, Ap	779	71.5	2.7	584	6	US-10-489-448-2995	Sequence 2995, Ap
707	72	2.7	195	7	US-11-027-844-5169	Sequence 5169, Ap	780	71.5	2.7	613	6	US-10-450-763-47273	Sequence 47273, A
708	72	2.7	195	7	US-11-028-050-5169	Sequence 5169, Ap	781	71.5	2.7	614	7	US-11-027-399-5301	Sequence 5301, Ap
709	72	2.7	195	7	US-11-028-457-5169	Sequence 5169, Ap	782	71.5	2.7	614	7	US-11-027-843-5301	Sequence 5301, Ap
710	72	2.7	195	7	US-11-027-891-5169	Sequence 5169, Ap	783	71.5	2.7	614	7	US-11-027-878-5301	Sequence 5301, Ap
711	72	2.7	195	7	US-11-028-291-5169	Sequence 5169, Ap	784	71.5	2.7	614	7	US-11-028-169-5301	Sequence 5301, Ap
712	72	2.7	232	7	US-11-035-703-12	Sequence 12, Appl	785	71.5	2.7	614	7	US-11-028-204-5301	Sequence 5301, Ap
713	72	2.7	311	6	US-10-450-763-37329	Sequence 37329, A	786	71.5	2.7	614	7	US-11-027-877-5301	Sequence 5301, Ap
714	72	2.7	333	6	US-10-450-763-45557	Sequence 45557, A	787	71.5	2.7	614	7	US-11-027-879-5301	Sequence 5301, Ap
715	72	2.7	394	6	US-10-450-763-51564	Sequence 51564, A	788	71.5	2.7	614	7	US-11-028-149-5301	Sequence 5301, Ap
716	72	2.7	396	7	US-11-027-399-4759	Sequence 4759, Ap	789	71.5	2.7	614	7	US-11-027-802-5301	Sequence 5301, Ap
717	72	2.7	396	7	US-11-027-843-4759	Sequence 4759, Ap	790	71.5	2.7	614	7	US-11-027-890-5301	Sequence 5301, Ap
718	72	2.7	396	7	US-11-027-878-4759	Sequence 4759, Ap	791	71.5	2.7	614	7	US-11-027-892-5301	Sequence 5301, Ap
719	72	2.7	396	7	US-11-028-169-4759	Sequence 4759, Ap	792	71.5	2.7	614	7	US-11-028-099-5301	Sequence 5301, Ap
720	72	2.7	396	7	US-11-028-204-4759	Sequence 4759, Ap	793	71.5	2.7	614	7	US-11-028-197-5301	Sequence 5301, Ap
721	72	2.7	396	7	US-11-027-877-4759	Sequence 4759, Ap	794	71.5	2.7	614	7	US-11-027-844-5301	Sequence 5301, Ap
722	72	2.7	396	7	US-11-027-879-4759	Sequence 4759, Ap	795	71.5	2.7	614	7	US-11-028-050-5301	Sequence 5301, Ap
723	72	2.7	396	7	US-11-028-149-4759	Sequence 4759, Ap	796	71.5	2.7	614	7	US-11-028-457-5301	Sequence 5301, Ap
724	72	2.7	396	7	US-11-027-802-4759	Sequence 4759, Ap	797	71.5	2.7	614	7	US-11-027-891-5301	Sequence 5301, Ap
725	72	2.7	396	7	US-11-027-890-4759	Sequence 4759, Ap	798	71.5	2.7	614	7	US-11-028-291-5301	Sequence 5301, Ap
726	72	2.7	396	7	US-11-027-892-4759	Sequence 4759, Ap	799	71.5	2.7	656	7	US-11-027-399-3258	Sequence 3258, Ap
727	72	2.7	396	7	US-11-028-099-4759	Sequence 4759, Ap	800	71.5	2.7	656	7	US-11-027-843-3258	Sequence 3258, Ap
728	72	2.7	396	7	US-11-028-197-4759	Sequence 4759, Ap	801	71.5	2.7	656	7	US-11-027-878-3258	Sequence 3258, Ap
729	72	2.7	396	7	US-11-027-844-4759	Sequence 4759, Ap	802	71.5	2.7	656	7	US-11-028-169-3258	Sequence 3258, Ap
730	72	2.7	396	7	US-11-028-050-4759	Sequence 4759, Ap	803	71.5	2.7	656	7	US-11-028-204-3258	Sequence 3258, Ap
731	72	2.7	396	7	US-11-028-457-4759	Sequence 4759, Ap	804	71.5	2.7	656	7	US-11-027-877-3258	Sequence 3258, Ap
732	72	2.7	396	7	US-11-027-891-4759	Sequence 4759, Ap	805	71.5	2.7	656	7	US-11-027-879-3258	Sequence 3258, Ap
733	72	2.7	396	7	US-11-028-291-4759	Sequence 4759, Ap	806	71.5	2.7	656	7	US-11-027-879-3258	Sequence 3258, Ap
734	72	2.7	465	7	US-11-031-175-12493	Sequence 12493, A	807	71.5	2.7	656	7	US-11-028-149-3258	Sequence 3258, Ap
735	72	2.7	513	6	US-10-450-763-33861	Sequence 33861, A	808	71.5	2.7	656	7	US-11-027-802-3258	Sequence 3258, Ap
736	72	2.7	564	7	US-11-031-175-16486	Sequence 16486, A	809	71.5	2.7	656	7	US-11-027-890-3258	Sequence 3258, Ap
737	72	2.7	600	6	US-10-718-359-14	Sequence 14, Appl	810	71.5	2.7	656	7	US-11-028-099-3258	Sequence 3258, Ap
738	72	2.7	663	6	US-10-450-763-59562	Sequence 59562, A	811	71.5	2.7	656	7	US-11-028-197-3258	Sequence 3258, Ap
739	72	2.7	712	6	US-10-450-763-57804	Sequence 57804, A	812	71.5	2.7	656	7	US-11-027-844-3258	Sequence 3258, Ap
740	72	2.7	732	6	US-10-450-763-40812	Sequence 40812, A	813	71.5	2.7	656	7	US-11-028-050-3258	Sequence 3258, Ap
741	72	2.7	994	7	US-11-031-175-13822	Sequence 13822, A	814	71.5	2.7	656	7	US-11-028-457-3258	Sequence 3258, Ap
742	72	2.7	1541	6	US-10-450-763-59612	Sequence 59612, A	815	71.5	2.7	656	7	US-11-027-891-3258	Sequence 3258, Ap
743	71.5	2.7	203	1	PCT-US04-09510-734	Sequence 734, App	816	71.5	2.7	656	7	US-11-028-291-3258	Sequence 3258, Ap
744	71.5	2.7	205	1	PCT-US04-09510-786	Sequence 786, App	817	71.5	2.7	706	6	US-10-450-763-47560	Sequence 47560, A
745	71.5	2.7	333	6	US-10-450-763-57904	Sequence 57904, A	818	71.5	2.7	732	7	US-11-033-545-291	Sequence 291, App
746	71.5	2.7	333	7	US-11-031-175-10854	Sequence 10854, A	819	71.5	2.7	746	6	US-10-476-264-69	Sequence 69, Appl
747	71.5	2.7	357	6	US-10-450-763-32547	Sequence 32547, A	820	71.5	2.7	746	6	US-10-476-264-70	Sequence 70, Appl
748	71.5	2.7	368	6	US-10-450-763-37458	Sequence 37458, A	821	71.5	2.7	746	6	US-10-476-264-72	Sequence 72, Appl
749	71.5	2.7	373	6	US-10-450-763-45445	Sequence 45445, A	822	71.5	2.7	780	6	US-11-031-175-13911	Sequence 13911, A
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751	71.5	2.7	481	7	US-11-027-399-2945	Sequence 2945, Ap	824	71.5	2.7	789	6	US-10-476-264-68	Sequence 68, Appl
752	71.5	2.7	481	7	US-11-027-843-2945	Sequence 2945, Ap	825	71.5	2.7	796	6	US-10-476-264-106	Sequence 106, App
753	71.5	2.7	481	7	US-11-027-878-2945	Sequence 2945, Ap	826	71.5	2.7	796	6	US-10-476-264-110	Sequence 110, App
754	71.5	2.7	481	7	US-11-028-169-2945	Sequence 2945, Ap	827	71.5	2.7	796	6	US-10-476-264-142	Sequence 142, App
755	71.5	2.7	481	7	US-11-028-204-2945	Sequence 2945, Ap	828	71.5	2.7	796	6	US-10-476-264-146	Sequence 146, App



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830	71.5	2.7	1003	1	PCT-US04-09510-874	Sequence 874, App	903	71	2.7	981	7	US-11-031-175-16812	Sequence 16812, A
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833	71.5	2.7	1037	6	US-10-450-763-35358	Sequence 35358, A	906	71	2.7	1188	7	US-11-031-175-10968	Sequence 10968, A
834	71.5	2.7	1045	6	US-10-450-763-42749	Sequence 42749, A	907	71	2.7	1235	6	US-10-450-763-47415	Sequence 47415, A
835	71.5	2.7	1114	7	US-11-031-175-16251	Sequence 16251, A	908	71	2.7	1285	6	US-10-450-763-46696	Sequence 46696, A
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837	71.5	2.7	1447	6	US-10-450-763-39341	Sequence 39341, A	910	71	2.7	8438	1	PCT-US04-29630-4	Sequence 4, Appli
838	71.5	2.7	1752	7	US-11-033-545-294	Sequence 294, App	911	70.5	2.7	256	7	US-11-031-175-10784	Sequence 10784, A
839	71	2.7	200	7	US-11-031-175-12552	Sequence 12552, A	912	70.5	2.7	288	7	US-11-031-175-16247	Sequence 16247, A
840	71	2.7	259	7	US-11-031-175-9885	Sequence 9885, Ap	913	70.5	2.7	297	7	US-11-031-175-12237	Sequence 12237, A
841	71	2.7	354	7	US-11-031-175-15411	Sequence 15411, A	914	70.5	2.7	321	6	US-10-450-763-34251	Sequence 34251, A
842	71	2.7	359	6	US-10-450-763-39633	Sequence 39633, A	915	70.5	2.7	325	7	US-11-027-399-3313	Sequence 3313, Ap
843	71	2.7	426	7	US-11-031-206-160	Sequence 160, App	916	70.5	2.7	325	7	US-11-027-843-3313	Sequence 3313, Ap
844	71	2.7	466	1	PCT-US04-03169-44	Sequence 44, Appl	917	70.5	2.7	325	7	US-11-027-878-3313	Sequence 3313, Ap
845	71	2.7	493	5	US-09-836-544B-34	Sequence 34, Appl	918	70.5	2.7	325	7	US-11-028-169-3313	Sequence 3313, Ap
846	71	2.7	494	1	PCT-US04-09510-378	Sequence 378, App	919	70.5	2.7	325	7	US-11-028-204-3313	Sequence 3313, Ap
847	71	2.7	496	1	PCT-US04-09510-354	Sequence 354, App	920	70.5	2.7	325	7	US-11-027-877-3313	Sequence 3313, Ap
848	71	2.7	497	1	PCT-US04-09510-437	Sequence 437, App	921	70.5	2.7	325	7	US-11-027-879-3313	Sequence 3313, Ap
849	71	2.7	506	7	US-11-027-399-4594	Sequence 4594, Ap	922	70.5	2.7	325	7	US-11-028-149-3313	Sequence 3313, Ap
850	71	2.7	506	7	US-11-027-843-4594	Sequence 4594, Ap	923	70.5	2.7	325	7	US-11-027-802-3313	Sequence 3313, Ap
851	71	2.7	506	7	US-11-027-878-4594	Sequence 4594, Ap	924	70.5	2.7	325	7	US-11-027-890-3313	Sequence 3313, Ap
852	71	2.7	506	7	US-11-028-169-4594	Sequence 4594, Ap	925	70.5	2.7	325	7	US-11-027-892-3313	Sequence 3313, Ap
853	71	2.7	506	7	US-11-028-204-4594	Sequence 4594, Ap	926	70.5	2.7	325	7	US-11-028-099-3313	Sequence 3313, Ap
854	71	2.7	506	7	US-11-027-877-4594	Sequence 4594, Ap	927	70.5	2.7	325	7	US-11-028-197-3313	Sequence 3313, Ap
855	71	2.7	506	7	US-11-027-879-4594	Sequence 4594, Ap	928	70.5	2.7	325	7	US-11-027-844-3313	Sequence 3313, Ap
856	71	2.7	506	7	US-11-028-149-4594	Sequence 4594, Ap	929	70.5	2.7	325	7	US-11-028-050-3313	Sequence 3313, Ap
857	71	2.7	506	7	US-11-027-802-4594	Sequence 4594, Ap	930	70.5	2.7	325	7	US-11-028-457-3313	Sequence 3313, Ap
858	71	2.7	506	7	US-11-027-890-4594	Sequence 4594, Ap	931	70.5	2.7	325	7	US-11-027-891-3313	Sequence 3313, Ap
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861	71	2.7	506	7	US-11-028-197-4594	Sequence 4594, Ap	934	70.5	2.7	371	6	US-10-450-763-47299	Sequence 47299, A
862	71	2.7	506	7	US-11-027-844-4594	Sequence 4594, Ap	935	70.5	2.7	478	7	US-11-031-175-15753	Sequence 15753, A
863	71	2.7	506	7	US-11-028-050-4594	Sequence 4594, Ap	936	70.5	2.7	494	7	US-11-027-399-4784	Sequence 4784, Ap
864	71	2.7	506	7	US-11-028-457-4594	Sequence 4594, Ap	937	70.5	2.7	494	7	US-11-027-843-4784	Sequence 4784, Ap
865	71	2.7	506	7	US-11-027-891-4594	Sequence 4594, Ap	938	70.5	2.7	494	7	US-11-027-878-4784	Sequence 4784, Ap
866	71	2.7	506	7	US-11-028-291-4594	Sequence 4594, Ap	939	70.5	2.7	494	7	US-11-028-169-4784	Sequence 4784, Ap
867	71	2.7	520	7	US-11-027-399-3457	Sequence 3457, Ap	940	70.5	2.7	494	7	US-11-028-204-4784	Sequence 4784, Ap
868	71	2.7	520	7	US-11-027-843-3457	Sequence 3457, Ap	941	70.5	2.7	494	7	US-11-027-877-4784	Sequence 4784, Ap
869	71	2.7	520	7	US-11-027-878-3457	Sequence 3457, Ap	942	70.5	2.7	494	7	US-11-027-879-4784	Sequence 4784, Ap
870	71	2.7	520	7	US-11-028-169-3457	Sequence 3457, Ap	943	70.5	2.7	494	7	US-11-028-149-4784	Sequence 4784, Ap
871	71	2.7	520	7	US-11-028-204-3457	Sequence 3457, Ap	944	70.5	2.7	494	7	US-11-027-802-4784	Sequence 4784, Ap
872	71	2.7	520	7	US-11-027-877-3457	Sequence 3457, Ap	945	70.5	2.7	494	7	US-11-027-890-4784	Sequence 4784, Ap
873	71	2.7	520	7	US-11-027-879-3457	Sequence 3457, Ap	946	70.5	2.7	494	7	US-11-027-892-4784	Sequence 4784, Ap
874	71	2.7	520	7	US-11-028-149-3457	Sequence 3457, Ap	947	70.5	2.7	494	7	US-11-028-099-4784	Sequence 4784, Ap
875	71	2.7	520	7	US-11-027-802-3457	Sequence 3457, Ap	948	70.5	2.7	494	7	US-11-028-197-4784	Sequence 4784, Ap
876	71	2.7	520	7	US-11-027-890-3457	Sequence 3457, Ap	949	70.5	2.7	494	7	US-11-027-844-4784	Sequence 4784, Ap
877	71	2.7	520	7	US-11-027-892-3457	Sequence 3457, Ap	950	70.5	2.7	494	7	US-11-028-050-4784	Sequence 4784, Ap
878	71	2.7	520	7	US-11-028-099-3457	Sequence 3457, Ap	951	70.5	2.7	494	7	US-11-028-457-4784	Sequence 4784, Ap
879	71	2.7	520	7	US-11-028-197-3457	Sequence 3457, Ap	952	70.5	2.7	494	7	US-11-027-891-4784	Sequence 4784, Ap
880	71	2.7	520	7	US-11-027-844-3457	Sequence 3457, Ap	953	70.5	2.7	494	7	US-11-028-291-4784	Sequence 4784, Ap
881	71	2.7	520	7	US-11-028-050-3457	Sequence 3457, Ap	954	70.5	2.7	539	6	US-10-450-763-36013	Sequence 36013, A
882	71	2.7	520	7	US-11-028-457-3457	Sequence 3457, Ap	955	70.5	2.7	566	6	US-10-450-763-48578	Sequence 48578, A
883	71	2.7	520	7	US-11-027-891-3457	Sequence 3457, Ap	956	70.5	2.7	581	7	US-11-027-399-3011	Sequence 3011, Ap
884	71	2.7	520	7	US-11-028-291-3457	Sequence 3457, Ap	957	70.5	2.7	581	7	US-11-027-843-3011	Sequence 3011, Ap
885	71	2.7	522	6	US-10-450-763-54682	Sequence 54682, A	958	70.5	2.7	581	7	US-11-028-169-3011	Sequence 3011, Ap
886	71	2.7	542	7	US-11-031-175-16134	Sequence 16134, A	959	70.5	2.7	581	7	US-11-027-878-3011	Sequence 3011, Ap
887	71	2.7	543	6	US-10-494-853-3	Sequence 3, Appli	960	70.5	2.7	581	7	US-11-027-879-3011	Sequence 3011, Ap
888	71	2.7	603	7	US-11-031-175-9826	Sequence 9826, Ap	961	70.5	2.7	581	7	US-11-027-877-3011	Sequence 3011, Ap
889	71	2.7	613	7	US-11-031-175-11783	Sequence 11783, A	962	70.5	2.7	581	7	US-11-028-204-3011	Sequence 3011, Ap
890	71	2.7	659	6	US-10-450-763-60468	Sequence 60468, A	963	70.5	2.7	581	7	US-11-027-879-3011	Sequence 3011, Ap
891	71	2.7	682	6	US-10-450-763-60109	Sequence 60109, A	964	70.5	2.7	581	7	US-11-028-149-3011	Sequence 3011, Ap
892	71	2.7	714	7	US-11-031-175-15419	Sequence 15419, A	965	70.5	2.7	581	7	US-11-027-802-3011	Sequence 3011, Ap
893	71	2.7	780	1	PCT-US04-42360-1227	Sequence 1227, Ap	966	70.5	2.7	581	7	US-11-027-892-3011	Sequence 3011, Ap
894	71	2.7	792	7	US-11-031-175-12692	Sequence 12692, A	967	70.5	2.7	581	7	US-11-028-099-3011	Sequence 3011, Ap
895	71	2.7	794	6	US-10-499-353A-545	Sequence 545, App	968	70.5	2.7	581	7	US-11-028-197-3011	Sequence 3011, Ap
896	71	2.7	861	6	US-10-450-763-47789	Sequence 47789, A	969	70.5	2.7	581	7	US-11-027-844-3011	Sequence 3011, Ap
897	71	2.7	878	7	US-11-031-175-10577	Sequence 10577, A	970	70.5	2.7	581	7	US-11-028-050-3011	Sequence 3011, Ap
898	71	2.7	883	6	US-10-938-061-141	Sequence 141, App	971	70.5	2.7	581	7	US-11-028-457-3011	Sequence 3011, Ap
899	71	2.7	883	6	US-10-936-626-141	Sequence 141, App	972	70.5	2.7	581	7	US-11-027-891-3011	Sequence 3011, Ap
900	71	2.7	897	7	US-11-031-175-15636	Sequence 15636, A	973	70.5	2.7	581	7	US-11-028-291-3011	Sequence 3011, Ap
901	71	2.7	901	6	US-10-489-448-1474	Sequence 1474, Ap	974	70.5	2.7	583	7	US-11-031-175-10782	Sequence 10782, A



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976	70.5	2.7	610	6	US-10-450-763-34626	Sequence 34626, A	1049	70	2.7	307	7	US-11-031-175-10066	Sequence 10066, A
977	70.5	2.7	645	6	US-10-489-448-994	Sequence 994, App	1050	70	2.7	313	1	PCT-US03-15712-258	Sequence 258, App
978	70.5	2.7	651	6	US-10-450-763-48295	Sequence 48295, A	1051	70	2.7	352	6	US-10-450-763-55845	Sequence 55845, A
979	70.5	2.7	652	7	US-11-027-399-3360	Sequence 3360, Ap	1052	70	2.7	365	7	US-11-031-206-164	Sequence 164, App
980	70.5	2.7	652	7	US-11-027-843-3360	Sequence 3360, Ap	1053	70	2.7	391	7	US-11-031-175-14025	Sequence 14025, A
981	70.5	2.7	652	7	US-11-027-878-3360	Sequence 3360, Ap	1054	70	2.7	446	6	US-10-450-763-40640	Sequence 40640, A
982	70.5	2.7	652	7	US-11-028-169-3360	Sequence 3360, Ap	1055	70	2.7	472	1	PCT-US04-17965-868	Sequence 868, App
983	70.5	2.7	652	7	US-11-028-204-3360	Sequence 3360, Ap	1056	70	2.7	485	7	US-11-031-175-9878	Sequence 9878, Ap
984	70.5	2.7	652	7	US-11-027-877-3360	Sequence 3360, Ap	1057	70	2.7	494	1	PCT-US04-09510-442	Sequence 442, App
985	70.5	2.7	652	7	US-11-027-879-3360	Sequence 3360, Ap	1058	70	2.7	627	6	US-10-450-763-34171	Sequence 34171, A
986	70.5	2.7	652	7	US-11-028-149-3360	Sequence 3360, Ap	1059	70	2.7	627	6	US-10-450-763-42533	Sequence 42533, A
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988	70.5	2.7	652	7	US-11-027-890-3360	Sequence 3360, Ap	1061	70	2.7	745	6	US-10-450-763-34211	Sequence 34211, A
989	70.5	2.7	652	7	US-11-027-892-3360	Sequence 3360, Ap	1062	70	2.7	745	6	US-10-450-763-39468	Sequence 39468, A
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991	70.5	2.7	652	7	US-11-028-197-3360	Sequence 3360, Ap	1064	70	2.7	745	6	US-10-450-763-45249	Sequence 45249, A
992	70.5	2.7	652	7	US-11-027-844-3360	Sequence 3360, Ap	1065	70	2.7	755	7	US-11-031-175-11169	Sequence 11169, A
993	70.5	2.7	652	7	US-11-028-050-3360	Sequence 3360, Ap	1066	70	2.7	780	6	US-10-450-763-45448	Sequence 45448, A
994	70.5	2.7	652	7	US-11-028-457-3360	Sequence 3360, Ap	1067	70	2.7	798	6	US-10-450-763-58262	Sequence 58262, A
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998	70.5	2.7	668	6	US-10-450-763-52689	Sequence 52689, A	1071	70	2.7	898	7	US-11-027-843-3327	Sequence 3327, Ap
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1016	70.5	2.7	740	7	US-11-028-050-3225	Sequence 3225, Ap	1089	70	2.7	930	7	US-11-027-843-2885	Sequence 2885, Ap
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1178	69	2.6	242	7	US-11-027-878-4609	Sequence 4609, Ap	1251	2.6	466	1	PCT-US04-03169-41	Sequence 41, Appl
1179	69	2.6	242	7	US-11-028-169-4609	Sequence 4609, Ap	1252	2.6	466	1	PCT-US04-03169-45	Sequence 45, Appl
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1181	69	2.6	242	7	US-11-027-877-4609	Sequence 4609, Ap	1254	2.6	471	6	US-10-048-917A-1	Sequence 1, Appli
1182	69	2.6	242	7	US-11-027-879-4609	Sequence 4609, Ap	1255	2.6	471	6	US-10-048-917A-4	Sequence 4, Appli
1183	69	2.6	242	7	US-11-028-149-4609	Sequence 4609, Ap	1256	2.6	471	6	US-10-048-917A-5	Sequence 5, Appli
1184	69	2.6	242	7	US-11-027-802-4609	Sequence 4609, Ap	1257	2.6	471	6	US-10-048-917A-6	Sequence 6, Appli
1185	69	2.6	242	7	US-11-027-890-4609	Sequence 4609, Ap	1258	2.6	471	6	US-10-048-917A-7	Sequence 7, Appli
1186	69	2.6	242	7	US-11-027-892-4609	Sequence 4609, Ap	1259	2.6	471	6	US-10-048-917A-8	Sequence 8, Appli
1187	69	2.6	242	7	US-11-028-099-4609	Sequence 4609, Ap	1260	2.6	472	5	US-09-836-544B-21	Sequence 21, Appl
1188	69	2.6	242	7	US-11-028-197-4609	Sequence 4609, Ap	1261	2.6	492	1	PCT-US04-09510-427	Sequence 427, App
1189	69	2.6	242	7	US-11-027-844-4609	Sequence 4609, Ap	1262	2.6	493	1	PCT-US04-09510-376	Sequence 376, App
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Searched: 283416 seqs, 96216763 residues

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3: pir3:\*  
4: pir4:\*

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2	1044	39.8	481	2 S56299	hypothetical prote
3	889.5	33.9	372	2 T42426	conserved hypotet
4	583.5	22.2	458	2 C84134	hypothetical prote
5	574.5	21.9	878	2 S44543	hypothetical prote
6	570	21.7	459	2 E75324	ArgE/DapE/Acyl fam
7	457.5	17.4	437	2 A90449	deacetylase, proba
8	451.5	17.2	493	2 H72011	hypothetical prote
9	438.5	16.7	457	2 C95017	hypothetical prote
10	434.5	16.6	457	2 D97890	peptidase, M20/M25
11	426.5	16.3	470	2 G70870	hypothetical prote
12	424.5	16.2	463	2 E75327	ArgE/DapE/Acyl fam
13	420.5	16.0	483	2 AE3480	aminoacylase (EC 3
14	397	15.1	442	2 C87058	conserved hypotet
15	395	15.1	463	2 AG2589	hypothetical prote
16	395	15.1	507	2 G97371	hypothetical prote
17	395	15.1	507	2 G97371	hypothetical prote
18	228.5	8.7	378	2 AB1469	hypothetical prote
19	221	8.4	410	2 H90312	hypothetical prote
20	215	8.2	375	2 A42959	hypothetical prote
21	213	8.1	375	2 A85890	hypothetical prote
22	213	8.1	375	2 F91045	hypothetical prote
23	211.5	8.1	379	2 AB1108	hypothetical prote
24	211	8.0	375	2 AG0816	hypothetical prote
25	201	7.7	465	2 B97235	hypothetical prote
26	197.5	7.5	470	2 AD1277	hypothetical prote
27	196	7.5	381	2 F81073	hypothetical prote
28	194.5	7.4	384	2 B82973	hypothetical prote
29	192	7.3	383	2 A71650	hypothetical prote

30	191.5	7.3	381	2 B81797	hypothetical prote
31	191.5	7.3	411	2 B71451	hypothetical prote
32	190.5	7.3	470	2 AD1640	hypothetical prote
33	190	7.2	396	2 H72224	hypothetical prote
34	189	7.2	436	2 H69588	hypothetical prote
35	187	7.1	375	2 AD0371	hypothetical prote
36	187	7.1	426	2 B69876	hypothetical prote
37	184	7.0	427	2 F83984	hypothetical prote
38	183	7.0	387	2 AG3218	hypothetical prote
39	181	6.9	375	2 F84940	hypothetical prote
40	181	6.9	377	2 B82846	hypothetical prote
41	180.5	6.9	376	2 E90252	hypothetical prote
42	178.5	6.8	377	2 C82113	hypothetical prote
43	174.5	6.7	382	2 C97868	hypothetical prote
44	172	6.6	377	2 F64048	hypothetical prote
45	172	6.6	463	2 B69994	hypothetical prote
46	171.5	6.5	450	2 S43914	hypothetical prote
47	170.5	6.5	386	2 B87283	hypothetical prote
48	170.5	6.5	407	2 E89991	hypothetical prote
49	169	6.4	383	2 G83500	hypothetical prote
50	165	6.3	400	2 B72650	hypothetical prote
51	157.5	6.0	466	2 F95072	hypothetical prote
52	156	5.9	410	2 A64357	hypothetical prote
53	155.5	5.9	431	2 T29267	hypothetical prote
54	155.5	5.9	466	2 C97940	hypothetical prote
55	155	5.9	398	2 AB2622	hypothetical prote
56	155	5.9	398	2 B97404	hypothetical prote
57	154.5	5.9	474	2 E87650	hypothetical prote
58	153	5.8	389	2 AD0478	hypothetical prote
59	152	5.8	423	2 C83782	hypothetical prote
60	151	5.8	388	2 C71961	hypothetical prote
61	151	5.8	469	2 C89960	hypothetical prote
62	150.5	5.7	472	2 B86730	hypothetical prote
63	147.5	5.6	391	2 E87699	hypothetical prote
64	144	5.5	395	2 AB3543	hypothetical prote
65	143.5	5.5	407	2 JN0584	hypothetical prote
66	142.5	5.4	374	2 F98308	hypothetical prote
67	142.5	5.4	374	2 AE2974	hypothetical prote
68	142	5.4	455	2 E71074	hypothetical prote
69	141.5	5.4	365	2 E81307	hypothetical prote
70	141	5.4	408	2 A47488	hypothetical prote
71	140.5	5.4	401	2 B85200	hypothetical prote
72	140.5	5.4	753	2 T05649	hypothetical prote
73	139	5.3	474	2 F75133	hypothetical prote
74	138.5	5.3	403	2 H69362	hypothetical prote
75	137.5	5.2	399	2 T19180	hypothetical prote
76	137	5.2	383	2 D64546	hypothetical prote
77	135.5	5.2	467	2 B87070	hypothetical prote
78	135	5.1	299	2 C70349	hypothetical prote
79	133.5	5.1	412	2 C83297	hypothetical prote
80	132.5	5.1	470	2 S57902	hypothetical prote
81	132	5.0	383	2 B42377	hypothetical prote
82	132	5.0	383	2 F91239	hypothetical prote
83	132	5.0	383	2 C86087	hypothetical prote
84	131	5.0	374	2 D95388	hypothetical prote
85	130	5.0	443	2 H95251	hypothetical prote
86	130	5.0	443	2 E98116	hypothetical prote
87	129.5	4.9	384	2 A82996	hypothetical prote
88	127.5	4.9	441	2 E72579	hypothetical prote
89	127.5	4.9	471	2 E87340	hypothetical prote
90	126.5	4.8	448	2 A70578	hypothetical prote
91	125	4.8	414	2 D87448	hypothetical prote
92	123	4.7	383	2 AC0936	hypothetical prote
93	122.5	4.7	397	2 T19182	hypothetical prote
94	122	4.7	378	2 C82049	hypothetical prote
95	122	4.7	2291	1 A46147	hypothetical prote
96	121	4.6	369	2 C69256	hypothetical prote
97	121	4.6	592	2 E89772	hypothetical prote
98	119	4.5	346	2 D90156	hypothetical prote
99	119	4.5	381	2 B84935	hypothetical prote
100	118.5	4.5	394	2 T19181	hypothetical prote
101	118.5	4.5	443	2 T35974	hypothetical prote
102	117.5	4.5	362	2 H75398	hypothetical prote



103	113.5	4.3	435	2	A96506	probable aminoacyl	176	96.5	3.7	498	1	VHIV61	nucleoprotein - in
104	113	4.3	410	2	A41465	arginine deiminase	177	96.5	3.7	1622	2	T45240	hypothetical prote
105	113	4.3	465	2	H84058	Xaa-His dipeptidas	178	96.5	3.7	4613	2	T17409	polyketide synthas
106	112.5	4.3	337	2	G75160	acetyl ornithine d	179	96	3.7	485	2	E83775	aldehyde dehydroge
107	112.5	4.3	1176	2	JN0583	myosin-light-chain	180	96	3.7	633	2	E90244	hypothetical prote
108	110.5	4.2	596	2	T38349	carboxypeptidase s	181	95.5	3.6	325	2	F71179	hypothetical prote
109	110.5	4.2	1420	2	T17158	CL2AB protein - ra	182	95.5	3.6	406	2	S60962	hypothetical prote
110	110.5	4.2	1435	2	T46611	CL2BB protein - ra	183	95.5	3.6	480	2	G70302	conserved hypothet
111	110.5	4.2	1452	2	T17157	CL2AA protein - ra	184	95.5	3.6	498	1	VHIVX5	nucleoprotein - in
112	110.5	4.2	1463	2	T17159	CL2AC protein - ra	185	95.5	3.6	546	2	A95600	conserved hypothet
113	110.5	4.2	1467	2	T17160	CL2BA protein - ra	186	95.5	3.6	809	2	A55547	quinate-shikimate
114	110.5	4.2	1478	2	T17185	CL2BC protein - ra	187	95.5	3.6	901	2	AH2290	cyanophycin synthe
115	110.5	4.2	1487	2	T14324	alpha-latrototoxin r	188	95.5	3.6	955	2	F97861	excinuclease ABC s
116	110	4.2	438	2	C96507	hypothetical prote	189	95.5	3.6	1029	2	E85043	probable pre-mRNA
117	110	4.2	650	2	E82937	DNA topoisomerase,	190	95.5	3.6	1147	2	A59307	myosin-light-chain
118	110	4.2	1193	2	JC2489	peptidyl-dipeptida	191	95.5	3.6	1285	2	B72420	hypothetical prote
119	108.5	4.1	1003	2	JH0823	FL-160-2 protein -	192	95.5	3.6	1381	2	S71288	protoporphylin IX
120	108.5	4.1	2425	2	D69426	surface layer prot	193	95.5	3.6	1733	2	D70887	probable polyketid
121	106.5	4.1	321	2	AI1086	PTS system mannose	194	95	3.6	443	2	T27877	hypothetical prote
122	105.5	4.0	403	2	A91097	probable deacetyla	195	95	3.6	454	2	S01092	amine oxidase (cop
123	105.5	4.0	403	2	H65070	hypothetical prote	196	95	3.6	757	2	E64889	DNA polymerase I l
124	105.5	4.0	403	2	E85942	probable deacetyla	197	95	3.6	876	2	G89952	probable DNA-direc
125	105.5	4.0	453	2	AB1867	GTP binding protei	198	95	3.6	1416	2	D71350	mycocerosate synth
126	104.5	4.0	1218	2	E84537	hypothetical prote	199	95	3.6	2110	2	B44110	phosphoglycerate k
127	104.5	4.0	1430	2	T12449	hypothetical prote	200	94.5	3.6	402	2	B71830	N-acyl-L-amino aci
128	104	4.0	1155	2	D70148	DNA-directed RNA p	201	94.5	3.6	404	2	E83851	hypothetical prote
129	104	4.0	1380	2	S64721	protoporphylin IX	202	94.5	3.6	434	2	D83133	histone acetyltra
130	103.5	3.9	321	2	AH1450	PTS system mannose	203	94.5	3.6	473	2	B90193	T17H3.1 protein -
131	103.5	3.9	1415	2	S52267	DNA polymerase III	204	94.5	3.6	568	2	B86400	hypothetical prote
132	103.5	3.9	1438	2	C89900	DNA polymerase III	205	94.5	3.6	571	2	T29751	probable acetate-C
133	103	3.9	504	2	T36703	DNA polymerase III	206	94.5	3.6	662	2	T41215	probable sulfatase
134	103	3.9	979	2	G90459	formate dehydrogen	207	94.5	3.6	787	2	B70643	transcription-repa
135	102	3.9	383	2	T00674	hypothetical prote	208	94.5	3.6	1179	2	AG1463	1,3-beta-glucanase
136	101.5	3.9	393	2	H90291	thermostable carbo	209	94	3.6	342	2	S72529	hypothetical prote
137	101.5	3.9	629	2	A71023	arginine-tRNA liga	210	94	3.6	447	2	C86233	hypothetical prote
138	101.5	3.9	944	2	T18911	hypothetical prote	211	94	3.6	579	2	AB1855	hypothetical prote
139	101	3.9	151	2	S77763	hypothetical prote	212	94	3.6	733	2	E69007	translation elonga
140	101	3.9	2116	2	C86926	probable mycoceros	213	94	3.6	777	2	T38769	hypothetical prote
141	100.5	3.8	623	2	G95180	ABC transporter, A	214	94	3.6	785	2	AB1582	MutS protein (MutS
142	100.5	3.8	656	2	E71080	probable DNA-bindi	215	94	3.6	873	2	S75028	hypothetical prote
143	100.5	3.8	895	2	I53908	major vault protei	216	94	3.6	901	2	G71286	probable pyruvate,
144	100.5	3.8	1473	2	A20872	ovostatin precursor	217	94	3.6	1028	2	A45388	protein-tyrosine k
145	100	3.8	462	2	T02726	probable protein k	218	94	3.6	1058	2	AG2541	cation efflux syst
146	100	3.8	613	2	T35828	acetolactate synth	219	94	3.6	1331	1	XORTDH	xanthine dehydroge
147	100	3.8	887	2	S43196	[protein-P1I] urid	220	94	3.6	1546	2	F75461	DNA-directed RNA p
148	100	3.8	1075	2	S76433	cation efflux syst	221	94	3.6	4077	2	T17484	hypothetical prote
149	99.5	3.8	370	2	C75268	carboxypeptidase G	222	93.5	3.6	426	2	AE1535	3-hydroxy-3-methyl
150	99.5	3.8	452	2	T45448	probable serine pr	223	93.5	3.6	498	1	VHIVN7	nucleoprotein - in
151	99.5	3.8	466	2	AH3100	amidohydrolase [im	224	93.5	3.6	498	1	VHIVX6	threonine ammonia-
152	99.5	3.8	466	2	B98186	probable hydrolase	225	93.5	3.6	595	2	A38628	calcium-dependent
153	99.5	3.8	623	2	AF1473	transcription anti	226	93.5	3.6	639	1	T02784	env polyprotein pr
154	99.5	3.8	653	2	B75105	probable DNA helic	227	93.5	3.6	666	1	VCMVHL	chemotaxis protein
155	99	3.8	1276	2	S11455	botulinum neurotox	228	93.5	3.6	777	2	A35966	conserved hypothet
156	98.5	3.8	184	2	A99229	acetylornithine de	229	93.5	3.6	1613	2	E82193	ABC transporter (A
157	98.5	3.8	351	2	E87317	hypothetical prote	230	93	3.5	255	2	AH1709	N-acyl-L-amino aci
158	98.5	3.8	793	2	H91051	hypothetical prote	231	93	3.5	393	2	AF1500	hypothetical prote
159	98.5	3.8	793	2	D85896	probable peptide s	232	93	3.5	413	2	F70211	hypothetical prote
160	98.5	3.8	873	1	JH0182	nitrate reductase	233	93	3.5	414	2	A83745	N-carbamyl-L-amino
161	98.5	3.8	1617	2	T28153	complement C4 - ch	234	93	3.5	498	1	VHIVX3	nucleoprotein - in
162	98.5	3.8	10797	2	T30192	probable peptidase	235	93	3.5	498	1	VHIVX4	nucleoprotein - in
163	98	3.7	372	2	E83833	hypothetical prote	236	93	3.5	767	2	S63182	hypothetical prote
164	98	3.7	498	1	VHIVX2	nucleoprotein - in	237	93	3.5	896	2	S57723	lrp protein - huma
165	98	3.7	2111	2	A70568	mycocerosate synth	238	93	3.5	1309	1	S35484	peptidyl-dipeptida
166	97.5	3.7	400	2	T41596	probable acetylorn	239	92.5	3.5	382	2	H86930	probable secreted
167	97.5	3.7	402	2	A64688	probable phosphogl	240	92.5	3.5	393	2	AC1142	N-acyl-L-amino aci
168	97.5	3.7	959	2	S32016	flagellum-associat	241	92.5	3.5	489	1	S66088	conserved hypothet
169	97.5	3.7	2672	2	A48126	translational activa	242	92.5	3.5	498	1	VHIV68	nucleoprotein - in
170	97	3.7	344	2	E71291	flagellar motor sw	243	92.5	3.5	837	2	JN0292	antigen 332 - mala
171	97	3.7	385	2	E64436	conserved hypothet	244	92.5	3.5	843	2	A47132	major vault protei
172	97	3.7	1541	2	T02831	AAA protein I4171.	245	92.5	3.5	953	2	D71645	excinuclease ABC c
173	97	3.7	1628	2	T43682	nucleoporin - fiss	246	92.5	3.5	1354	2	T48198	hypothetical prote
174	96.5	3.7	372	2	D86695	acetylornithine de	247	92.5	3.5	1501	2	S50992	SNQ2 protein - yea
175	96.5	3.7	498	1	VHIV8H	nucleoprotein - in	248	92.5	3.5	1900	2	AG2391	serine/threonine k

249 92 3.5 411 2 T49883 glutamate dehydrog  
250 92 3.5 423 2 E75103 phosphoesterase ho  
251 92 3.5 571 1 A36829 hemagglutinin-neur  
252 92 3.5 576 2 G72277 NH(3)-dependent NA  
253 92 3.5 588 1 E64061 aspartate-tRNA lig  
254 92 3.5 687 2 T47403 amine oxidase-like  
255 92 3.5 690 2 E72337 translation initia  
256 92 3.5 844 2 T05227 hypothetical prote  
257 92 3.5 880 2 E69680 DNA polymerase I p  
258 92 3.5 889 2 H84506 probable retroelem  
259 92 3.5 1036 2 T30311 S-layer protein -  
260 92 3.5 1059 2 T12195 sucrose-phosphate  
261 92 3.5 1117 2 S33851 fibronectin-bindin  
262 92 3.5 1568 2 T08616 aggregation factor  
263 91.5 3.5 370 2 I40358 N-acyl-L-amino aci  
264 91.5 3.5 391 2 C72220 conserved hypothet  
265 91.5 3.5 500 1 A53377 transcription term  
266 91.5 3.5 565 2 H82610 sodium/proton exch  
267 91.5 3.5 702 1 JU0401 cryptophan synthas  
268 91.5 3.5 730 2 E83951 translation initia  
269 91.5 3.5 959 2 AB0111 glycine dehydrogen  
270 91.5 3.5 1732 2 T14039 protein kinase (EC  
271 91.5 3.5 3418 1 G02334 breast cancer tumo  
272 91 3.5 234 2 B29792 adenylate kinase (  
273 91 3.5 241 2 JS0422 adenylate kinase (  
274 91 3.5 319 2 T38793 glycerophosphoryl  
275 91 3.5 414 2 B97245 probable selenocys  
276 91 3.5 604 2 B90289 conserved hypothet  
277 91 3.5 621 2 AC1654 asparagine synthet  
278 91 3.5 732 2 T19570 hypothetical prote  
279 91 3.5 737 1 A34402 peptidyl-dipeptida  
280 91 3.5 871 2 E97035 DNA polymerase I,  
281 91 3.5 1071 2 T18597 hypothetical prote  
282 90.5 3.5 500 2 AI0901 L factor imported  
283 90.5 3.5 505 2 AC3361 GRP-binding protei  
284 90.5 3.5 519 2 T51496 hypothetical prote  
285 90.5 3.5 560 1 F69059 arginine-tRNA liga  
286 90.5 3.5 603 2 AD1582 excinuclease ABC c  
287 90.5 3.5 711 2 A72375 hypothetical prote  
288 90.5 3.5 1167 1 A35066 streptococcal C5a  
289 90.5 3.5 1496 2 T45808 helicase-like prot  
290 90.5 3.5 1504 2 T17426 FK506 polyketide s  
291 90.5 3.5 1513 2 A70982 probable ATP-depen  
292 90.5 3.5 1679 2 S49802 probable membrane  
293 90.5 3.5 1963 2 T49914 callose synthase c  
294 90 3.4 372 2 T08273 conserved hypothet  
295 90 3.4 426 2 H70390 conserved hypothet  
296 90 3.4 435 2 C70509 hypothetical prote  
297 90 3.4 455 2 E64454 proline-tRNA ligas  
298 90 3.4 621 2 AG1282 asparagine synthet  
299 90 3.4 647 2 AF1488 transcription anti  
300 90 3.4 1092 1 JN0635 neural cell adhesi  
301 90 3.4 1120 2 H71664 transcription-repa  
302 90 3.4 1260 2 A86323 protein F14D16.3 [  
303 90 3.4 1850 2 AC1917 serine/threonine k  
304 90 3.4 2410 2 T43731 cell wall alpha-gl  
305 89.5 3.4 335 2 S63612 probable acyltrans  
306 89.5 3.4 374 2 H83693 carboxypeptidase G  
307 89.5 3.4 380 2 H72374 probable phosphori  
308 89.5 3.4 393 2 A99361 thermostable carbo  
309 89.5 3.4 396 2 AC1751 phosphoglycerate k  
310 89.5 3.4 401 2 F65063 Cysteine sulfinate  
311 89.5 3.4 460 2 F71292 probable GTP-bindi  
312 89.5 3.4 478 2 F71171 probable pyruvate  
313 89.5 3.4 480 2 B70446 hypothetical prote  
314 89.5 3.4 481 2 H97054 ribonucleases G/E  
315 89.5 3.4 527 2 AI3494 chromosomal replic  
316 89.5 3.4 542 2 E90604 hypothetical prote  
317 89.5 3.4 711 2 F86373 protein T23E23.12  
318 89.5 3.4 715 2 S73637 ATP-dependent prot  
319 89.5 3.4 941 2 S78633 isoleucine-tRNA li  
320 89.5 3.4 1120 2 T01863 hypothetical prote  
321 89.5 3.4 1179 2 AG1101 transcription-repa

322 89.5 3.4 1309 2 F82207 ATP-dependent heli  
323 89.5 3.4 1344 2 S47412 gene P2 protein -  
324 89.5 3.4 1742 2 T49451 kinesin-like prote  
325 89 3.4 410 2 S68515 probable arginine  
326 89 3.4 424 2 B99262 conserved hypothet  
327 89 3.4 441 2 G98348 n-carbamoyl-beta-a  
328 89 3.4 478 2 T12683 embryogenesis prot  
329 89 3.4 493 2 A87459 cytosol aminopepti  
330 89 3.4 574 1 B42374 phosphotransferase  
331 89 3.4 732 1 A35655 peptidyl-dipeptida  
332 89 3.4 794 2 T39171 probable peroxisom  
333 89 3.4 829 2 T19494 hypothetical prote  
334 89 3.4 876 2 A84044 DNA polymerase I p  
335 89 3.4 1312 1 A34171 peptidyl-dipeptida  
336 89 3.4 1313 1 JC2038 peptidyl-dipeptida  
337 89 3.4 1383 2 T07126 magnesium chelatas  
338 89 3.4 15281 2 S41309 cyclosporin synthe  
339 88.5 3.4 396 2 AB1382 phosphoglycerate k  
340 88.5 3.4 449 2 C69086 chorismate mutase  
341 88.5 3.4 487 1 A64472 carbamoyl-phosphat  
342 88.5 3.4 500 1 JT0482 glucokinase (EC 2.  
343 88.5 3.4 520 2 AD2616 chromosomal replic  
344 88.5 3.4 529 2 D97398 dnaA protein (L254  
345 88.5 3.4 603 2 AB1229 excinuclease ABC c  
346 88.5 3.4 623 2 C98048 hypothetical prote  
347 88.5 3.4 755 2 B41836 amine oxidase (fla  
348 88.5 3.4 901 2 F89910 aconitate hydratase  
349 88.5 3.4 3746 1 YGPLV3 alpha-aminoadipyl-  
350 88 3.4 357 2 A39875 alpha-2-macroglobu  
351 88 3.4 358 2 C72626 hypothetical prote  
352 88 3.4 426 2 AE2446 processing protein  
353 88 3.4 444 2 E69102 sensory transducti  
354 88 3.4 505 2 F70104 hypothetical prote  
355 88 3.4 510 2 T47704 pyruvate kinase-li  
356 88 3.4 562 2 E72608 probable hyuB APE1  
357 88 3.4 576 2 G86893 cell division regu  
358 88 3.4 653 2 AB1128 transcription anti  
359 88 3.4 721 2 AF1254 penicillin-binding  
360 88 3.4 780 1 KIHUFM 6-phosphofructokin  
361 88 3.4 802 2 I39665 penicillin amidase  
362 88 3.4 838 2 D75304 probable alpha-glu  
363 88 3.4 992 2 A42318 glycogen phosphory  
364 88 3.4 1134 2 D75014 hypothetical prote  
365 88 3.4 1241 2 F97286 DNA-dependent RNA  
366 88 3.4 1816 2 F83901 hypothetical prote  
367 87.5 3.3 160 2 A89883 hypothetical prote  
368 87.5 3.3 331 2 AI0505 probable transcrip  
369 87.5 3.3 350 2 D72259 hypothetical prote  
370 87.5 3.3 392 2 A44852 pectate lyase (EC  
371 87.5 3.3 393 1 WZWC6A pectate lyase (EC  
372 87.5 3.3 401 2 F91087 hypothetical prote  
373 87.5 3.3 449 2 AB1546 glutathione-disulf  
374 87.5 3.3 498 1 VHIVAK nucleoprotein - in  
375 87.5 3.3 498 1 VHIVN5 nucleoprotein - in  
376 87.5 3.3 499 2 T10680 cytochrome P450 mo  
377 87.5 3.3 610 2 T37956 probable vacuolar  
378 87.5 3.3 725 2 JE0100 neural cell adhesi  
379 87.5 3.3 732 1 S05238 peptidyl-dipeptida  
380 87.5 3.3 766 2 H83141 probable two-compo  
381 87.5 3.3 925 2 S69539 hypothetical prote  
382 87.5 3.3 1027 2 AC1841 glycerophosphoryl  
383 87.5 3.3 1052 2 I53012 focal adhesion kin  
384 87.5 3.3 1168 2 H89816 transcription-repa  
385 87.5 3.3 1234 2 G70622 probable transcrip  
386 87.5 3.3 1306 1 A31759 peptidyl-dipeptida  
387 87.5 3.3 1377 2 AG3345 DNA-directed RNA p  
388 87.5 3.3 1587 2 G86467 hypothetical prote  
389 87.5 3.3 2150 2 T08165 RNA1 polypeptide -  
390 87.5 3.3 2712 2 T30949 hypothetical prote  
391 87.5 3.3 3864 2 D87757 protein C44E4.1a l  
392 87.5 3.3 5762 2 A41819 proline-rich pepti  
393 87.5 3.3 5762 2 A41819 proline-rich pepti  
394 87 3.3 334 2 H75362 hypothetical prote

395	87	3.3	363	2	C90197	transposase ISCl35	468	86	3.3	903	2	T47316	hypothetical prote
396	87	3.3	382	2	F71008	probable sarcosine	469	86	3.3	911	1	RDTONH	nitrate reductase
397	87	3.3	399	2	H75207	26S proteinase reg	470	86	3.3	923	2	B87629	preprotein translo
398	87	3.3	495	1	P1WLB	L1 protein - bovin	471	86	3.3	1247	2	A33812	interphotoreceptor
399	87	3.3	514	2	G01026	serine-trNA ligase	472	86	3.3	1344	2	AD2103	two-component hybr
400	87	3.3	544	2	F82557	hypothetical prote	473	86	3.3	1946	2	AE1449	hypothetical prote
401	87	3.3	576	2	S16693	Gly-X carboxypepti	474	85.5	3.3	259	1	PMHUBM	bisphosphoglycerat
402	87	3.3	631	2	A53623	yolk protein facto	475	85.5	3.3	357	2	B71003	hypothetical prote
403	87	3.3	637	2	B95878	probable adenylate	476	85.5	3.3	416	2	T36130	probable PTS trans
404	87	3.3	646	2	G85056	probable receptor-	477	85.5	3.3	451	2	T16162	hypothetical prote
405	87	3.3	672	2	S46276	acetate-CoA ligase	478	85.5	3.3	484	2	S25002	1-aminocyclopropan
406	87	3.3	700	2	A56976	transfer complex p	479	85.5	3.3	552	2	D82421	conserved hypothet
407	87	3.3	704	2	G96587	hypothetical prote	480	85.5	3.3	633	2	B69961	conserved hypothet
408	87	3.3	738	2	A87516	dipeptidyl peptida	481	85.5	3.3	655	2	E75206	alpha-amylase (or
409	87	3.3	912	2	C71004	probable ATP-depen	482	85.5	3.3	662	2	D54078	methyl-accepting c
410	87	3.3	1117	2	AE0075	hypothetical prote	483	85.5	3.3	696	2	B97227	glutamine syntheta
411	87	3.3	1224	2	A25884	DNA-directed RNA p	484	85.5	3.3	719	1	MNXR3D	nonstructural prot
412	87	3.3	1507	2	D97106	large chain of NAD	485	85.5	3.3	732	2	F87469	TonB-dependent rec
413	87	3.3	4639	1	A54794	dyein heavy chain	486	85.5	3.3	732	2	D86506	exodeoxyribonuclea
414	87	3.3	6359	2	T31679	bacitracin synthet	487	85.5	3.3	843	2	S38364	membrane alanyl am
415	86.5	3.3	267	2	S38373	interleukin-1 beta	488	85.5	3.3	867	2	A81707	ATP-dependent Clp
416	86.5	3.3	284	2	B69945	phage-related prot	489	85.5	3.3	867	2	B96625	hypothetical prote
417	86.5	3.3	285	2	B90445	regucalcin homolog	490	85.5	3.3	867	2	D75091	large helicase-rel
418	86.5	3.3	334	2	A75495	6-phosphofructokin	491	85.5	3.3	933	2	H90247	ATP-dependent heli
419	86.5	3.3	401	2	H85932	hypothetical prote	492	85.5	3.3	1019	2	F70342	cation efflux syst
420	86.5	3.3	404	2	AD0032	probable type-III	493	85.5	3.3	1105	2	S76557	carbamoyl-phosphat
421	86.5	3.3	411	2	S71217	glutamate dehydrog	494	85.5	3.3	1230	2	S53974	hypothetical prote
422	86.5	3.3	412	2	JC6317	glutamate dehydrog	495	85.5	3.3	1232	2	I38496	anion exchanger 3
423	86.5	3.3	415	2	S28088	gene B protein - Y	496	85.5	3.3	1233	2	T04251	p-glycoprotein 2 -
424	86.5	3.3	468	2	T10595	hypothetical prote	497	85.5	3.3	1433	2	B83952	DNA polymerase III
425	86.5	3.3	479	2	A84588	probable tyrosine	498	85.5	3.3	1780	2	A85045	probable glucan sy
426	86.5	3.3	516	2	JC5375	orphan nuclear rec	499	85.5	3.3	2670	2	T37919	GCN1 homolog - fis
427	86.5	3.3	533	2	A70464	D-3-phosphoglycera	500	85	3.2	284	2	D72413	thioredoxin reduct
428	86.5	3.3	635	2	AI0625	ABC transporter At	501	85	3.2	332	2	T51269	hypothetical prote
429	86.5	3.3	638	2	A36929	virulence regulato	502	85	3.2	338	2	T04891	hyuC protein homol
430	86.5	3.3	679	2	S64258	hypothetical prote	503	85	3.2	405	2	B30768	tryptophan synthas
431	86.5	3.3	705	2	B82044	guanosine-3',5'-bi	504	85	3.2	408	1	JQ2126	tryptophan synthas
432	86.5	3.3	732	2	A72118	exodeoxyribonuclea	505	85	3.2	443	2	F71549	hypothetical prote
433	86.5	3.3	802	2	S49252	penicillin amidase	506	85	3.2	451	1	C64186	pmbA protein - Hae
434	86.5	3.3	1046	2	T34566	hypothetical prote	507	85	3.2	485	2	C89978	glutamyl-trNAGln a
435	86.5	3.3	1075	2	T07448	hypothetical prote	508	85	3.2	495	1	FJEC	transcription term
436	86.5	3.3	1169	2	G72571	probable DNA-direc	509	85	3.2	495	2	B91135	transcription term
437	86.5	3.3	1420	2	T18385	latrophilin-2 (spl	510	85	3.2	495	2	B85980	transcription term
438	86.5	3.3	1426	2	A99580	hypothetical prote	511	85	3.2	498	1	VHIV34	nucleoprotein - in
439	86.5	3.3	1435	2	T18387	latrophilin-2 (spl	512	85	3.2	529	2	A69025	translation elonga
440	86.5	3.3	1444	2	AD1602	DNA polymerase III	513	85	3.2	547	2	F69964	amino acid degrada
441	86.5	3.3	1448	2	F83237	probable ATP-depen	514	85	3.2	592	2	D70327	glutamine-fructose
442	86.5	3.3	1463	2	T18386	latrophilin-2 (spl	515	85	3.2	695	2	G87316	nuclease, probable
443	86.5	3.3	1478	2	T18388	latrophilin-2 (spl	516	85	3.2	713	2	D85503	lysine decarboxyla
444	86.5	3.3	1944	2	AH3098	rhizobiocin/RTX to	517	85	3.2	713	2	D90652	lysine decarboxyla
445	86.5	3.3	1990	2	A96188	probable phosphoes	518	85	3.2	713	2	B64743	lysine decarboxyla
446	86.5	3.3	2137	1	SJHUB	spectrin beta chai	519	85	3.2	734	2	F88098	protein F18A12.4 l
447	86	3.3	332	2	C90497	transposase ISC135	520	85	3.2	818	2	F89819	endopeptidase limp
448	86	3.3	334	2	T41209	thioredoxin-disulf	521	85	3.2	932	2	F69552	leucyl-tRNA synthe
449	86	3.3	363	2	T41209	mannose-1-phosphat	522	85	3.2	960	2	AF1940	isoleucyl-tRNA syn
450	86	3.3	393	1	IBBYFC	ferrochelatase (EC	523	85	3.2	1141	2	T24176	hypothetical prote
451	86	3.3	432	2	AC0161	serine-type D-Ala-	524	85	3.2	1266	2	T27024	hypothetical prote
452	86	3.3	468	2	C83774	succinate-semialde	525	85	3.2	1285	2	S70582	botulinum neurotox
453	86	3.3	470	2	B83991	glycolate oxidase	526	85	3.2	1291	2	T21267	hypothetical prote
454	86	3.3	491	1	JN0491	X-Pro aminopeptida	527	85	3.2	1498	2	AF1082	B. subtilis Yuka p
455	86	3.3	520	2	T20226	hypothetical prote	528	85	3.2	1576	2	AE0249	probable hemolysin
456	86	3.3	571	2	S40164	hemagglutinin-neur	529	85	3.2	1692	2	G01449	probable mucin G2
457	86	3.3	618	2	B83853	hypothetical prote	530	85	3.2	1768	2	T27023	hypothetical prote
458	86	3.3	658	1	S73805	DNA ligase (NAD) (	531	85	3.2	1926	2	JC4842	DNA-binding nuclea
459	86	3.3	697	2	T37946	tryptophan synthas	532	84.5	3.2	226	2	F85842	probable tail comp
460	86	3.3	702	1	SHECGD	guanosine-3',5'-bi	533	84.5	3.2	226	2	C90877	probable tail asse
461	86	3.3	702	2	E91194	(p)ppGpp synthetas	534	84.5	3.2	281	2	A72472	probable electron
462	86	3.3	702	2	F86041	guanosine-3',5'-bi	535	84.5	3.2	332	2	E95033	PTS system, mannos
463	86	3.3	760	2	T31556	hypothetical prote	536	84.5	3.2	332	2	E97904	phosphotransferase
464	86	3.3	847	2	S51965	hypothetical prote	537	84.5	3.2	334	2	G75069	cytochrome-c3 hydr
465	86	3.3	867	2	H90524	preprotein translo	538	84.5	3.2	335	2	T12460	hypothetical prote
466	86	3.3	881	2	B82097	protein-P-II uridy	539	84.5	3.2	343	2	F84653	hypothetical prote
467	86	3.3	898	1	RDBJNH	nitrate reductase	540	84.5	3.2	401	2	B87503	acyl-CoA dehydroge





687	82.5	3.1	236	2	D70783	probable two compo
688	82.5	3.1	267	2	A75217	hypothetical prote
689	82.5	3.1	372	2	G84220	glutamate dehydrog
690	82.5	3.1	448	2	T03776	tat binding protei
691	82.5	3.1	481	2	A84294	Htr9 transducer [i
692	82.5	3.1	482	2	T44973	transducer protein
693	82.5	3.1	487	2	S65811	finger protein (cl
694	82.5	3.1	503	2	D64478	hypothetical prote
695	82.5	3.1	514	2	C90060	1-pyrroline-5-carb
696	82.5	3.1	521	2	A37806	amidase (EC 3.5.1.
697	82.5	3.1	521	2	S15070	amidase (EC 3.5.1.
698	82.5	3.1	566	2	B70469	type IV pilus asse
699	82.5	3.1	584	2	A90451	conserved hypothet
700	82.5	3.1	592	2	E70455	sulfur oxidation p
701	82.5	3.1	648	1	DJBP82	DNA-directed DNA p
702	82.5	3.1	667	2	F70124	guanosine-3',5'-bi
703	82.5	3.1	688	2	D96930	methyl-accepting c
704	82.5	3.1	691	2	D84889	probable receptor-
705	82.5	3.1	705	1	I39759	xylan 1,4-beta-xyl
706	82.5	3.1	738	2	AC1265	(p)ppGpp synthetas
707	82.5	3.1	738	2	AE1627	(p)ppGpp synthetas
708	82.5	3.1	755	1	S20922	photosystem I prot
709	82.5	3.1	757	2	S68142	probable transcrip
710	82.5	3.1	783	2	AH3592	ribonuclease R (EC
711	82.5	3.1	843	2	S44868	kinesin heavy chai
712	82.5	3.1	856	2	G71133	probable alpha-man
713	82.5	3.1	875	1	S66672	phosphatidylinosit
714	82.5	3.1	889	2	AB0790	probable two-compo
715	82.5	3.1	1047	2	B71402	hypothetical prote
716	82.5	3.1	1052	2	JC4200	protein-tyrosine k
717	82.5	3.1	1097	2	JQ0301	hypothetical 127K
718	82.5	3.1	1099	2	T30307	rexB protein - Lac
719	82.5	3.1	1222	2	S56030	SCP160 protein - Y
720	82.5	3.1	1338	2	A49634	aldehyde oxidase (
721	82.5	3.1	1544	2	G96904	DNA segregation AT
722	82.5	3.1	1646	1	WMTMS2	186K protein - cuc
723	82.5	3.1	1906	1	S68235	myosin-light-chain
724	82.5	3.1	2165	1	RNRZA2	genome polyprotein
725	82.5	3.1	2351	2	G71415	hypothetical prote
726	82.5	3.1	2500	2	G88493	protein F57B9.2 [i
727	82	3.1	201	1	DAPSAA	protocatechuate 3,
728	82	3.1	268	2	AD3496	ABC transporter su
729	82	3.1	288	2	S73455	fructose-bisphosph
730	82	3.1	295	2	S67860	gumK protein - Xan
731	82	3.1	324	2	S28309	hypothetical prote
732	82	3.1	332	2	AE1396	zinc-binding dehyd
733	82	3.1	334	4	PRHVER	retrovirus-related
734	82	3.1	345	2	C71651	uroporphyrinogen d
735	82	3.1	379	2	C84253	hypothetical prote
736	82	3.1	392	2	T24240	hypothetical prote
737	82	3.1	406	2	E72545	hypothetical prote
738	82	3.1	442	2	H72209	hypothetical prote
739	82	3.1	452	2	C97162	UDP-N-acetylmuramy
740	82	3.1	468	2	D83218	hypothetical prote
741	82	3.1	471	2	T48743	probable 26S ATP/u
742	82	3.1	498	1	VHIVN8	nucleoprotein - in
743	82	3.1	543	1	TVHUYS	protein-tyrosine k
744	82	3.1	558	2	I56545	glypican precursor
745	82	3.1	586	1	E69314	replication licens
746	82	3.1	597	2	D70100	phosphoglucomutase
747	82	3.1	616	1	HNNZU1	hemagglutinin-neur
748	82	3.1	631	2	T37384	nucleoside triphos
749	82	3.1	631	2	C72163	OLL protein - vari
750	82	3.1	631	2	H36847	nucleoside-triphos
751	82	3.1	631	2	T28539	hypothetical prote
752	82	3.1	635	2	C71021	hypothetical prote
753	82	3.1	647	2	C69102	DNA mismatch recog
754	82	3.1	649	2	A49512	alpha-amylase (EC
755	82	3.1	664	2	AD1494	NADH flavin oxidor
756	82	3.1	703	2	AC2430	hypothetical prote
757	82	3.1	707	2	S78538	site-specific reco
758	82	3.1	721	2	AD1617	penicillin-binding
759	82	3.1	760	2	D87553	exoribonuclease, v
760	82	3.1	760	2	probable two compo	
761	82	3.1	761	1	hypothetical prote	
762	82	3.1	762	2	glutamate dehydrog	
763	82	3.1	763	2	tat binding protei	
764	82	3.1	764	2	Htr9 transducer [i	
765	82	3.1	765	2	transducer protein	
766	82	3.1	766	2	finger protein (cl	
767	82	3.1	767	2	hypothetical prote	
768	82	3.1	768	2	1-pyrroline-5-carb	
769	82	3.1	769	2	amidase (EC 3.5.1.	
770	82	3.1	770	2	amidase (EC 3.5.1.	
771	82	3.1	771	2	type IV pilus asse	
772	82	3.1	772	2	conserved hypothet	
773	82	3.1	773	2	sulfur oxidation p	
774	82	3.1	774	2	DNA-directed DNA p	
775	81.5	3.1	775	2	guanosine-3',5'-bi	
776	81.5	3.1	776	2	methyl-accepting c	
777	81.5	3.1	777	2	probable receptor-	
778	81.5	3.1	778	2	xylan 1,4-beta-xyl	
779	81.5	3.1	779	2	(p)ppGpp synthetas	
780	81.5	3.1	780	2	(p)ppGpp synthetas	
781	81.5	3.1	781	2	photosystem I prot	
782	81.5	3.1	782	2	probable transcrip	
783	81.5	3.1	783	2	ribonuclease R (EC	
784	81.5	3.1	784	2	kinesin heavy chai	
785	81.5	3.1	785	2	probable alpha-man	
786	81.5	3.1	786	2	phosphatidylinosit	
787	81.5	3.1	787	2	probable two-compo	
788	81.5	3.1	788	2	hypothetical prote	
789	81.5	3.1	789	2	protein-tyrosine k	
790	81.5	3.1	790	2	hypothetical 127K	
791	81.5	3.1	791	2	rexB protein - Lac	
792	81.5	3.1	792	2	SCP160 protein - Y	
793	81.5	3.1	793	2	aldehyde oxidase (	
794	81.5	3.1	794	2	DNA segregation AT	
795	81.5	3.1	795	2	186K protein - cuc	
796	81.5	3.1	796	2	myosin-light-chain	
797	81.5	3.1	797	2	genome polyprotein	
798	81.5	3.1	798	2	hypothetical prote	
799	81.5	3.1	799	2	protein F57B9.2 [i	
800	81.5	3.1	800	2	protocatechuate 3,	
801	81.5	3.1	801	2	ABC transporter su	
802	81.5	3.1	802	2	fructose-bisphosph	
803	81.5	3.1	803	2	gumK protein - Xan	
804	81.5	3.1	804	2	hypothetical prote	
805	81.5	3.1	805	2	zinc-binding dehyd	
806	81.5	3.1	806	2	retrovirus-related	
807	81.5	3.1	807	2	uroporphyrinogen d	
808	81.5	3.1	808	2	hypothetical prote	
809	81.5	3.1	809	2	hypothetical prote	
810	81.5	3.1	810	2	hypothetical prote	
811	81.5	3.1	811	2	hypothetical prote	
812	81.5	3.1	812	2	UDP-N-acetylmuramy	
813	81	3.1	813	2	hypothetical prote	
814	81	3.1	814	2	probable 26S ATP/u	
815	81	3.1	815	2	nucleoprotein - in	
816	81	3.1	816	2	protein-tyrosine k	
817	81	3.1	817	2	glypican precursor	
818	81	3.1	818	2	replication licens	
819	81	3.1	819	2	phosphoglucomutase	
820	81	3.1	820	2	hemagglutinin-neur	
821	81	3.1	821	2	nucleoside triphos	
822	81	3.1	822	2	OLL protein - vari	
823	81	3.1	823	2	nucleoside-triphos	
824	81	3.1	824	2	hypothetical prote	
825	81	3.1	825	2	hypothetical prote	
826	81	3.1	826	2	DNA mismatch recog	
827	81	3.1	827	2	alpha-amylase (EC	
828	81	3.1	828	2	NADH flavin oxidor	
829	81	3.1	829	2	hypothetical prote	
830	81	3.1	830	2	site-specific reco	
831	81	3.1	831	2	penicillin-binding	
832	81	3.1	832	2	exoribonuclease, v	
792	3.1	792	2	2	subtilisin-type al	
913	3.1	913	1	1	DNA-directed DNA p	
913	3.1	913	2	2	DNA-directed DNA p	
949	3.1	949	2	2	excinuclease ABC c	
973	3.1	973	2	2	probable leucyl tr	
1122	3.1	1122	2	2	transcription-repa	
1128	3.1	1128	1	1	plasmid replicatio	
1157	3.1	1157	2	2	NUP133 protein - y	
1258	3.1	1258	2	2	nuclear protein SA	
1652	3.1	1652	2	2	hypothetical prote	
1660	3.1	1660	2	2	vitellogenin vit-6	
2368	3.1	2368	2	2	ESR1 protein - yea	
2626	3.1	2626	2	2	myosin-RhoGAP prot	
4930	3.1	4930	2	2	polyketide synthet	
5369	3.1	5369	2	2	mycosubtilin synth	
226	3.1	226	2	2	probable tail asse	
309	3.1	309	2	2	phosphoribosylanth	
346	3.1	346	2	2	hypothetical prote	
350	3.1	350	2	2	hypothetical prote	
358	3.1	358	2	2	cell division prot	
391	3.1	391	2	2	hypothetical prote	
413	3.1	413	1	1	hypothetical prote	
428	3.1	428	2	2	probable phosphoes	
442	3.1	442	1	1	exopolyposphatase	
468	3.1	468	2	2	transcription enha	
509	3.1	509	2	2	3-phosphoshikimate	
539	3.1	539	2	2	leucine aminopepti	
586	3.1	586	1	1	hypothetical prote	
596	3.1	596	2	2	CCT (chaperonin co	
610	3.1	610	2	2	NADH2 dehydrogenas	
619	3.1	619	2	2	TPR domain protein	
619	3.1	619	2	2	probable cystathio	
619	3.1	619	2	2	conserved hypothet	
619	3.1	619	2	2	CT858 hypothetical	
665	3.1	665	2	2	CT858 hypothetical	
671	3.1	671	2	2	transketolase (EC	
671	3.1	671	2	2	chemotaxis sensor	
671	3.1	671	2	2	methyl-accepting c	
724	3.1	724	2	2	ATP-dependent prot	
780	3.1	780	2	2	6-phosphofructokin	
793	3.1	793	2	2	probable DNA methy	
800	3.1	800	2	2	gyrase-like protei	
837	3.1	837	2	2	DNA-Binding Protei	
976	3.1	976	2	2	2-oxoglutarate deh	
1000	3.1	1000	2	2	hypothetical prote	
1102	3.1	1102	2	2	virG protein - Shi	
1111	3.1	1111	1	1	phytochrome C - Ar	
1174	3.1	1174	2	2	probable membrane	
1312	3.1	1312	2	2	hypothetical prote	
1503	3.1	1503	2	2	chloroplast outer	
1819	3.1	1819	2	2	uncharacterized pr	
2793	3.1	2793	2	2	hypothetical prote	
2806	3.1	2806	2	2	hypothetical prote	
3791	3.1	3791	1	1	alpha-aminoadipyl-	
184	3.1	184	2	2	hypothetical prote	
278	3.1	278	2	2	probable enoyl-CoA	
346	3.1	346	2	2	MCP-glutamate meth	
363	3.1	363	1	1	probable hexosyltr	
364	3.1	364	2	2	aminotripeptidase	
384	3.1	384	2	2	probable H+-export	
402	3.1	402	2	2	tryptophan synthas	
406	3.1	406	2	2	tryptophan synthas	
414	3.1	414	2	2	protein F23F12.6 [	
415	3.1	415	2	2	Leu/Ile/Val-bindin	
417	3.1	417	2	2	tryptophan synthas	
419	3.1	419	1	1	diaminopimel	

833	81	3.1	492	2	T30066	hypothetical prote	906	80.5	3.1	662	2	A54078	methy1-accepting c
834	81	3.1	496	2	G87546	acid-CoA ligase, p	907	80.5	3.1	677	2	T50022	sulfate transporte
835	81	3.1	500	2	S77243	hypothetical prote	908	80.5	3.1	717	2	B32838	DNA-directed RNA p
836	81	3.1	502	2	I39876	lipoprotein lpla -	909	80.5	3.1	725	2	T44992	translation elonga
837	81	3.1	523	1	S17949	glutamate dehydrog	910	80.5	3.1	728	2	B83805	GTP pyrophosphokin
838	81	3.1	558	1	DEHUE	glutamate dehydrog	911	80.5	3.1	740	2	B86638	GTP diphosphokinas
839	81	3.1	571	1	B36829	hemagglutinin-neur	912	80.5	3.1	750	1	D72530	probable nicotine
840	81	3.1	577	1	S64250	probable membrane	913	80.5	3.1	750	2	S55180	phospholipase D ho
841	81	3.1	586	2	T19075	hypothetical prote	914	80.5	3.1	770	2	T22944	hypothetical prote
842	81	3.1	609	1	A43458	replication protei	915	80.5	3.1	780	1	A31070	6-phosphofructokin
843	81	3.1	630	2	S77148	hypothetical prote	916	80.5	3.1	784	2	T22939	hypothetical prote
844	81	3.1	633	2	JQ1242	Virai replicase 2	917	80.5	3.1	810	2	B71639	virb4 protein prec
845	81	3.1	636	2	JC4960	DNA topoisomerase	918	80.5	3.1	863	2	B72344	tRNA nucleotidyl t
846	81	3.1	655	2	A48468	dnak-type molecula	919	80.5	3.1	889	2	C86257	resistance to pseu
847	81	3.1	658	2	AD2096	heat shock protein	920	80.5	3.1	933	2	T41122	nucleoporin - fiss
848	81	3.1	664	2	AB1136	NADH flavin oxidor	921	80.5	3.1	942	2	D96814	trehalose-6-phosph
849	81	3.1	674	1	KIMSCD	protein kinase C (	922	80.5	3.1	944	2	S01909	hairy wing suppres
850	81	3.1	676	2	S23807	alpha-amylase (EC	923	80.5	3.1	1012	2	S68259	DNA polymerase gam
851	81	3.1	706	2	S62933	hypothetical prote	924	80.5	3.1	1023	2	AE1643	ATP-dependent dsDN
852	81	3.1	740	1	JC6010	formate C-acetyltr	925	80.5	3.1	1057	2	S72648	sucrose-phosphate
853	81	3.1	745	2	T37458	VCP-like ATPase -	926	80.5	3.1	1146	2	A55532	myosin-heavy-chain
854	81	3.1	751	2	AG1329	penicillin-binding	927	80.5	3.1	1159	2	S22768	130K protein - mai
855	81	3.1	755	2	T32971	hypothetical prote	928	80.5	3.1	1178	2	S08405	hypothetical prote
856	81	3.1	778	2	E97224	ATP-dependent Lon	929	80.5	3.1	1186	2	T12737	tail protein - Met
857	81	3.1	785	2	AH1228	MutS protein (MutS	930	80.5	3.1	1207	2	C70013	conserved hypothet
858	81	3.1	785	2	G96825	hypothetical prote	931	80.5	3.1	1361	2	A29959	DNA-directed RNA p
859	81	3.1	835	2	F70363	cation transportin	932	80.5	3.1	1378	2	AB2817	DNA-directed RNA p
860	81	3.1	858	2	S30571	DNA topoisomerase	933	80.5	3.1	1403	2	T17372	plasma membrane-as
861	81	3.1	974	2	T35045	bacteriophage phiC	934	80.5	3.1	1411	2	C97595	RNA polymerase bet
862	81	3.1	974	2	T35045	methylenetetrahydr	935	80.5	3.1	1417	2	F96613	hypothetical prote
863	81	3.1	1013	2	B96544	hypothetical prote	936	80.5	3.1	1437	2	F69680	DNA-directed DNA p
864	81	3.1	1029	2	F86359	hypothetical prote	937	80.5	3.1	1444	1	A30588	140K adhesin precu
865	81	3.1	1034	1	GNLJCA	HIV-1 retropepsin	938	80.5	3.1	1530	2	AD1663	glutamate synthase
866	81	3.1	1044	2	E86613	ribonucleoside red	939	80.5	3.1	2013	2	AD1129	probable peptidogl
867	81	3.1	1044	2	A72010	ribonucleoside-dip	940	80.5	3.1	2347	1	TVHURS	kinase-related pro
868	81	3.1	1096	2	C87263	hypothetical prote	941	80.5	3.1	3739	2	T17410	polyketide synthas
869	81	3.1	1170	2	C96599	protein F20N2.14 f	942	80.5	3.1	5175	2	T20992	hypothetical prote
870	81	3.1	1193	2	F69698	DNA-directed RNA p	943	80.5	3.1	5198	2	T43290	hemimentin precurs
871	81	3.1	1203	2	C95229	DNA-directed RNA p	944	80	3.0	249	2	F97338	3-ketoacyl-acyl ca
872	81	3.1	1216	2	G98093	DNA polymerase bet	945	80	3.0	251	2	A97070	precorrin-4 methyl
873	81	3.1	1468	2	F70466	RNA polymerase bet	946	80	3.0	316	2	F70441	capsular polysacch
874	81	3.1	2092	2	S30026	genome polyprotein	947	80	3.0	342	2	D87280	aspartate-semialde
875	81	3.1	2149	2	S18676	genome polyprotein	948	80	3.0	345	2	F98013	3-isopropylmalate
876	81	3.1	2264	1	GNVVTB	genome polyprotein	949	80	3.0	345	2	AB1448	gp18 (Bacteriophag
877	80.5	3.1	278	2	H87402	spoU rRNA methylas	950	80	3.0	354	2	A75087	acetyl ornithine d
878	80.5	3.1	294	2	A96016	probable DNA ligas	951	80	3.0	373	1	AJHUQ	glutamate-ammonia
879	80.5	3.1	372	2	F70150	mannose-6-phosphat	952	80	3.0	377	2	H89930	hypothetical prote
880	80.5	3.1	390	2	C90573	cell division prot	953	80	3.0	382	2	AE2754	two component sens
881	80.5	3.1	394	2	B72419	conserved hypothet	954	80	3.0	382	2	C97535	nitrogen regulatio
882	80.5	3.1	400	2	H81936	probable tryptopha	955	80	3.0	397	2	JW0075	cysteine-dependent
883	80.5	3.1	408	2	A99238	conserved hypothet	956	80	3.0	409	2	E69309	ATPase AAA homolog
884	80.5	3.1	411	2	G75150	3-hydroxy-3-methyl	957	80	3.0	451	2	D83960	signal recognition
885	80.5	3.1	413	2	B82587	D-3-phosphoglycera	958	80	3.0	452	2	S03829	nifB protein - Rho
886	80.5	3.1	422	2	AD3504	tryptophan synthas	959	80	3.0	465	2	H84198	proline-tRNA synth
887	80.5	3.1	428	2	C64080	hemY protein homol	960	80	3.0	472	2	T15515	hypothetical prote
888	80.5	3.1	466	2	H96991	secreted protein c	961	80	3.0	475	2	G72274	glutamyl tRNA-Gln
889	80.5	3.1	469	2	D87493	glutamine syntheta	962	80	3.0	485	2	AB0543	aminoacyl-histidin
890	80.5	3.1	475	2	A71110	hypothetical prote	963	80	3.0	487	2	F82065	RNA polymerase sig
891	80.5	3.1	478	2	G75052	pyruvate kinase (E	964	80	3.0	487	2	G83827	stage V sporulatio
892	80.5	3.1	500	2	B85488	L-arabinose isomer	965	80	3.0	489	2	F70401	Flagellar M-ring p
893	80.5	3.1	500	2	B90637	L-arabinose isomer	966	80	3.0	492	1	A27727	trypanothione-disu
894	80.5	3.1	503	2	A97802	n utilization subs	967	80	3.0	523	1	DEFFG6	glucose-6-phosphat
895	80.5	3.1	509	2	T40835	hypothetical prote	968	80	3.0	536	2	T16428	propionyl-CoA carb
896	80.5	3.1	509	2	A95985	probable sugar kin	969	80	3.0	544	2	T32568	hypothetical prote
897	80.5	3.1	542	2	JC5507	monocarboxylate tr	970	80	3.0	552	1	S19647	T-complex protein
898	80.5	3.1	548	2	AD1216	ABC transporters,	971	80	3.0	569	2	B99587	hypothetical prote
899	80.5	3.1	555	2	C72512	probable thermosom	972	80	3.0	571	1	I46328	hemagglutinin-neur
900	80.5	3.1	578	2	A35810	alpha,alpha-trehal	973	80	3.0	575	1	HMIVBH	threonine ammonia-
901	80.5	3.1	590	2	H70170	hypothetical prote	974	80	3.0	576	1	DWBYT	hypothetical prote
902	80.5	3.1	619	2	A91113	glutathionylspermi	975	80	3.0	585	2	S48951	Bira protein/Bvg a
903	80.5	3.1	619	2	A85958	glutathionylspermi	976	80	3.0	592	2	B81009	intracellular prot
904	80.5	3.1	619	2	A57538	glutathionylspermi	977	80	3.0	594	2	I49127	conserved hypothet
905	80.5	3.1	642	2	C89124	protein K07C11.9 f	978	80	3.0	598	2	E86697	



979	80	3.0	616	1	C46328	hemagglutinin-neur
980	80	3.0	626	2	Tl3444	trehalase homolog
981	80	3.0	644	2	S15464	gp70 protein - mur
982	80	3.0	647	2	S58225	skeletal muscle ab
983	80	3.0	665	1	A42792	succinate dehydrog
984	80	3.0	702	2	G83386	elongation factor
985	80	3.0	721	2	S49789	hypothetical prote
986	80	3.0	724	2	AE1199	ATP-dependent prot
987	80	3.0	725	2	T20526	glutamine-fructose
988	80	3.0	747	2	A71440	hypothetical prote
989	80	3.0	775	2	T37848	probable cleavage
990	80	3.0	785	2	T52059	ent-kaurene syntha
991	80	3.0	828	2	G64556	flagellin B homolo
992	80	3.0	831	2	S50163	nitrate reductase
993	80	3.0	868	2	H81775	aconitate hydratase
994	80	3.0	894	2	F84870	hypothetical prote
995	80	3.0	906	2	T01440	hypothetical prote
996	80	3.0	911	2	S77659	DNA-directed DNA p
997	80	3.0	917	1	RDMUNH	nitrate reductase
998	80	3.0	976	2	S57725	respiration defici
999	80	3.0	981	2	S55132	hypothetical prote
1000	80	3.0	1019	2	C96519	probable disease r
1001	80	3.0	1056	2	S55151	probable membrane
1002	80	3.0	1056	2	B82557	hypothetical prote
1003	80	3.0	1107	2	S61667	probable membrane
1004	80	3.0	1164	2	B71429	phytochrome D - Ar
1005	80	3.0	1242	2	D90186	reverse gyrase (to
1006	80	3.0	1280	2	E95031	alkaline amylopull
1007	80	3.0	1289	1	GUBPT4	proximal tail fibe
1008	80	3.0	1377	2	C70148	DNA-directed RNA p
1009	80	3.0	1382	2	T01789	protoporphyrin IX
1010	80	3.0	1634	2	E64410	DNA-directed DNA p
1011	80	3.0	2269	1	JQ1750	genome polyprotein
1012	80	3.0	2325	2	T02235	acetyl-CoA carboxy
1013	80	3.0	2617	2	AE2136	peptide synthetase
1014	79.5	3.0	131	2	T04415	profilin - barley
1015	79.5	3.0	178	2	B84769	hypothetical prote
1016	79.5	3.0	240	2	T45727	hypothetical prote
1017	79.5	3.0	248	2	A86786	conserved hypothet
1018	79.5	3.0	263	2	C75217	probable short-cha
1019	79.5	3.0	300	2	C85631	hypothetical prote
1020	79.5	3.0	304	2	H70769	hypothetical prote
1021	79.5	3.0	312	2	B90248	deoxyhypusine synt
1022	79.5	3.0	323	2	D83708	phosphonates trans
1023	79.5	3.0	336	2	AB0280	probable membrane
1024	79.5	3.0	349	2	S74439	iron(III) dicitrat
1025	79.5	3.0	364	2	G82734	acetylornithine de
1026	79.5	3.0	385	2	S56224	hypothetical prote
1027	79.5	3.0	387	2	B97201	iron (III) ABC tra
1028	79.5	3.0	400	2	S76929	hypothetical prote
1029	79.5	3.0	413	2	C69160	phosphoenolpyruvat
1030	79.5	3.0	415	1	YXPSF2	carboxypeptidase G
1031	79.5	3.0	434	2	B69271	hypothetical prote
1032	79.5	3.0	435	2	C89857	conserved hypothet
1033	79.5	3.0	445	2	G70371	UDP-MURNAC-pentape
1034	79.5	3.0	448	2	S39348	26S ATP/ubiquitin-
1035	79.5	3.0	451	2	E85866	o-succinylbenzoate
1036	79.5	3.0	461	2	E84017	glutamate-1-semial
1037	79.5	3.0	462	2	E71891	probable GTP bindi
1038	79.5	3.0	472	2	AG3171	conserved hypothet
1039	79.5	3.0	492	2	C90985	probable export pr
1040	79.5	3.0	492	2	F85830	probable export pr
1041	79.5	3.0	496	2	AH3254	acetyl-CoA:acetoac
1042	79.5	3.0	500	2	AC0515	L-arabinose isomer
1043	79.5	3.0	502	2	T45852	hypothetical prote
1044	79.5	3.0	504	2	AG1413	gluconate kinase h
1045	79.5	3.0	510	2	T19577	hypothetical prote
1046	79.5	3.0	511	1	VGBE1K	glycoprotein C - h
1047	79.5	3.0	513	1	A45333	exopolysphatase
1048	79.5	3.0	513	2	D91049	exopolysphatase
1049	79.5	3.0	513	2	H85893	exopolysphatase
1050	79.5	3.0	515	2	A83992	1-pyrroline-5-carb
1051	79.5	3.0	516	2	JE0266	L-amino-acid oxida
1052	79.5	3.0	527	2	1052	hypothetical prote
1053	79.5	3.0	571	2	1053	probable oxaloacet
1054	79.5	3.0	573	2	1054	hydroxymethylgluta
1055	79.5	3.0	585	2	1055	hypothetical prote
1056	79.5	3.0	586	2	1056	Sarcophaga-derived
1057	79.5	3.0	587	2	1057	alpha-glucosidase
1058	79.5	3.0	629	2	1058	methionine-tRNA li
1059	79.5	3.0	629	2	1059	hypothetical prote
1060	79.5	3.0	660	2	1060	probable lipopolys
1061	79.5	3.0	708	1	1061	tryptophan synthas
1062	79.5	3.0	726	2	1062	nuclear pore prote
1063	79.5	3.0	737	2	1063	heavy metal-transp
1064	79.5	3.0	739	2	1064	F14O10.2 protein -
1065	79.5	3.0	749	2	1065	probable dehydroge
1066	79.5	3.0	807	2	1066	phenylalanyl-tRNA
1067	79.5	3.0	807	2	1067	phenylalanyl-tRNA
1068	79.5	3.0	865	1	1068	DNA-directed RNA p
1069	79.5	3.0	906	2	1069	NADH2 dehydrogenas
1070	79.5	3.0	911	1	1070	band 3 anion trans
1071	79.5	3.0	911	2	1071	nitrate reductase
1072	79.5	3.0	953	2	1072	pyruvate, phosphat
1073	79.5	3.0	969	2	1073	hypothetical prote
1074	79.5	3.0	1052	2	1074	protein-tyrosine k
1075	79.5	3.0	1084	1	1075	DNA-directed DNA p
1076	79.5	3.0	1111	2	1076	hypothetical prote
1077	79.5	3.0	1230	2	1077	TBP-interacting pr
1078	79.5	3.0	1402	2	1078	chemotaxis protein
1079	79.5	3.0	1447	2	1079	UDPglucose-glycopr
1080	79.5	3.0	1557	2	1080	hypothetical prote
1081	79.5	3.0	1627	1	1081	adhesin P1 precurs
1082	79.5	3.0	1635	2	1082	adhesin P1, group
1083	79.5	3.0	2013	2	1083	probable peptidogl
1084	79.5	3.0	2140	2	1084	serine proteinase,
1085	79.5	3.0	2295	2	1085	probable membrane
1086	79.5	3.0	3562	2	1086	chondroitin sulfat
1087	79.5	3.0	3898	1	1087	genome polyprotein
1088	79.5	3.0	4180	2	1088	hypothetical prote
1089	79	3.0	192	2	1089	hypothetical prote
1090	79	3.0	248	2	1090	hypothetical prote
1091	79	3.0	275	2	1091	glutamine ABC tran
1092	79	3.0	289	2	1092	methionyl-trna for
1093	79	3.0	297	2	1093	formylmethanofuran
1094	79	3.0	309	2	1094	ABC transporter, A
1095	79	3.0	311	2	1095	carbohydrate kinas
1096	79	3.0	326	1	1096	microbial serine p
1097	79	3.0	331	2	1097	transcription regu
1098	79	3.0	355	2	1098	hypothetical prote
1099	79	3.0	356	2	1099	probable hexosyltr
1100	79	3.0	359	2	1100	3-isopropylmalate
1101	79	3.0	365	2	1101	probable GTPase, Y
1102	79	3.0	366	2	1102	iron-regulated ABC
1103	79	3.0	394	2	1103	conserved hypothet
1104	79	3.0	399	2	1104	hypothetical prote
1105	79	3.0	399	2	1105	probable 26S prote
1106	79	3.0	401	1	1106	tryptophan synthas
1107	79	3.0	413	2	1107	N-carbamoyl-beta-a
1108	79	3.0	415	2	1108	UDP-N-acetylmuramo
1109	79	3.0	416	2	1109	conserved hypothet
1110	79	3.0	425	2	1110	transcription enha
1111	79	3.0	434	2	1111	D-nopaline dehydro
1112	79	3.0	435	2	1112	hypothetical prote
1113	79	3.0	438	2	1113	transcription enha
1114	79	3.0	443	2	1114	proteinase homolog
1115	79	3.0	443	2	1115	26S proteasome sub
1116	79	3.0	443	2	1116	histidine kinase (
1117	79	3.0	455	2	1117	replicative DNA he
1118	79	3.0	472	2	1118	D-nopaline dehydro
1119	79	3.0	492	2	1119	pyruvate kinase-li
1120	79	3.0	494	2	1120	protein R08F11.3 [
1121	79	3.0	498	1	1121	nucleoprotein - in
1122	79	3.0	501	1	1122	L1 protein - bovin
1123	79	3.0	539	2	1123	hypothetical prote
1124	79	3.0	543	2	1124	hypothetical prote



1271	78	3.0	358	2	E71686	hypothetical prote	1344	78	3.0	1374	2	A84888	hypothetical prote
1272	78	3.0	359	2	F72418	basic membrane pro	1345	78	3.0	1409	2	S74916	alkaline phosphata
1273	78	3.0	361	2	S23346	hypothetical prote	1346	78	3.0	1411	2	S55123	hypothetical prote
1274	78	3.0	365	2	B48945	recombination prot	1347	78	3.0	1424	2	S11480	hypothetical prote
1275	78	3.0	372	2	S24996	phosphopyruvate hy	1348	78	3.0	1464	2	T07050	hypothetical prote
1276	78	3.0	373	2	A19157	hypothetical prote	1349	78	3.0	1536	2	E72310	hypothetical prote
1277	78	3.0	389	2	T41420	26S proteinase reg	1350	78	3.0	1624	2	C70867	probable Helix-tur
1278	78	3.0	398	2	T38233	probable cystathio	1351	78	3.0	1698	2	S51869	probable membrane
1279	78	3.0	400	2	G64104	pantothenate metab	1352	78	3.0	1706	2	B75633	probable RNA helic
1280	78	3.0	411	2	T16981	glutamate dehydrog	1353	78	3.0	1740	2	T43215	ribonucleotide red
1281	78	3.0	411	2	S54797	glutamate dehydrog	1354	78	3.0	1796	2	AC1895	serine/threonine k
1282	78	3.0	424	2	T35924	hypothetical prote	1355	78	3.0	2168	2	D88131	protein F10G7.10 l
1283	78	3.0	430	2	T41054	probable chromosom	1356	78	3.0	2207	2	T24629	glutamate synthase
1284	78	3.0	435	2	B83958	glucose-inhibited	1357	78	3.0	2477	1	SJCHA	spectrin alpha cha
1285	78	3.0	444	2	AC1792	conserved hypothet	1358	78	3.0	3519	2	S43048	polyketide synthas
1286	78	3.0	458	2	G69581	acetoin dehydrogen	1359	78	3.0	4351	2	T00252	MEGF1 protein - ra
1287	78	3.0	464	2	C70821	probable serine pr	1360	78	3.0	4385	2	T29042	hypothetical prote
1288	78	3.0	470	2	AC2457	hypothetical prote	1361	78	3.0	4568	2	T08030	dynein beta heavy
1289	78	3.0	477	2	E97670	conserved hypothet	1362	78	3.0	131	2	S35798	profilin 3 - maize
1290	78	3.0	477	2	AB2895	nucleoprotein - in	1363	77.5	3.0	131	2	S35796	profilin 1 - maize
1291	78	3.0	498	1	VHIVN4	transcription term	1364	77.5	3.0	208	2	A98225	hypothetical prote
1292	78	3.0	503	2	H71659	phosphoglycerate k	1365	77.5	3.0	208	2	AF3061	ribonuclease D lim
1293	78	3.0	505	1	TVUT2B	lysine-tRNA ligase	1366	77.5	3.0	232	2	A87363	dnaJ family protei
1294	78	3.0	521	2	B70182	ubiquinol-cytochro	1367	77.5	3.0	265	2	C69978	glutamate racemase
1295	78	3.0	534	1	A48529	phosphoglucutase	1368	77.5	3.0	274	2	B70695	probable enoyl-coA
1296	78	3.0	542	2	AE3057	55K protein precur	1369	77.5	3.0	308	2	AE0566	hypothetical lysR-
1297	78	3.0	542	2	S07386	hypothetical prote	1370	77.5	3.0	320	2	G82293	lytB protein VC068
1298	78	3.0	546	2	A69484	glutamate dehydrog	1371	77.5	3.0	325	2	E64998	hypothetical prote
1299	78	3.0	558	1	A53719	carboxylesterase (	1372	77.5	3.0	332	2	T21279	hypothetical prote
1300	78	3.0	559	1	JC5408	2-isopropylmalate	1373	77.5	3.0	334	1	S15318	transcription regu
1301	78	3.0	565	2	T08590	phosphoglucutase	1374	77.5	3.0	361	2	S67590	mannose-1-phosphat
1302	78	3.0	567	2	A96229	hypothetical prote	1375	77.5	3.0	367	2	F87293	deoxyhypusine synt
1303	78	3.0	570	2	B86827	hypothetical prote	1376	77.5	3.0	376	2	D83099	probable RND efflu
1304	78	3.0	576	2	AC3038	biotin carboxylase	1377	77.5	3.0	386	1	A29984	alanine racemase (
1305	78	3.0	576	2	H98247	biotin carboxylase	1378	77.5	3.0	409	2	C87319	hypothetical prote
1306	78	3.0	597	2	C69283	hypothetical prote	1379	77.5	3.0	421	2	E83108	probable type II s
1307	78	3.0	609	2	S72845	H+-transporting tw	1380	77.5	3.0	434	2	H72358	lipopolysaccharide
1308	78	3.0	623	2	F87287	hypothetical prote	1381	77.5	3.0	435	2	A84824	probable nematode-
1309	78	3.0	636	2	F69027	hypothetical prote	1382	77.5	3.0	439	2	G82859	chromosomal replic
1310	78	3.0	660	2	S70904	cleavage and polya	1383	77.5	3.0	448	2	H90536	hypothetical prote
1311	78	3.0	676	2	F91185	transferrin-bindin	1384	77.5	3.0	451	2	B64997	o-succinylbenzoate
1312	78	3.0	693	2	D97122	alpha-amylase limp	1385	77.5	3.0	452	2	F64053	4-chlorobenzoate-C
1313	78	3.0	693	2	D97122	translation IF2, G	1386	77.5	3.0	459	2	AB3373	glutamate-tRNA lig
1314	78	3.0	703	2	AG0969	guanosine-3',5'-bi	1387	77.5	3.0	459	2	G81946	probable DNA repai
1315	78	3.0	717	2	T28829	hypothetical prote	1388	77.5	3.0	463	2	S33528	aspartate transami
1316	78	3.0	764	2	T45793	hypothetical prote	1389	77.5	3.0	475	2	D86450	hypothetical prote
1317	78	3.0	780	1	KIRBF	6-phosphofructokin	1390	77.5	3.0	492	2	T36429	nucleoprotein - in
1318	78	3.0	786	2	S71091	acetyl-CoA carboxy	1391	77.5	3.0	498	1	VHIVN9	L-arabinose isomer
1319	78	3.0	795	2	D64343	hypothetical prote	1392	77.5	3.0	500	1	ISECAB	glycoprotein C - h
1320	78	3.0	801	2	T47774	hypothetical prote	1393	77.5	3.0	511	1	VGBEF4	signal recognition
1321	78	3.0	807	2	T42924	glycoprotein B - a	1394	77.5	3.0	541	2	JX0112	CTP synthetase UU2
1322	78	3.0	809	2	S67665	ubiquitin-specific	1395	77.5	3.0	542	2	B82910	probable trehalose
1323	78	3.0	810	2	A97852	virB4 protein prec	1396	77.5	3.0	544	2	C95854	probable anti-mull
1324	78	3.0	822	2	D95141	DNA gyrase chain A	1397	77.5	3.0	557	2	S41627	proline-tRNA ligas
1325	78	3.0	879	2	AI0728	conserved hypothet	1398	77.5	3.0	570	2	D81847	acetolactate synth
1326	78	3.0	889	2	C72565	probable valyl-tRN	1399	77.5	3.0	575	2	F81801	acetolactate synth
1327	78	3.0	912	2	F71433	probable growth re	1400	77.5	3.0	575	2	A81067	hypothetical prote
1328	78	3.0	921	2	C81153	type I restriction	1401	77.5	3.0	583	2	D90052	topoisomerase I-re
1329	78	3.0	948	2	B81883	excinuclease ABC c	1402	77.5	3.0	584	2	S51882	probable AMP-bindi
1330	78	3.0	1013	2	C83771	hypothetical prote	1403	77.5	3.0	601	2	AG0066	FEt112-like protei
1331	78	3.0	1019	1	A32856	collagen alpha 1(V	1404	77.5	3.0	619	2	D69194	dnak-type molecula
1332	78	3.0	1067	2	D82436	transporter, AcrB/	1405	77.5	3.0	630	2	A35388	hypothetical prote
1333	78	3.0	1073	2	H82300	probable multidrug	1406	77.5	3.0	634	2	T18711	hypothetical prote
1334	78	3.0	1117	2	A71032	hypothetical prote	1407	77.5	3.0	634	2	T18702	hypothetical prote
1335	78	3.0	1151	2	F84605	hypothetical prote	1408	77.5	3.0	635	2	H81793	hypothetical prote
1336	78	3.0	1153	2	F84468	hypothetical prote	1409	77.5	3.0	637	2	S66953	protein T7N9.18 li
1337	78	3.0	1159	1	H64089	DNA-directed DNA p	1410	77.5	3.0	657	2	G86397	tail fiber protein
1338	78	3.0	1196	1	GNMVRV	HIV-1 retropepsin	1411	77.5	3.0	669	2	B42291	hypothetical prote
1339	78	3.0	1251	2	C82721	conserved hypothet	1412	77.5	3.0	670	2	T33304	hypothetical prote
1340	78	3.0	1259	2	T06521	pitrilysin (EC 3.4	1413	77.5	3.0	679	2	S21764	heat shock protein
1341	78	3.0	1278	2	A47462	probable DNA-direc	1414	77.5	3.0	682	2	T12294	NADH2 dehydrogenas
1342	78	3.0	1344	2	H84557	hypothetical prote	1415	77.5	3.0	694	1	C65137	4-alpha-glucanotra
1343	78	3.0	1365	2	T00833	RNA-directed DNA p	1416	77.5	3.0	705	2	S76729	hypothetical prote













Db 187 PTITGVRLSYVEIHVQGANRDHLHSGSYGGAAPNPINALCEIIAGLKDDQGRVTIPGFY 246

Qy 297 DEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAF 356

Db 247 DGIEPLTDEERQMWALPHSDEEFAASIGVPELPGEEGYTTLERLWGRPTLDVNGIWGGY 306

Qy 357 DEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLH 416

Db 307 QGEGSKTVIAAKAGAKVSMRLVPGQDPERITRLIQEYVPTIAPK--GVKAEVLSHHGGQ 363

Qy 417 PWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDG 476

Db 364 PVKFDTSVWVQGANRALKRVYGRDAAFARTGGSIPIVADFDRILQTPVLFVDFGLNEDA 423

Qy 477 EHSQNEKINRWNYIEGTKLFAAFLE 502

Db 424 PHSPNESFAVDYHNGI-LTSAYLLQ 448

RESULT 7

A90449

deacetylase, probable [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 16-Aug-2004

C:Accession: A90449

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: A90449

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-437 <KUR>

A:Cross-references: UNIPROT:Q97V97; GB:AB006641; NID:g13816063; PIDN:AAK42848.1; GSPDB:G

C:Genetics:

A:Gene: SSO2737

C:Superfamily: Peptidase V

Query Match 17.4%; Score 457.5; DB 2; Length 437;

Best Local Similarity 29.5%; Pred. No. 3.5e-25;

Matches 114; Conservative 80; Mismatches 177; Indels 15; Gaps 9;

Qy 112 PVILAEIGSDPTKGTVCYFGHLDVQPADRGDGLWTDPPYVLTEVDGKLYGRGATDNKGPVL 171

Db 52 PVVYAEINVN-AKKTLLIYNHYDVQVPDPISEWKRAFFSATIENDRIYARGASDNKGILM 110

Qy 172 AWINAVSAFRALEQDLPVNIKFIIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLW 231

Db 111 ARLFAIKHLDD-KNEINNVNKLLEYEGEEIGSVNLEDYIEKNTNKL--KADSVIMEGAGL 167

Qy 232 ISQRPKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHIL 291

Db 168 DPKGRPQIVLGVKGLLYVELVDYGTCDLHSSN-APLVRNPCIDLAKIISTLVDMGGRVL 226

Qy 292 VPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHG 351

Db 227 IEGFYDDVRELTEERELIKKYDIDVEELKKALGFELKELKYNEKEIAEALLTYPTCNVDG 286

Qy 352 IEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVS 411

Db 287 FECGYTGKSKTIVPHRAFAKLDFRLVPNQDPYKVFELLKKHLQ---KAGFNGEILAH- 341

Qy 412 TLGL-HPWIANIDDTQYLAAKRAIRTVFGTEPDMI-RDGSTIPIAKMFQEI-VHKSVVLI 468

Db 342 --GFEYPVRTSVNSTVVKAMIESAKKVCYGTPEQVIPNSAGTQPMGLFVYKLGIRDASAI 399

Qy 469 PLGAVDDGEHSQNEKINRWNYIEGTK 494

Db 400 GAGGYYSNAHAPNENIKIDDYYKAIK 425

RESULT 8

H72011

hypothetical protein - Chlamydophila pneumoniae (strain CWL029)

C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C:Accession: H72011

R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999

A:Title: Comparative Genomes of Clamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: H72011

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-493 <ARN>

A:Cross-references: UNIPROT:Q9Z6S9; GB:AE001678; GB:AE001363; NID:g4377301; PIDN:AAD1911

A:Experimental source: strain CWL029

C:Genetics:

A:Gene: CPn0980

Query Match 17.2%; Score 451.5; DB 2; Length 493;

Best Local Similarity 27.0%; Pred. No. 1.1e-24;

Matches 137; Conservative 91; Mismatches 203; Indels 77; Gaps 15;

Qy 24 MFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI-----ESDSVQVPVPRFRQELFRMM 78

Db 29 IFNCSGKPMNLDS--KHFDINSANFLEEFKFISSPISADSDHLQDCENCAHEL---- 82

Qy 79 AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGS-DPTKGTVCYFGHLDVQP 137

Db 83 ---VDHVNKI-----FDVELWETPGH-----PPIYASYKSEDLPSPTLMLYNHYDVQP 128

Qy 138 ADRGDGWLTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIEG 197

Db 129 AQLSDGWKGDPIFLREENGNYARGASDNKGQCFFYLKALQHYYESQGNFPLNIWLIEG 188

Qy 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRPKPAITYGTRGNSYFMVEVKCRD 257

Db 189 EEEGSLALFTWLEKKKEAL--RADYLLIVDGGFLSEKHPYVSI GARGIVSMKISLEEGN 246

Qy 258 QDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV-VPLTEEEINTYKAIHLD 316

Db 247 KDMHSGVLGGIAYNTNRALSEILSSLHHPDNSIAIEGPDYDDLALPSDSRDPDKSDFLR 306

Qy 317 LEEYRNSRVEKF--LFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374

Db 307 ECEENLGRFPQGYEASYPESALR----PTVEINGISGGYTGPGFKTVIPYRATAYLS 361

Qy 375 IRLVPHMNVSAVEKQVTRHLED-----VFSK-----RNSSNKMVVSMTLGLHPW 418

Db 362 CRLVPNQDPDKAAHQVVIHLKQQVPSSLKFSYEILPGSRGRWSSANLPVKKVLQEIYSD 421

Qy 419 IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEH 478

Db 422 LVN-----EECLRLVM-----PATIPIGILLGEAAQTSPICGTSYLSDDIH 463

Qy 479 SQNEKINRWNYIEGTKLFAAFLEMAQL 506

Db 464 AAEHFMSMDQLKKG-----FLSICQL 484

RESULT 9

A86613

hypothetical protein CPj0980 [imported] - Chlamydophila pneumoniae (strain J138)

C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 16-Aug-2004

C:Accession: A86613

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: A86613

A>Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-493 <STO>  
A;Cross-references: UNIPROT:Q9Z6S9; GB:BA000008; NID:g8979353; PIDN:BAA99187.1; GSPDB:GN  
A;Experimental source: strain J138  
C;Genetics:  
A;Gene: CPj0980  
C;Superfamily: Peptidase V

Query Match 17.2%; Score 451.5; DB 2; Length 493;  
Best Local Similarity 27.0%; Pred. No. 1.1e-24;  
Matches 137; Conservative 91; Mismatches 203; Indels 77; Gaps 15;

QY 24 MFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI-----ESDSVQVPVPRFRQELFRMM 78  
Db 29 IFNCSGKPMNLD--KHPDINSANFLEEFKAFISFESISADSDHLQDCENCAHFL----- 82

QY 79 AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPPVILAEGLS-DPTKGTVCYGHLDVQP 137  
Db 83 ---VDHVNKI-----FDVELWETPGH-----PPIYASYKSEDP LSP TLM LYNHYDVQP 128

QY 138 ADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIIEG 197  
Db 129 AQLSDGWKGDPPFILRENGNLYARGASDNKGQCFFYTLKALQHYYESQGNFPLNIWLIEG 188

QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRD 257  
Db 189 EEESGSLALFTWLEKKEAL--RADYLLIVDGGFLSEKHPYVVSIGARGIVSMKISLEEGN 246

QY 258 QDFHSGTFGGILHEPMADLVALGSLVDSSGHILVPGIYDEV-VPLTEEEINITYKAHLD 316  
Db 247 KDMHSGVLGGIAYNTNRALSEILSLHHPDNSIATEGFYDDLALPDSDRDLPKSDTLR 306

QY 317 LEEYRNSRVEKF--LPDTKEEILMHLWRYP SLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 307 ECEENLGRPQGYEASYSPEESALR-----PTVEINGISGGYTGPGFKTVIPRATAYLS 361

QY 375 IRLVPHMNVSAVEKQVTRHLED-----VFSK-----RNSSNMVVMVMTLGLHPW 418  
Db 362 CRLVPNQDPDKAAHQVIHHLKQVPSLKFSEILPGGSRGWRSSANLPVVKVLEIYSD 421

QY 419 IANIDDTQYLAAKRAINTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDDGEH 478  
Db 422 LYN-----EECLRLVM-----PATIPIGLLGEAAQTSPIICGTSYLSDDIH 463

QY 479 SQNEKINRWNYIEGTKLFAAFFLEMAQL 506.  
Db 464 AAEHFMDQLKKG-----FLSICQL 484

RESULT 10  
C95017  
peptidase, M20/M25/M40 family [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 16-Aug-2004  
C;Accession: C95017  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: C95017  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-457 <KUR>  
A;Cross-references: UNIPROT:Q97T10; GB:AE005672; PIDN:AAK74332.1; PID:g14971616; GSPDB:G  
C;Genetics:  
A;Gene: SP0150  
C;Superfamily: Peptidase V

Query Match 16.7%; Score 438.5; DB 2; Length 457;

Best Local Similarity 27.6%; Pred. No. 8.7e-24;  
Matches 133; Conservative 80; Mismatches 180; Indels 89; Gaps 15;

QY 41 YIDLHQDEFVQTL--KEWVAIESDSVQVPVPRFRQELFRMMVAADTLQRLGARVASVDMG 98  
Db 17 HVAQHYFEVLRTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID-- 63

QY 99 PQQLPDGQSLPIPPVILAEGLSDPTKGTVCYGHLDVQPADRGDGLTDPYVLTEVDGKL 158  
Db 64 -----ESYTAPFVMAHFKSSRPDAKTLIFYNHYDTPADGDQVWTEDPFTLSVRNGFM 116

QY 159 YRGATDNKGPVLAWINAVSAFRALEQDLPNVNIKFIEGMEEGSVALEELVEKEKDRFF 218  
Db 117 YGRGVDDDKGHITARLSALRKYMQHDDLPVNIISFIMEGAESASTDLDKYLEKHADK-L 175

QY 219 SGVDYIVISDNLWISQKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPM 273  
Db 176 RGADLLV-----WEOGTKNALEQL EISGNGKGI VTFDAKVKSADVDIHS-SYGGVVESAP 229

QY 274 ADLVALGSLVDSSGHILVPGIYDEVVPLTE-----EEINTYKAHLDLEE 319  
Db 230 WYLLQALQSLRAADGRILVEGLYEEVQEPNEREMALLETYGQRNPPEVSRIYGLLEPLLQ 289

QY 320 YRNSRVEKFLDPTKEEILMHLWRYP SLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVP 379  
Db 290 EERMAFLKRFFD-----PALNIEGISQSGYQGQGVKTILPAEASAKLEVRLVP 337

QY 380 HMNVSAVEKQVTRHLEDVFSKRNSNMVVMVMTLG-----LHPWIANIDDTQ---YL 428  
Db 338 GLEPHDVLEKIRKQLD-----KNGFDKVELYITLGEMSYRSDMSAPAILNVIELAKKFYP 392

QY 429 AAKRAIRTVFGTEP-DMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDDGEHSQNEKINRW 487  
Db 393 QGVSVLPTTAGTGPMTVFDALVP-----MVAFGLGNANSRDRHGGDENVRIA 440

QY 488 NY 489  
Db 441 DY 442

RESULT 11  
D97890  
succinyl-diaminopimelate desuccinylase (EC 3.5.1.18) [imported] - Streptococcus pneumon  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 16-Aug-2004  
C;Accession: D97890  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: D97890  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-457 <KUR>  
A;Cross-references: UNIPROT:Q8DRG0; GB:AE007317; PIDN:AAK98952.1; PID:g15457689; GSPDB:G  
C;Genetics:  
A;Gene: dape  
C;Superfamily: Peptidase V  
C;Keywords: hydrolase

Query Match 16.6%; Score 434.5; DB 2; Length 457;  
Best Local Similarity 28.9%; Pred. No. 1.7e-23;  
Matches 138; Conservative 77; Mismatches 183; Indels 79; Gaps 17;

QY 41 YIDLHQDEFVQTL--KEWVAIESDSVQVPVPRFRQELFRMMVAADTLQRLGARVASVDMG 98  
Db 17 HVAQHYFEVLRTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID-- 63

QY 99 PQQLPDGQSLPIPPVILAEGLSDPTKGTVCYGHLDVQPADRGDGLTDPYVLTEVDGKL 158







Db 429 EHFARG----VAFGVEL 441

RESULT 14  
AE3480  
aminoacylase (EC 3.5.1.14) [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 16-Aug-2004  
C;Accession: AE3480  
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AE3480  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-483 <KUR>  
A;Cross-references: UNIPROT:Q8YEQ1; GB:AE008917; PIDN:AAL53008.1; PID:g17983863; GSPDB:G  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BMEI1827  
A;Map position: 1  
C;Superfamily: Peptidase V  
C;Keywords: hydrolase

Query Match 16.0%; Score 420.5; DB 2; Length 483;  
Best Local Similarity 25.6%; Pred. No. 1.9e-22;  
Matches 128; Conservative 85; Mismatches 238; Indels 49; Gaps 11;

QY 26 SSPSPPPAL-LEKVQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADT 84  
Db 8 SSGSPMSTLSLDKVLNHLNLANLKSRLRLFNLRISISTDPA--YKADCRKAAEWLVED 65

QY 85 LQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFCYGHLDVQPADRGDGW 144  
Db 66 LKSIG-----FDASVRDTPGH-----PMVVAHHDGATADAPHVLFYGHYDVQVPDPLSLW 115

QY 145 LTDPY--VLTEV-----DGK--LYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI 195  
Db 116 ENDPFDPAIKDVGDASNGRKILTGRGTSDDKQLMTFVEACRAYKAVNGSLPVKVTLLF 175

QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255  
Db 176 EGEEESGSPSLKPFLEANRQEL--KADVALVCDTAMWDAETPAISVGLRGLVGEEIVIKA 233

QY 256 RDQDFHSGTGGILHEPMDLALLGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAIHL 315  
Db 234 ADRDLHSGFFGGAANPIHILTKILADLHDETRITIPDFYEGVEETPTQILKSWSLGR 293

QY 316 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375  
Db 294 TAESFLGPIGLSIPAGEKGRSVLELTWARPTAEVNGIIGGYTGEGFKTVIAAEASAKVSF 353

QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNS-----SNKMVVSMTLGLHPWIAN-----IDD 424  
Db 354 RLV-----HKQDPVKIREAFRAFKERVVPADCSVEFHFGGSPAQLPYDS 399

QY 425 TQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIVLPLGAVDGGEHSQNEKI 484  
Db 400 PLVSKAKNALSDWPKPAPVLIAMGGSIPVGFNTFLGMESLLVGFGLGLEDRIHSPNEKY 459

QY 485 NRWNYIEGTKLFAAFLEMA 504  
Db 460 ELNSFHKGQRSWARILAAIA 479

RESULT 15  
C87058  
conserved hypothetical protein ML1193 [imported] - Mycobacterium leprae  
C;Species: Mycobacterium leprae  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 16-Aug-2004

C;Accession: C87058  
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S A;Title: Massive gene decay in the leprosy bacillus.  
A;Reference number: A86909; MUID:21128732; PMID:11234002  
A;Accession: C87058  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-442 <STO>  
A;Cross-references: UNIPROT:Q9X7E4; GB:AL450380; NID:g13093158; PIDN:CAC31574.1; GSPDB: C;Genetics:  
A;Gene: ML1193  
C;Superfamily: Peptidase V

Query Match 15.1%; Score 397; DB 2; Length 442;  
Best Local Similarity 28.2%; Pred. No. 8.1e-21;  
Matches 130; Conservative 78; Mismatches 203; Indels 50; Gaps 15;

QY 34 LLEKVQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVA 93  
Db 4 LIERVREVLPLVR---RDLENLVRIE--SWADPGRRNEVHRSQVVLDSLQAGNFV 57

QY 94 SVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFCYGHLDVQPADRGDGLTDPYVLTE 153  
Db 58 RI-----VSEGA---PAVIARYPAPLGTPTVLLYAHHDVQPEGDRDQWASPPPEPTE 107

QY 154 VDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKE 213  
Db 108 RDGRIYGRGSADDKAGIATHL--AAFRAHGGRPPVGVTVFVEGEEESGSPSLGRLLAAH 164

QY 214 KDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPM 273  
Db 165 RDALAADVILIIADSDN-W-STDVPALTVSLRGLVDCVVEVATLDHGLHSLGMLGGVVPDAL 222

QY 274 ADLVALIGSLVDSSGHILVPGIYDEVVPLTTEEEINTYKAIHLDLEEYRNSS-RVEKFLFD 332  
Db 223 SVLMRLLASLHDDDDGNVAVAGLHEST---TAADVN-----YPHERVRADSGLLD 268

QY 333 TKEEI-----LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVE 387  
Db 269 GVSEIGSGSVQRLWAKPAITVIGIDTTSVAAAASNNMLIP-RARAKISMRIAPGGDAAVHL 327

QY 388 QKVTRHLEDVFSKRNSNNKMVVSMTLG--LHPWIANIDDTQYLAAKRAIRTVFGTEPDMI 445  
Db 328 DALTAHLQ-----RYAPWGAQVSVIRGEVSQPYAIEASGGVYDTARTAFRQAWGADPTDM 382

QY 446 RDGSTIPIAKMFQEIIVHKSIVLIP-LGAVDGGEHSQNEKIN 485  
Db 383 GMGGSIPFIAEFASAFPQAKILVTGVGDPATQAHGVNESVH 423

Search completed: February 8, 2005, 23:23:13  
Job time : 72 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: February 8, 2005, 23:18:35 ; Search time 178 Seconds  
(without alignments)  
1458.563 Million cell updates/sec

Title: US-10-036-342-57  
Perfect score: 2623  
Sequence: 1 MDPKLGMAASLLAVLLLLL.....NYIEGTKLFAAFLEMAQLH 507

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2623	100.0	507	2	Q6UWK2	Q6uwk2 homo sapien
2	2585.5	98.6	508	1	CGL2_HUMAN	Q96kn2 homo sapien
3	2100.5	80.1	492	2	Q66HG3	Q66hg3 rattus norv
4	2097	79.9	492	2	Q8BUG2	Q8bug2 mus musculus
5	2091	79.7	492	2	Q80XP5	Q80xp5 mus musculus
6	1598	60.9	494	2	Q6PA54	Q6pa54 xenopus lae
7	1416	54.0	474	2	Q6DH98	Q6dh98 brachydanio
8	1396.5	53.2	499	2	Q6P336	Q6p336 xenopus tro
9	1391.5	53.0	489	2	Q8AWF8	Q8awf8 xenopus lae
10	1391.5	53.0	494	2	Q7ZXA6	Q7zxa6 xenopus lae
11	1391.5	53.0	500	2	Q801E4	Q801e4 xenopus lae
12	1388	52.9	474	2	Q7T0R7	Q7t0r7 xenopus lae
13	1382	52.7	474	2	Q6P358	Q6p358 xenopus tro
14	1382	52.7	475	1	CGL1_MOUSE	Q9dia2 mus musculus
15	1379	52.6	474	2	Q6TNV3	Q6tnv3 brachydanio
16	1377	52.5	474	2	Q6DJK5	Q6djk5 xenopus lae
17	1369	52.2	475	2	Q6Q0N1	Q6q0n1 rattus norv
18	1363	52.0	475	1	CGL1_HUMAN	Q96kp4 homo sapien
19	1267.5	48.3	503	2	Q7QJQ9	Q7qjq9 anopheles g
20	1231.5	47.0	478	2	Q9V9H1	Q9v9h1 drosophila
21	1199	45.7	471	2	Q8I1J9	Q8ilj9 drosophila
22	1154.5	44.0	473	2	O18000	O18000 caenorhabdi
23	1081	41.2	401	2	Q6KAT3	Q6kat3 mus musculus
24	1064	40.6	474	1	CPGL_SCHPO	Q9p6i2 schizosacch
25	1044	39.8	481	1	CPGL_YEAST	P43616 saccharomyc
26	1039	39.6	476	2	Q870Z2	Q870z2 neurospora
27	1030	39.3	478	2	Q6C1A8	Q6cla8 yarrowia li
28	1029	39.2	443	2	Q9BL46	Q9bl46 caenorhabdi
29	1010	38.5	391	2	Q8WY59	Q8wy59 homo sapien
30	1000	38.1	528	2	Q753S4	Q753s4 ashbya goss
31	984	37.5	483	2	Q6FWY0	Q6fwy0 candida gla

32	983	37.5	533	2	Q6CYE6	Q6cye6 kluyveromyc
33	975	37.2	481	2	Q6BHB5	Q6bhb5 debaryomyce
34	919.5	35.1	357	2	Q8I1B0	Q8ilb0 drosophila
35	889.5	33.9	372	2	P78801	P78801 schizosacch
36	882	33.6	311	2	Q9NW02	Q9nw02 homo sapien
37	766	29.2	171	2	Q6ZND4	Q6znd4 homo sapien
38	705	26.9	276	2	Q9H7K8	Q9h7k8 homo sapien
39	630.5	24.0	867	2	Q6C2N8	Q6c2n8 yarrowia li
40	583.5	22.2	458	2	Q9K657	Q9k657 bacillus ha
41	582.5	22.2	468	2	Q7UJ49	Q7uj49 rhodopirell
42	578	22.0	957	2	Q6BQB3	Q6bbq3 debaryomyce
43	575.5	21.9	457	2	Q67Q20	Q67q20 symbiobacte
44	574.5	21.9	878	1	YB9X_YEAST	P38149 saccharomyc
45	570	21.7	459	2	Q9RSU7	Q9rsu7 deinococcus
46	549	20.9	957	2	Q6NE94	Q6ne94 neurospora
47	542	20.7	432	2	Q72LC6	Q72lc6 thermus the
48	539.5	20.6	870	2	Q6FXK1	Q6fxk1 candida gla
49	539	20.5	184	2	Q7ZZU2	Q7zzu2 oreochromis
50	535	20.4	888	2	Q758A6	Q758a6 ashbya goss
51	528	20.1	480	2	Q6MBN6	Q6mbn6 parachlamyd
52	528	20.1	868	2	Q6CLL9	Q6cll9 kluyveromyc
53	525.5	20.0	467	2	Q82IQ8	Q82iq8 streptomyce
54	521	19.9	451	2	Q7MWN9	Q7mwn9 porphyromon
55	514.5	19.6	1065	2	Q7S5Y4	Q7s5y4 neurospora
56	513.5	19.6	470	2	Q9FCX3	Q9fck3 streptomyce
57	507	19.3	170	2	Q9NUV1	Q9nuv1 homo sapien
58	506.5	19.3	453	2	Q8CUJ6	Q8cuju6 oceanobacil
59	506.5	19.3	716	2	Q6CF83	Q6cf83 yarrowia li
60	503	19.2	454	2	Q64PP6	Q64pp6 bacteroides
61	503	19.2	454	2	Q8A601	Q8a601 bacteroides
62	487.5	18.6	459	2	Q67PY8	Q67py8 symbiobacte
63	487.5	18.6	486	2	Q98AF9	Q98af9 rhizobium l
64	484	18.5	464	2	Q89QR0	Q89qr0 bradyrhizob
65	457.5	17.4	437	2	Q97V97	Q97v97 sulfolobus
66	456	17.4	468	2	Q6N8Q9	Q6n8q9 rhodopseudo
67	451.5	17.2	493	2	Q9Z6S9	Q9z6s9 chlamydia p
68	450.5	17.2	441	2	Q72JK7	Q72jk7 thermus the
69	448	17.1	458	2	Q8E3R9	Q8e3r9 streptococc
70	445	17.0	173	2	Q6XHG1	Q6xhg1 drosophila
71	441	16.8	458	2	Q8DY53	Q8dy53 streptococc
72	438.5	16.7	457	2	Q97T10	Q97t10 streptococc
73	434.5	16.6	457	2	Q8DRG0	Q8drg0 streptococc
74	432	16.5	454	2	Q822A3	Q822a3 chlamydophi
75	431.5	16.5	473	2	Q73XH9	Q73xh9 mycobacteri
76	426.5	16.3	470	2	O53227	O53227 mycobacteri
77	426.5	16.3	470	2	Q7TYD9	Q7tyd9 mycobacteri
78	424.5	16.2	463	2	Q9RSV5	Q9rsv5 deinococcus
79	421.5	16.1	462	2	Q6G0L2	Q6g0l2 bartonella
80	420.5	16.0	483	2	Q8YEQ1	Q8yeq1 brucella me
81	419.5	16.0	438	2	Q6L031	Q6l031 picrophilus
82	417.5	15.9	462	2	Q6G4T1	Q6g4t1 bartonella
83	414	15.8	471	2	Q8G331	Q8g331 brucella su
84	413.5	15.8	455	2	Q8G5E2	Q8g5e2 bifidobacte
85	407.5	15.5	457	2	Q93DA3	Q93da3 streptococc
86	399	15.2	447	2	Q6A6C5	Q6a6c5 propionibac
87	399	15.2	464	2	Q92T12	Q92t12 rhizobium m
88	397	15.1	442	2	Q9X7E4	Q9x7e4 mycobacteri
89	395	15.1	463	2	Q8UJ30	Q8uj30 agrobacteri
90	395	15.1	507	2	Q7D266	Q7d266 agrobacteri
91	393	15.0	461	2	Q98GJ6	Q98gj6 rhizobium l
92	389	14.8	426	2	Q972L9	Q972l9 sulfolobus
93	356.5	13.6	422	2	Q974N2	Q974n2 sulfolobus
94	354.5	13.5	451	2	Q9K425	Q9k425 streptomyce
95	349	13.3	514	2	Q6D5Q3	Q6d5q3 erwinia car
96	339	12.9	451	2	Q6AE81	Q6ae81 leifsonia x
97	332.5	12.7	451	2	Q82N32	Q82n32 streptomyce
98	326.5	12.4	446	2	Q83NH1	Q83nh1 tropheryma
99	323.5	12.3	446	2	Q83GM1	Q83gm1 tropheryma
100	323	12.3	453	2	Q6NF63	Q6nif63 corynebacte
101	307	11.7	461	2	Q89D44	Q89d44 bradyrhizob
102	306.5	11.7	473	2	Q6D5G6	Q6d5g6 erwinia car
103	302.5	11.5	457	2	Q8NM54	Q8nm54 corynebacte
104	281.5	10.7	490	2	Q7WAX1	Q7wax1 bordetella



105	281	10.7	471	2	Q8FME3	Q8fme3 corynebacte	178	180.5	6.9	384	2	Q8EEB6	Q8eeb6 shewanella
106	278.5	10.6	490	2	Q7WK27	Q7wk27 bordetella	179	180	6.9	375	2	Q6D7N4	Q6d7n4 erwinia car
107	273	10.4	472	2	Q63LU1	Q63lu1 burkholderi	180	178.5	6.8	189	2	Q9EUW1	Q9euw1 listeria in
108	269.5	10.3	497	2	Q8PIE6	Q8pie6 xanthomonas	181	178.5	6.8	377	2	Q9KQ52	Q9kq52 vibrio chol
109	269	10.3	497	2	Q8P732	Q8p732 xanthomonas	182	176.5	6.7	381	2	Q7PA85	Q7pa85 rickettsia
110	259.5	9.9	475	2	Q882Q4	Q882q4 pseudomonas	183	176.5	6.7	392	2	Q7VF72	Q7vf72 helicobacte
111	256.5	9.8	483	2	Q63MK2	Q63mk2 burkholderi	184	176	6.7	432	2	Q836F6	Q836f6 enterococcu
112	250.5	9.6	483	2	Q62CN6	Q62cn6 burkholderi	185	176	6.7	434	2	Q64B38	Q64b38 uncultured
113	237.5	9.1	480	2	Q83F46	Q83f46 coxiella bu	186	175	6.7	383	2	Q7WD03	Q7wd03 bordetella
114	228.5	8.7	378	2	Q92F19	Q92f19 listeria in	187	175	6.7	397	2	Q8ZVD7	Q8zvd7 pyrobaculum
115	223	8.5	465	2	Q8XL31	Q8xl31 clostridium	188	174.5	6.7	382	2	Q92FY0	Q92fy0 rickettsia
116	221.5	8.4	467	2	Q6SHW5	Q6shw5 uncultured	189	174.5	6.7	383	2	Q886Q4	Q886q4 pseudomonas
117	221	8.4	410	2	Q97Y12	Q97y12 sulfolobus	190	174	6.6	379	2	Q9ZEX1	Q9zex1 bordetella
118	218	8.3	375	2	Q7N3J4	Q7n3j4 photorhabdu	191	174	6.6	387	2	Q6NC49	Q6nc49 rhodopseudo
119	217	8.3	375	2	Q8FF82	Q8ff82 escherichia	192	173	6.7	390	2	Q7W5G7	Q7ws57 bordetella
120	215	8.2	375	1	DAPE ECOLI	P24176 escherichia	193	172.5	6.6	398	2	Q73GZ0	Q73gz0 wolbachia p
121	215	8.2	464	2	Q8RSR5	Q8r5r5 thermoanaer	194	172	6.6	374	2	Q83DN2	Q83dn2 coxiella bu
122	215	8.2	480	2	Q6BFV7	Q6bfv7 paramecium	195	172	6.6	377	1	DAPE HAEIN	P44514 haemophilus
123	213	8.1	379	2	Q8XBE0	Q8xbe0 escherichia	196	172	6.6	390	2	Q7VTF2	Q7vtf2 bordetella
124	211.5	8.1	379	2	Q9ZFY0	Q9zey0 listeria mo	197	172	6.6	463	2	O34944	O34944 bacillus su
125	211	8.0	375	2	Q8Z4S2	Q8z4s2 salmonella	198	171.5	6.5	377	2	Q65US9	Q65us9 mannheimia
126	210.5	8.0	395	2	Q724E0	Q724e0 listeria mo	199	171.5	6.5	405	1	DAPE STAEP	Q8cqc2 staphylococ
127	210	8.0	375	2	Q8CN75	Q8cn75 salmonella	200	171.5	6.5	413	2	Q64CX5	Q64cx5 uncultured
128	208.5	7.9	414	2	Q8CMV9	Q8cmv9 staphylococ	201	171.5	6.5	444	2	Q8GND1	Q8gnd1 streptococc
129	207	7.9	426	2	Q81YY6	Q81yy6 bacillus an	202	171.5	6.5	450	2	Q45631	Q45631 bacillus st
130	204	7.8	376	2	Q82XY4	Q82xy4 nitrosomona	203	171	6.5	468	2	Q8DZ92	Q8dz92 streptococc
131	203.5	7.8	379	2	Q9EXP4	Q9exf4 listeria mo	204	171	6.5	468	2	Q8E4V2	Q8e4v2 streptococc
132	201.5	7.7	425	2	Q98L43	Q98l43 rhizobium l	205	171	6.5	493	2	Q6NCQ7	Q6ncq7 rhodopseudo
133	201	7.7	465	2	Q97FL3	Q97fl3 clostridium	206	170.5	6.5	386	2	Q9ABF3	Q9abf3 caulobacter
134	200.5	7.6	378	2	Q87MI6	Q87mi6 vibrio para	207	170.5	6.5	400	1	DAPE STAAM	Q931i4 staphylococ
135	200.5	7.6	401	2	Q7MIL6	Q7mil6 vibrio vuln	208	170.5	6.5	407	1	DAPE STAAN	Q99sn6 staphylococ
136	200	7.6	452	2	Q7P724	Q7p724 fusobacteri	209	170.5	6.5	467	2	Q6RJS3	Q6rjs3 streptococc
137	198	7.5	386	2	Q8XZK5	Q8xzks ralstonia s	210	170.5	6.5	510	2	Q8XSI7	Q8xsi7 ralstonia s
138	197.5	7.5	470	2	Q8Y6R4	Q8y6r4 listeria mo	211	169	6.4	383	2	Q9I4H5	Q9i4h5 pseudomonas
139	197	7.5	481	2	Q892Y8	Q892y8 clostridium	212	168.5	6.4	372	2	Q74M62	Q74m62 nanoarchaeu
140	196	7.5	381	2	Q9JYL2	Q9jyl2 neisseria m	213	168.5	6.4	407	1	DAPE STAAM	Q8nv17 staphylococ
141	195.5	7.5	377	2	Q6LTL8	Q6ltw8 photobacter	214	168.5	6.4	407	2	Q6G7T6	Q6g7t6 staphylococ
142	195	7.4	424	2	Q63GE6	Q63ge6 bacillus ce	215	168.5	6.4	455	2	Q6L NK8	Q6lnk8 photobacter
143	194.5	7.4	384	2	Q9HTH4	Q9hth4 pseudomonas	216	168	6.4	469	2	Q8K7L6	Q8k7l6 streptococc
144	194.5	7.4	452	2	Q8RGL3	Q8rgl3 fusobacteri	217	168	6.4	469	2	Q8P162	Q8p162 streptococc
145	193.5	7.4	377	2	Q8DBA6	Q8dba6 vibrio vuln	218	167.5	6.4	263	2	Q6YRJ0	Q6yrj0 onion yello
146	193.5	7.4	379	2	Q6SHP2	Q6shp2 uncultured	219	167.5	6.4	374	2	Q96XG6	Q96xg6 sulfolobus
147	193.5	7.4	399	2	Q8PAU0	Q8pau0 xanthomonas	220	166.5	6.3	407	2	Q6GF48	Q6gff48 staphylococ
148	192.5	7.3	377	2	Q6FEI4	Q6fei4 acinetobact	221	166	6.3	469	2	Q99ZU1	Q99zul streptococc
149	192	7.3	383	2	Q9ZC93	Q9zcn93 rickettsia	222	166	6.3	508	2	Q6GQN3	Q6gqn3 brachydanio
150	191.5	7.3	381	2	Q9JTL0	Q9jtl0 neisseria m	223	165	6.3	159	2	Q9F8K6	Q9f8k6 carboxydoth
151	191.5	7.3	411	2	Q58003	Q58003 pyrococcus	224	165	6.3	400	2	Q9YEE4	Q9yee4 aeropyrum p
152	190.5	7.3	470	2	Q92B89	Q92b89 listeria in	225	165	6.3	458	2	Q6YQT3	Q6yqt3 onion yello
153	190	7.2	396	2	Q9X1Z4	Q9xlz4 thermotoga	226	165	6.3	469	2	Q8CNV2	Q8cnv2 staphylococ
154	189	7.2	391	2	Q88GZ4	Q88gz4 pseudomonas	227	164.5	6.3	385	1	ARGE PHOLL	Q7myd5 photorhabdu
155	189	7.2	424	2	Q6HNV0	Q6hnw0 bacillus th	228	164.5	6.3	390	2	Q6G1H9	Q6glh9 bartonella
156	189	7.2	434	2	Q7BVV8	Q7bvv8 bacillus su	229	164.5	6.3	470	2	Q8DTT4	Q8dtt4 streptococc
157	189	7.2	436	2	Q34984	Q34984 bacillus su	230	163.5	6.2	418	2	Q7WJY2	Q7wjy2 bordetella
158	188	7.2	383	2	Q68VN9	Q68vn9 rickettsia	231	163.5	6.2	422	2	Q7WAS3	Q7was3 bordetella
159	188	7.2	467	2	Q88XA5	Q88xa5 lactobacill	232	163.5	6.2	467	2	O84914	O84914 lactobacill
160	188	7.2	471	2	Q838A2	Q838a2 enterococcu	233	162.5	6.2	378	2	Q9CM22	Q9cm22 pasteurella
161	187	7.1	375	2	Q668G5	Q668g5 yersinia ps	234	162.5	6.2	472	2	O07121	O07121 lactococcus
162	187	7.1	375	2	Q8ZCD8	Q8zcd8 yersinia pe	235	162.5	6.2	472	2	Q84BV1	Q84bv1 lactococcus
163	187	7.1	426	2	O31724	O31724 bacillus su	236	162	6.2	377	1	DAPE BUCBP	Q89ay1 buchnera ap
164	186	7.1	379	2	Q7VXJ5	Q7vxj5 bordetella	237	162	6.2	468	2	Q816W3	Q816w3 bacillus ce
165	186	7.1	424	2	Q73E12	Q73e12 bacillus ce	238	161.5	6.2	375	1	DAPE BUCAP	Q8ka25 buchnera ap
166	185	7.1	379	2	Q7W8Y3	Q7w8y3 bordetella	239	161.5	6.2	377	2	Q7NYI9	Q7ny19 chromobacte
167	184.5	7.0	470	2	Q71Z48	Q71z48 listeria mo	240	161.5	6.2	472	2	Q7DFZ2	Q7dfz2 lactococcus
168	184	7.0	379	2	Q7WKC6	Q7wkc6 bordetella	241	161.5	6.2	472	2	Q84BV0	Q84bv0 lactococcus
169	184	7.0	427	2	Q9K9G9	Q9k9g9 bacillus ha	242	161	6.1	468	2	Q72Z23	Q72z23 bacillus ce
170	184	7.0	439	2	Q9FVL5	Q9fvl5 cucurbita p	243	160.5	6.1	377	2	Q87F49	Q87f49 xylella fas
171	183	7.0	387	2	Q8UJU8	Q8ujj8 agrobacteri	244	160.5	6.1	390	2	Q6G567	Q6g567 bartonella
172	182.5	7.0	376	2	Q9EZ94	Q9ez94 zymomonas m	245	160.5	6.1	472	2	Q83UN9	Q83un9 lactococcus
173	182	6.9	438	2	Q9MB49	Q9mb49 citrullus l	246	160	6.1	379	2	Q62JB1	Q62jb1 burkholderi
174	181.5	6.9	406	2	Q81IB8	Q81ib8 bacillus ce	247	160	6.1	383	2	Q63T00	Q63t00 burkholderi
175	181	6.9	375	1	DAPE BUCAI	P57196 buchnera ap	248	160	6.1	385	2	Q88AX7	Q88ax7 pseudomonas
176	181	6.9	377	2	Q9PH30	Q9ph30 xylella fas	249	159	6.1	422	2	Q81DV3	Q81dv3 bacillus ce
177	180.5	6.9	376	2	Q97ZB7	Q97zb7 sulfolobus	250	158.5	6.0	159	2	Q84GK9	Q84gk9 listeria mo

251	158.5	6.0	383	2	Q88MP5	Q88mp5 pseudomonas	324	141.5	5.4	365	2	Q9PNP3	Q9pnp3 campylobact
252	157.5	6.0	159	2	Q84GL0	Q84gl0 listeria mo	325	141.5	5.4	397	2	Q8XYW5	Q8xyw5 ralstonia s
253	157.5	6.0	397	2	Q17686	Q17686 caenorhabdi	326	141	5.4	345	2	Q6HS42	Q6hs42 bacillus an
254	157.5	6.0	466	2	Q97S02	Q97s02 streptococ	327	141	5.4	408	1	ACY1_HUMAN	Q03154 homo sapien
255	157	6.0	446	2	Q8TZE7	Q8tze7 pyrococcus	328	140.5	5.4	381	2	Q88VV9	Q88vv9 lactobacill
256	157	6.0	468	2	Q6HCH6	Q6hch6 bacillus th	329	140.5	5.4	401	2	O49682	O49682 arabidopsis
257	156.5	6.0	159	2	Q83UJ0	Q83uj0 listeria mo	330	140.5	5.4	443	2	Q6ZGS9	Q6zgs9 oryza sativ
258	156.5	6.0	378	2	Q6VE94	Q6ve94 pseudomonas	331	140.5	5.4	753	2	Q9SZM2	Q9szm2 arabidopsis
259	156	5.9	410	1	Y457_METJA	Q57899 methanococc	332	140	5.3	382	1	ARGE_PASMU	Q9clt9 pasteurella
260	156	5.9	415	2	Q6LXF3	Q6lxf3 methanococc	333	140	5.3	423	2	Q7QEF5	Q7qef5 anopheles g
261	156	5.9	469	2	Q8NW23	Q8nw23 staphylococ	334	139	5.3	474	2	Q9V0C1	Q9v0c1 pyrococcus
262	156	5.9	469	2	Q6G8H6	Q6g8h6 staphylococ	335	138.5	5.3	403	2	O29358	O29358 archaeoglob
263	155.5	5.9	157	2	Q6QMP6	Q6qmp6 listeria mo	336	138	5.3	408	2	Q9CR15	Q9cr15 m mus muscu
264	155.5	5.9	411	2	Q73RM0	Q73rm0 treponema d	337	138	5.3	408	2	Q99JW2	Q99jw2 mus musculu
265	155.5	5.9	466	2	Q8DQ06	Q8dqg6 streptococc	338	137.5	5.2	397	2	Q98D57	Q98d57 rhizobium l
266	155	5.9	398	2	Q8UIC7	Q8uic7 agrobacteri	339	137.5	5.2	399	2	Q17898	Q17898 caenorhabdi
267	155	5.9	468	2	Q632Y6	Q632y6 bacillus ce	340	137.5	5.2	401	2	Q9VCR2	Q9vcr2 drosophila
268	154.5	5.9	157	2	Q6QM03	Q6qmq3 listeria mo	341	137.5	5.2	413	2	Q7JUX5	Q7jux5 drosophila
269	154.5	5.9	474	2	Q9A3G5	Q9a3g5 caulobacter	342	137.5	5.2	502	2	Q6GTS8	Q6gts8 homo sapien
270	153.5	5.9	156	2	Q6QMP8	Q6qmp8 listeria mo	343	137	5.2	383	2	O25002	O25002 helicobacte
271	153.5	5.9	157	2	Q6QM00	Q6qmq0 listeria mo	344	137	5.2	420	2	Q6NYR6	Q6nyr6 brachydanio
272	153	5.8	378	2	Q82Z92	Q82z92 enterococcu	345	137	5.2	420	2	Q7ZVV2	Q7zvv2 brachydanio
273	153	5.8	389	1	ARGE_YERPE	Q8za85 yersinia pe	346	137	5.2	576	2	Q88RC9	Q88rc9 pseudomonas
274	153	5.8	389	2	Q66G73	Q66g73 yersinia ps	347	136.5	5.2	380	2	Q65W20	Q65w20 mannheimia
275	153	5.8	465	2	Q74KT4	Q74kt4 lactobacill	348	136.5	5.2	395	2	Q6J680	Q6j680 collimonas
276	153	5.8	469	2	Q6GFV0	Q6gfv0 staphylococ	349	136.5	5.2	432	2	Q6N7D3	Q6n7d3 rhodopseudo
277	152.5	5.8	159	2	Q83U78	Q83u78 listeria mo	350	136.5	5.2	450	2	Q6F127	Q6f127 mesoplasma
278	152.5	5.8	159	2	Q84GK7	Q84gk7 listeria mo	351	136	5.2	422	2	Q81QW8	Q81qw8 bacillus an
279	152.5	5.8	364	2	Q7MSC2	Q7msc2 wolinella s	352	136	5.2	422	2	Q6HJ69	Q6hj69 bacillus th
280	152.5	5.8	390	2	Q7WE47	Q7we47 bordetella	353	136	5.2	442	2	Q93RZ9	Q93rz9 streptomyce
281	152	5.8	423	2	Q9KE02	Q9ke02 bacillus ha	354	135.5	5.2	389	2	Q63T68	Q63t68 burkholderi
282	151.5	5.8	157	2	Q6QMP7	Q6qmp7 listeria mo	355	135.5	5.2	405	2	Q62JI2	Q62ji2 burkholderi
283	151.5	5.8	159	2	Q84GK8	Q84gk8 listeria mo	356	135.5	5.2	467	2	Q9CC46	Q9cc46 mycobacteri
284	151.5	5.8	376	2	Q8PMJ5	Q8pmj5 xanthomonas	357	135	5.1	299	2	O66823	O66823 aquifex aeo
285	151.5	5.8	390	2	Q7VS04	Q7vs04 bordetella	358	135	5.1	381	1	ARGE_BUCAP	P59085 buchnera ap
286	151	5.8	383	2	Q6DAR2	Q6dar2 erwinia car	359	134.5	5.1	374	2	Q6W106	Q6w106 rhizobium s
287	151	5.8	388	2	Q9ZMM0	Q9zmm0 helicobacte	360	134	5.1	408	2	Q6PTT1	Q6ptt1 rattus norv
288	151	5.8	469	2	Q7A2R1	Q7a2r1 staphylococ	361	134	5.1	443	2	Q99YT8	Q99yt8 streptococc
289	151	5.8	469	2	Q7A522	Q7a522 staphylococ	362	134	5.1	443	2	Q8K6Q8	Q8k6g8 streptococc
290	151	5.8	469	2	Q9KWZ7	Q9kwz7 staphylococ	363	133.5	5.1	412	2	Q9I056	Q9i056 pseudomonas
291	150.5	5.7	472	2	Q83U23	Q83u23 lactococcus	364	132.5	5.1	361	1	LYSK_THET2	Q8vus5 thermus the
292	150.5	5.7	472	2	Q84BU9	Q84bu9 lactococcus	365	132.5	5.1	417	2	Q88TR8	Q88tr8 lactobacill
293	150.5	5.7	472	2	Q9CH96	Q9ch96 lactococcus	366	132.5	5.1	463	2	Q65G02	Q65g02 bacillus li
294	150	5.7	388	2	O32633	Q32633 helicobacte	367	132.5	5.1	470	1	PEPV_LACDL	P45494 lactobacill
295	149.5	5.7	157	2	Q6QM01	Q6qmq1 listeria mo	368	132	5.0	382	2	Q88AR3	Q88ar3 pseudomonas
296	149.5	5.7	157	2	Q6QM02	Q6qmq2 listeria mo	369	132	5.0	383	1	ARGE_ECO57	Q8x742 escherichia
297	149.5	5.7	159	2	Q84GK6	Q84gk6 listeria mo	370	132	5.0	383	1	ARGE_ECOLI	P23908 escherichia
298	149.5	5.7	384	2	Q7VRT2	Q7vrt2 candidatus	371	132	5.0	408	2	Q6AYS7	Q6ays7 rattus norv
299	149	5.7	388	2	Q89BP2	Q89bp2 bradyrhizob	372	131.5	5.0	351	2	Q8TZI3	Q8tzl3 methanopyru
300	149	5.7	413	2	Q880D7	Q880d7 pseudomonas	373	131.5	5.0	356	2	Q72H05	Q72h05 thermus the
301	148.5	5.7	157	2	Q6QMP5	Q6qmp5 listeria mo	374	131.5	5.0	422	2	Q63BQ0	Q63bq0 bacillus ce
302	148.5	5.7	430	2	Q8S9L3	Q8s9l3 arabidopsis	375	131	5.0	340	2	Q7VNH0	Q7vnh0 haemophilus
303	148.5	5.7	488	2	Q8RTT1	Q8rtt1 uncultured	376	131	5.0	374	2	Q92Y75	Q92y75 rhizobium m
304	147.5	5.6	391	2	Q9A2D4	Q9a2d4 caulobacter	377	130.5	5.0	409	2	Q89J35	Q89j35 bradyrhizob
305	147.5	5.6	456	2	Q6Z8P2	Q6z8p2 oryza sativ	378	130	5.0	387	2	Q7NVG4	Q7nvq4 chromobacte
306	147	5.6	376	2	Q7VNB3	Q7vnb3 haemophilus	379	130	5.0	397	2	Q92SH1	Q92sh1 rhizobium m
307	147	5.6	448	1	ARGE_DICDI	P54638 dictyosteli	380	130	5.0	400	2	Q8MYW6	Q8myw6 drosophila
308	147	5.6	503	2	Q8C165	Q8cl65 mus musculu	381	130	5.0	400	2	Q9VCR0	Q9vcr0 drosophila
309	146.5	5.6	494	2	Q6SFC6	Q6sfc6 uncultured	382	130	5.0	402	2	O8T490	Q8t490 drosophila
310	146	5.6	408	2	Q6PTT0	Q6ptt0 rattus norv	383	130	5.0	443	2	Q8P053	Q8p053 streptococc
311	146	5.6	422	2	Q65ID8	Q65id8 bacillus li	384	130	5.0	443	2	Q97NA0	Q97na0 streptococc
312	146	5.6	422	2	Q738R3	Q738r3 bacillus ce	385	130	5.0	443	2	Q8DN27	Q8dn27 streptococc
313	145.5	5.5	432	2	Q64EN7	Q64en7 uncultured	386	130	5.0	482	2	O8GQE3	Q8gqe3 leptospira
314	145	5.5	440	2	Q9C5C4	Q9c5c4 arabidopsis	387	130	5.0	482	2	Q72LR2	Q72lr2 leptospira
315	144.5	5.5	421	2	Q7UM22	Q7um22 rhodopirell	388	130	5.0	482	2	Q8EY68	Q8ey68 leptospira
316	144	5.5	380	1	ARGE_MYXXA	Q68873 myxococcus	389	129.5	4.9	119	2	Q9EUV7	Q9euv7 listeria iv
317	144	5.5	395	2	Q8YDB0	Q8ydb0 brucella me	390	129.5	4.9	384	2	Q9HTY4	Q9hty4 pseudomonas
318	144	5.5	395	2	Q8FV22	Q8fv22 brucella su	391	129	4.9	382	2	Q6UB09	Q6ub09 pseudomonas
319	143.5	5.5	406	1	ACY1_FIG	P37111 sus scrofa	392	129	4.9	383	1	ARGE_SHIFL	P59600 shigella fl
320	143	5.5	407	2	Q6DDE1	Q6dde1 xenopus lae	393	129	4.9	1052	2	Q8PZR1	Q8pzt1 methanosarc
321	143	5.5	407	2	Q6P7J0	Q6p7j0 xenopus lae	394	128.5	4.9	433	2	Q986X8	Q986x8 rhizobium l
322	142.5	5.4	374	2	Q8UAH6	Q8uah6 agrobacteri	395	128.5	4.9	502	2	Q6P4E3	Q6p4e3 homo sapien
323	142	5.4	455	2	O59016	O59016 pyrococcus	396	128	4.9	341	1	LYSK_PYRAE	Q8zug2 pyrobaculum



397	128	4.9	383	1	ARGE_ECOL6	Q8fb97	escherichia
398	127.5	4.9	383	1	ARGE_SALTY	Q8zk19	salmonella
399	127.5	4.9	441	2	Q9YAM6	Q9yam6	aeropyrum p
400	127.5	4.9	471	2	Q9AAV0	Q9aa70	caulobacter
401	127.5	4.9	509	2	Q87PY5	Q87py5	vibrio para
402	126.5	4.8	394	2	Q8XT42	Q8xt42	ralstonia s
403	126.5	4.8	448	2	Q7D7G7	Q7d7g7	mycobacteri
404	126.5	4.8	448	2	Q7TYZ8	Q7tyz8	mycobacteri
405	125.5	4.8	418	2	Q8CN41	Q8cn41	staphylococ
406	125.5	4.8	432	2	Q88A71	Q88a71	pseudomonas
407	125	4.8	376	2	Q8D2S2	Q8d2s2	wiggleswort
408	125	4.8	414	2	Q9A7W4	Q9a7w4	caulobacter
409	124.5	4.7	401	2	Q9VCO9	Q9vcq9	drosophila
410	124.5	4.7	448	2	Q6NKC8	Q6nkc8	corynebacte
411	124	4.7	378	1	ARGE_VIBVY	Q7mh69	vibrio vuln
412	124	4.7	381	2	Q8TV20	Q8tv20	methanopyru
413	124	4.7	579	2	Q6X7U2	Q6x7u2	staphylococ
414	123	4.7	383	1	ARGE_SALTI	Q8z308	salmonella
415	122.5	4.7	397	2	Q17899	Q17899	caenorhabdi
416	122.5	4.7	426	2	Q6NSE6	Q6nse6	rhodopseudo
417	122.5	4.7	440	2	Q82LW1	Q82lw1	streptomyce
418	122.5	4.7	1332	2	Q97897	Q97897	tragelaphus
419	122	4.7	344	2	Q6KYZ9	Q6kyz9	picrophilus
420	122	4.7	378	1	ARGE_VIBCH	Q9knt5	vibrio chol
421	122	4.7	575	2	Q8XZU3	Q8xxu3	ralstonia s
422	122	4.7	2291	1	SPCB_DROME	Q00963	drosophila
423	121.5	4.6	911	2	Q975L8	Q975l8	sulfolobus
424	121	4.6	369	2	Q30185	Q30185	archaeoglob
425	121	4.6	378	1	ARGE_VIBVU	Q8dcn1	vibrio vuln
426	121	4.6	592	2	Q99X94	Q99x94	staphylococ
427	121	4.6	592	2	Q7A864	Q7a864	staphylococ
428	120	4.6	441	2	Q93H22	Q93h22	streptomyce
429	120	4.6	451	2	Q73YR9	Q73yr9	mycobacteri
430	120	4.6	592	2	Q8NYS4	Q8nys4	staphylococ
431	120	4.6	592	2	Q6GD04	Q6gd04	staphylococ
432	120	4.6	592	2	Q7PSH4	Q7psh4	anopheles g
433	120	4.6	2296	2	Q7PFH9	Q7pfh9	anopheles g
434	119.5	4.6	361	2	Q96DM4	Q96dm4	homo sapien
435	119.5	4.6	436	2	Q8XUU2	Q8xuu2	ralstonia s
436	119.5	4.6	1133	2	Q93VS9	Q93vs9	phaseolus v
437	119	4.5	346	1	LYSK_SULSO	Q980w5	sulfolobus
438	119	4.5	381	1	ARGE_EUCAI	P57155	buchnera ap
439	119	4.5	592	2	Q6BHI4	Q6bhi4	debaryomyce
440	119	4.5	592	2	Q6GKI4	Q6gki4	staphylococ
441	118.5	4.5	377	2	Q7W3B6	Q7w3b6	bordetella
442	118.5	4.5	377	2	Q7WEN5	Q7wen5	bordetella
443	118.5	4.5	397	2	Q17900	Q17900	caenorhabdi
444	118.5	4.5	443	2	Q9ZBI7	Q9zbi7	streptomyce
445	118.5	4.5	1131	2	Q6DCK9	Q6dck9	xenopus lae
446	117.5	4.5	346	1	LYSK_SULTO	Q976k1	sulfolobus
447	117.5	4.5	362	1	LYSK_DEIRA	Q9ruh3	deinococcus
448	117.5	4.5	382	2	Q970S3	Q970s3	sulfolobus
449	117.5	4.5	407	2	Q72B12	Q72b12	desulfovibr
450	117.5	4.5	432	2	Q6VE96	Q6ve96	pseudomonas
451	117.5	4.5	515	2	Q8EB06	Q8eb06	shewanella
452	117	4.5	372	2	Q8XHM0	Q8xhm0	clostridium
453	117	4.5	445	2	Q9AD91	Q9ad91	streptomyce
454	116.5	4.4	377	2	Q7VU38	Q7vu38	bordetella
455	116.5	4.4	509	2	Q8PTG6	Q8ptg6	methanosarc
456	116	4.4	139	2	Q6RKI5	Q6rk15	erwinia car
457	115.5	4.4	378	1	ARGE_VIBPA	P59601	vibrio para
458	115.5	4.4	461	2	Q6MT56	Q6mt56	mycoplasma
459	115.5	4.4	469	2	Q8RNM5	Q8rnm5	legionella
460	115.5	4.4	579	2	Q93LM7	Q93lm7	pseudomonas
461	114.5	4.4	397	2	Q979Q6	Q979q6	thermoplasm
462	114.5	4.4	477	2	Q73QJ3	Q73qj3	treponema d
463	114.5	4.4	566	2	Q8RAC1	Q8rac1	thermoanaer
464	114.5	4.4	579	2	Q887F3	Q887f3	pseudomonas
465	114	4.3	1424	2	Q73JU8	Q73jj8	treponema d
466	113.5	4.3	435	2	Q9C6Y8	Q9c6y8	arabidopsis
467	113.5	4.3	516	2	Q8A7B0	Q8a7b0	bacteroides
468	113	4.3	374	2	Q987H6	Q987h6	rhizobium l
469	113	4.3	409	1	ARCA_MYCAR	P23793	mycoplasma

470	113	4.3	441	2	Q8NLV7	Q8nlv7	corynebacte
471	113	4.3	465	2	Q9K7T7	Q9k7t7	bacillus ha
472	112.5	4.3	337	1	LYSK_PYRAB	Q9vli3	pyrococcus
473	112.5	4.3	379	2	Q6F727	Q6f727	acinetobact
474	112.5	4.3	1066	2	Q93W58	Q93w58	phaseolus v
475	112.5	4.3	1176	1	KMLS_BOVIN	Q28824	bos taurus
476	112	4.3	446	2	Q69TX7	Q69tx7	oryza sativ
477	112	4.3	1328	2	Q97896	Q97896	syncerus ca
478	112	4.3	1425	2	Q8REY5	Q8rey5	fusobacteri
479	111.5	4.3	380	2	Q88CJ5	Q88cj5	pseudomonas
480	111.5	4.3	425	2	Q89MN6	Q89mn6	bradyrhizob
481	111.5	4.3	727	2	Q8BYY6	Q8bvy6	mus musculu
482	111.5	4.3	941	2	Q6NAK2	Q6nak2	rhodopseudo
483	111.5	4.3	1085	2	Q8R3B4	Q8r3b4	mus musculu
484	111.5	4.3	1163	2	Q8K3G8	Q8k3g8	mus musculu
485	111.5	4.3	2061	1	MYOF_HUMAN	Q9nzm1	homo sapien
486	111.5	4.3	2078	2	Q69ZN7	Q69zn7	mus musculu
487	111	4.2	1179	2	Q7S9M2	Q7s9m2	neurospora
488	110.5	4.2	401	2	Q9I7K3	Q9i7k3	drosophila
489	110.5	4.2	596	2	Q13968	Q13968	schizosacch
490	110.5	4.2	1487	1	LHN2_RAT	Q88923	rattus norv
491	110	4.2	438	2	Q9LPE9	Q9lpe9	arabidopsis
492	110	4.2	650	2	Q9PR64	Q9pr64	ureaplasma
493	110	4.2	992	2	Q9C0L5	Q9c0l5	homo sapien
494	110	4.2	1193	1	ACE_CHICK	Q10751	gallus gall
495	110	4.2	1914	1	KMLS_HUMAN	Q15746	homo sapien
496	110	4.2	1914	2	Q7Z4J0	Q7z4j0	homo sapien
497	109	4.2	396	2	Q6NIX2	Q6nix2	corynebacte
498	109	4.2	428	2	Q8G5X6	Q8g5x6	bifidobacte
499	109	4.2	882	2	Q7RHT9	Q7rht9	plasmodium
500	108.5	4.1	401	2	Q9VCQ8	Q9vcq8	drosophila
501	108.5	4.1	405	2	Q6LQN1	Q6lqn1	photobacter
502	108.5	4.1	720	2	Q7TNB7	Q7tnb7	mus musculu
503	108.5	4.1	1003	2	Q9060	Q9060	trypanosoma
504	108.5	4.1	1162	2	Q8BGM9	Q8bgm9	mus musculu
505	108.5	4.1	2425	2	Q28859	Q28859	archaeoglob
506	108	4.1	378	2	Q6L017	Q6l017	picrophilus
507	107.5	4.1	385	2	Q89WA3	Q89wa3	bradyrhizob
508	107.5	4.1	735	2	Q822N1	Q822n1	chlamydophi
509	107.5	4.1	944	2	Q7SAH8	Q7sah8	neurospora
510	107.5	4.1	1118	2	Q93VL6	Q93vl6	phaseolus v
511	107	4.1	420	2	Q831D3	Q831d3	enterococcu
512	107	4.1	552	2	Q6P4A8	Q6p4a8	homo sapien
513	106.5	4.1	321	2	Q8YAM2	Q8yam2	listeria mo
514	106.5	4.1	321	2	Q724W0	Q724w0	listeria mo
515	106.5	4.1	363	2	Q6BMA2	Q6bma2	debaryomyce
516	106.5	4.1	565	2	Q8TXX8	Q8txx8	methanopyru
517	106.5	4.1	577	2	Q6CPD8	Q6cpd8	kluyveromyc
518	106.5	4.1	886	2	Q8D2N1	Q8d2n1	wiggleswort
519	106	4.0	381	2	Q6HFD6	Q6hfd6	bacillus th
520	106	4.0	599	2	Q6CXP9	Q6cxp9	kluyveromyc
521	105.5	4.0	403	1	YGEY_ECO57	P65809	escherichia
522	105.5	4.0	403	1	YGEY_ECOL6	P65808	escherichia
523	105.5	4.0	403	1	YGEY_ECOLI	P65807	escherichia
524	105.5	4.0	453	1	ENGA_ANASP	Q8yzh7	anabaena sp
525	105.5	4.0	485	2	Q64Y95	Q64y95	bacteroides
526	105	4.0	641	2	Q9BE69	Q9be69	macaca fasc
527	105	4.0	852	1	MVP_DISOM	Q90405	discopyge o
528	105	4.0	1129	2	Q80UX0	Q80ux0	mus musculu
529	105	4.0	4083	1	DYHC_ASHGO	Q9clm7	ashbya goes
530	104.5	4.0	401	2	Q8MRB5	Q8mrbs	drosophila
531	104.5	4.0	572	2	Q6C2B3	Q6c2b3	yarrowia li
532	104.5	4.0	572	2	Q6D1B9	Q6dlb9	erwinia car
533	104.5	4.0	762	1	METE_BACAN	Q6kna9	bacillus an
534	104.5	4.0	762	2	Q635S6	Q635s6	bacillus ce
535	104.5	4.0	1083	2	Q64J33	Q64j33	turicella o
536	104.5	4.0	1218	2	Q9XIH2	Q9xih2	arabidopsis
537	104	4.0	355	2	Q8A1V9	Q8a1v9	bacteroides
538	104	4.0	475	2	Q9EWF0	Q9ewf0	streptomyce
539	104	4.0	995	2	Q75QN2	Q75qn2	homo sapien
540	104	4.0	1155	1	RPOB_BORBU	Q59191	borrelia bu
541	104	4.0	1380	2	Q40001	Q40001	hordeum vul
542	104	4.0	1381	2	Q94C01	Q94c01	hordeum vul



543	104	4.0	1449	1	DPO3_CLOPE	Q8xjr3 clostridium	616	100	3.8	1263	2	Q8JIY6	Q8jiy6 brachydanio
544	104	4.0	1940	2	Q6PDN3	Q6pdn3 mus musculus	617	99.5	3.8	370	2	Q9RRJ7	Q9rrj7 deinococcus
545	103.5	3.9	321	2	Q92FG3	Q92fg3 listeria in	618	99.5	3.8	437	2	Q9HEX2	Q9hex2 pneumocysti
546	103.5	3.9	343	2	Q637G3	Q637g3 bacillus ce	619	99.5	3.8	452	2	Q9Z5G6	Q9z5g6 mycobacteri
547	103.5	3.9	490	1	DNAA_RHILO	Q98bg9 rhizobium l	620	99.5	3.8	466	2	Q8U7M1	Q8u7m1 agrobacteri
548	103.5	3.9	498	2	Q8AZ75	Q8az75 influenza a	621	99.5	3.8	498	2	Q9QNB4	Q9qnb4 influenza a
549	103.5	3.9	656	2	Q6FIW6	Q6fiw6 candida gla	622	99.5	3.8	498	2	Q9QNB5	Q9qnb5 influenza a
550	103.5	3.9	1436	1	DPO3_STAAM	Q53665 staphylococ	623	99.5	3.8	619	2	Q8W0D6	Q8w0d6 oryza sativ
551	103.5	3.9	1438	1	DPO3_STAAM	P63981 staphylococ	624	99.5	3.8	623	2	Q92EY3	Q92ey3 listeria in
552	103.5	3.9	1438	1	DPO3_STAAN	P63982 staphylococ	625	99.5	3.8	650	2	Q8DBC7	Q8dbc7 vibrio vuln
553	103.5	3.9	1438	2	Q6G9U9	Q6g9u9 staphylococ	626	99.5	3.8	653	2	Q9UZB6	Q9uzb6 pyrococcus
554	103.5	3.9	1438	2	Q6GHH1	Q6ghh1 staphylococ	627	99.5	3.8	1179	2	Q724J9	Q724j9 listeria mo
555	103.5	3.9	4007	1	FRS1_HUMAN	Q86xx4 homo sapien	628	99.5	3.8	1190	2	Q9ZIM3	Q9zim3 listeria mo
556	103	3.9	330	2	Q839X9	Q839x9 enterococcu	629	99.5	3.8	1332	2	Q95325	Q95325 bos taurus
557	103	3.9	504	2	Q9XA30	Q9xa30 streptomyc	630	99	3.8	342	2	Q6D395	Q6d395 erwinia car
558	103	3.9	979	2	Q97V13	Q97v13 sulfolobus	631	99	3.8	498	2	Q89898	Q89898 influenza a
559	103	3.9	987	1	K6P1_CANAL	Q94201 candida alb	632	99	3.8	587	2	Q817G3	Q817g3 bacillus ce
560	103	3.9	1001	2	Q8IE06	Q8ie06 plasmodium	633	99	3.8	658	2	Q9KZN9	Q9kzn9 streptomyc
561	103	3.9	1031	2	Q80YN7	Q80yn7 mus musculu	634	99	3.8	745	2	Q6FHX2	Q6fhx2 homo sapien
562	103	3.9	1950	2	Q80YN8	Q80yn8 mus musculu	635	99	3.8	1155	2	Q661M9	Q661m9 borrelia ga
563	103	3.9	5239	2	Q7QJA9	Q7qja9 anopheles g	636	99	3.8	1275	2	Q9QTG7	Q9qtg7 clostridium
564	102.5	3.9	486	2	Q67EF2	Q67ef2 influenza a	637	99	3.8	1276	1	BXD_CLOBO	P19321 clostridium
565	102.5	3.9	578	2	Q898M0	Q898m0 clostridium	638	99	3.8	1382	2	Q6ZQA0	Q6zqa0 mus musculu
566	102.5	3.9	580	2	Q6FX49	Q6fx49 candida gla	639	99	3.8	1834	2	Q6FJK7	Q6fjk7 candida gla
567	102.5	3.9	762	1	METE_BACC1	Q731w2 bacillus ce	640	98.5	3.8	184	2	Q9UXH6	Q9uxh6 sulfolobus
568	102.5	3.9	762	2	Q6HEG3	Q6heg3 bacillus th	641	98.5	3.8	351	2	Q9AAP6	Q9aap6 caulobacter
569	102.5	3.9	889	1	IF2_NITEU	Q82wq0 nitrosomona	642	98.5	3.8	395	1	TRPB_FUSNN	Q8rgh8 fusobacteri
570	102.5	3.9	999	2	Q86525	Q86525 rice yellow	643	98.5	3.8	449	2	Q7MX_Y0	Q7mxy0 porphyromon
571	102	3.9	353	2	Q64ZF5	Q64zf5 bacteroides	644	98.5	3.8	491	2	Q919W2	Q919w2 influenza a
572	102	3.9	381	2	Q81AB5	Q81ab5 bacillus ce	645	98.5	3.8	498	2	Q6XTR3	Q6xtr3 influenza a
573	102	3.9	383	2	Q80564	Q80564 arabadopsis	646	98.5	3.8	498	2	Q6XTS6	Q6xts6 influenza a
574	102	3.9	391	2	Q723B2	Q723b2 listeria mo	647	98.5	3.8	498	2	Q77Y46	Q77y46 influenza a
575	102	3.9	539	2	Q8GMG0	Q8gmg0 streptomyc	648	98.5	3.8	498	2	Q8B674	Q8b674 influenza a
576	101.5	3.9	333	2	Q7MZR8	Q7mzr8 photorhabdu	649	98.5	3.8	498	2	Q8B677	Q8b677 influenza a
577	101.5	3.9	393	1	CBP1_SULSO	P80092 sulfolobus	650	98.5	3.8	498	2	Q9EA34	Q9ea34 influenza a
578	101.5	3.9	498	2	Q8QM08	Q8qm08 influenza a	651	98.5	3.8	498	2	Q9YIL3	Q9yil3 influenza a
579	101.5	3.9	498	2	Q75T93	Q75t93 influenza a	652	98.5	3.8	793	2	Q7ABM3	Q7abm3 escherichia
580	101.5	3.9	498	2	Q75TA3	Q75ta3 influenza a	653	98.5	3.8	793	2	Q8XA96	Q8xa96 escherichia
581	101.5	3.9	498	2	Q8B675	Q8b675 influenza a	654	98.5	3.8	801	2	Q7SDJ3	Q7sdj3 neurospora
582	101.5	3.9	629	1	SYR_PYRHO	O59147 pyrococcus	655	98.5	3.8	873	1	NIA_EMENI	Q72945 emericella
583	101.5	3.9	740	2	Q6PFQ0	Q6pfq0 brachydanio	656	98.5	3.8	1125	2	Q6L2N8	Q6l2n8 picrophilus
584	101.5	3.9	746	2	Q6L3T5	Q6l3t5 solanum dem	657	98.5	3.8	4912	2	Q94116	Q94116 aureobasidi
585	101.5	3.9	944	2	Q9XVF1	Q9xvf1 caenorhabdi	658	98	3.7	326	1	LYSK_PYRFU	Q8u0b3 pyrococcus
586	101	3.9	151	2	Q48969	Q48969 mycoplasma	659	98	3.7	372	2	Q9KCV0	Q9kcv0 bacillus ha
587	101	3.9	399	2	Q9HJN3	Q9hjn3 thermoplasma	660	98	3.7	463	2	Q6LJM6	Q6ljm6 photobacter
588	101	3.9	454	2	Q6A7U1	Q6a7u1 propionibac	661	98	3.7	475	2	Q821I8	Q821i8 streptomyc
589	101	3.9	1166	2	Q890Z1	Q890z1 clostridium	662	98	3.7	477	2	Q83AU7	Q83au7 coxiella bu
590	101	3.9	1511	2	Q897I5	Q897i5 clostridium	663	98	3.7	486	2	Q7MWQ8	Q7mwq8 porphyromon
591	101	3.9	2116	2	Q9CD78	Q9cd78 mycobacteri	664	98	3.7	498	1	VNUC_IAFOW	P18071 influenza a
592	100.5	3.8	382	1	ARGE_MORAB	Q9k4z2 moritella a	665	98	3.7	498	2	P90204	P90204 influenza a
593	100.5	3.8	623	2	Q97PQ0	Q97pq0 streptococc	666	98	3.7	677	2	Q6MB11	Q6mb11 parachlamyd
594	100.5	3.8	656	2	O58624	O58624 pyrococcus	667	98	3.7	903	2	Q8VTA5	Q8vta5 synechococc
595	100.5	3.8	731	2	Q8ZYN4	Q8zyn4 pyrobaculum	668	98	3.7	956	2	Q64DL1	Q64dl1 uncultured
596	100.5	3.8	861	1	MVP_MOUSE	Q9eqk5 mus musculu	669	98	3.7	1381	2	Q8RY14	Q8ry14 arabadopsis
597	100.5	3.8	861	1	MVP_RAT	Q62667 rattus norv	670	98	3.7	1381	2	Q9FNB0	Q9fnb0 arabadopsis
598	100.5	3.8	861	2	Q922X6	Q922x6 mus musculu	671	98	3.7	1484	2	Q9G0G0	Q9g0g0 roseophage
599	100.5	3.8	870	2	Q8C2S9	Q8c2s9 mus musculu	672	98	3.7	2095	2	Q6FVK1	Q6fvk1 candida gla
600	100.5	3.8	1030	2	Q8BYE3	Q8bye3 m mus muscu	673	98	3.7	2111	1	MCAS_MYCBO	Q02251 mycobacteri
601	100.5	3.8	1331	1	XDH_BOVIN	P80457 bos taurus	674	98	3.7	2111	2	P96291	P96291 mycobacteri
602	100.5	3.8	1473	1	OVO5_CHICK	P20740 gallus gall	675	97.5	3.7	376	2	Q6NAG8	Q6nag8 rhodopseudo
603	100.5	3.8	2369	2	Q96VL6	Q96vl6 candida alb	676	97.5	3.7	400	2	O74916	O74916 schizosacch
604	100	3.8	372	2	Q6C8S2	Q6c8s2 yarrowia li	677	97.5	3.7	402	1	PGK_HELPY	P56154 helicobacte
605	100	3.8	381	1	ARGE_MORPR	Q9k4z7 moritella p	678	97.5	3.7	491	2	Q919W0	Q919w0 influenza a
606	100	3.8	415	2	Q884H3	Q884h3 pseudomonas	679	97.5	3.7	546	2	Q7VCD2	Q7vcd2 prochloroco
607	100	3.8	462	2	O81064	O81064 arabadopsis	680	97.5	3.7	674	1	RGS9_HUMAN	O75916 homo sapien
608	100	3.8	498	2	Q995Q0	Q995q0 influenza a	681	97.5	3.7	819	1	ADVL_HUMAN	O75366 homo sapien
609	100	3.8	612	2	Q75HW4	Q75hw4 oryza sativ	682	97.5	3.7	829	2	Q8D9G3	Q8d9g3 vibrio vuln
610	100	3.8	613	2	Q9Z567	Q9z567 streptomyc	683	97.5	3.7	834	2	Q6BST4	Q6bat4 debaryomyce
611	100	3.8	815	2	Q9KY60	Q9ky60 streptomyc	684	97.5	3.7	841	2	Q89E16	Q89el6 bradyrhizob
612	100	3.8	887	1	GLND_KLEOX	P41393 klebsiella	685	97.5	3.7	960	2	Q05507	Q05507 trypanosoma
613	100	3.8	1028	2	Q8THY1	Q8thy1 methanosarc	686	97.5	3.7	1105	2	Q6BT28	Q6bt28 debaryomyce
614	100	3.8	1075	2	P74461	Q74461 synechocyst	687	97.5	3.7	1618	2	Q7MKX5	Q7mkx5 vibrio vuln
615	100	3.8	1223	1	RPB2_CANGA	Q6fld5 candida gla	688	97.5	3.7	1735	2	Q6M931	Q6m931 neurospora

689	97.5	3.7	2405	2	Q8L3E9	Q8L3e9 streptococc
690	97.5	3.7	2672	1	GCN1_YEAST	P33892 saccharomyc
691	97	3.7	344	1	FLIM_TREPA	P74927 treponema p
692	97	3.7	365	2	O85036	Q85036 mycoplasma
693	97	3.7	385	1	YA94_METJA	Q58494 methanococc
694	97	3.7	428	2	Q6D355	Q6d355 erwinia car
695	97	3.7	498	2	Q67230	Q67230 influenza a
696	97	3.7	524	2	Q8ZZA1	Q8zza1 pyrobaculum
697	97	3.7	527	2	Q74J63	Q74j63 lactobacill
698	97	3.7	589	2	Q75HI7	Q75hi7 oryza sativ
699	97	3.7	611	2	Q91XS9	Q91xs9 cavia porce
700	97	3.7	695	2	Q72JF3	Q72jf3 thermus the
701	97	3.7	773	2	Q877G7	Q877g7 sulfolobus
702	97	3.7	1541	2	O15837	O15837 leishmania
703	96.5	3.7	372	2	Q9CI04	Q9ci04 lactococcus
704	96.5	3.7	421	2	Q7VX91	Q7vx91 bordetella
705	96.5	3.7	430	2	Q7W858	Q7w858 bordetella
706	96.5	3.7	430	2	Q7WLK6	Q7wlk6 bordetella
707	96.5	3.7	486	2	Q67EF3	Q67ef3 influenza a
708	96.5	3.7	486	2	Q67EF4	Q67ef4 influenza a
709	96.5	3.7	486	2	Q67EF5	Q67ef5 influenza a
710	96.5	3.7	486	2	Q67EF6	Q67ef6 influenza a
711	96.5	3.7	486	2	Q67EF7	Q67ef7 influenza a
712	96.5	3.7	486	2	Q67EF8	Q67ef8 influenza a
713	96.5	3.7	486	2	Q67EF9	Q67ef9 influenza a
714	96.5	3.7	486	2	Q67EG0	Q67ego influenza a
715	96.5	3.7	486	2	Q67EG1	Q67eg1 influenza a
716	96.5	3.7	493	2	Q08026	Q08026 influenza a
717	96.5	3.7	495	2	Q89NL6	Q89nl6 bradyrhizob
718	96.5	3.7	498	1	VNUC_IAHO1	P22435 influenza a
719	96.5	3.7	498	1	VNUC_IAVI6	P26073 influenza a
720	96.5	3.7	498	2	Q91MA6	Q91ma6 influenza a
721	96.5	3.7	498	2	Q6XT82	Q6xt82 influenza a
722	96.5	3.7	498	2	Q6XT83	Q6xt83 influenza a
723	96.5	3.7	498	2	Q6XT84	Q6xt84 influenza a
724	96.5	3.7	498	2	Q6XT88	Q6xt88 influenza a
725	96.5	3.7	498	2	Q6XT90	Q6xt90 influenza a
726	96.5	3.7	498	2	Q6XT91	Q6xt91 influenza a
727	96.5	3.7	498	2	Q6XT92	Q6xt92 influenza a
728	96.5	3.7	498	2	Q6XT93	Q6xt93 influenza a
729	96.5	3.7	498	2	Q6XT94	Q6xt94 influenza a
730	96.5	3.7	498	2	Q6XT96	Q6xt96 influenza a
731	96.5	3.7	498	2	Q6XT97	Q6xt97 influenza a
732	96.5	3.7	498	2	Q6XT98	Q6xt98 influenza a
733	96.5	3.7	498	2	Q6XT99	Q6xt99 influenza a
734	96.5	3.7	498	2	Q6XTA0	Q6xta0 influenza a
735	96.5	3.7	498	2	Q6XTA1	Q6xta1 influenza a
736	96.5	3.7	498	2	Q6XTA2	Q6xta2 influenza a
737	96.5	3.7	498	2	Q6XTA3	Q6xta3 influenza a
738	96.5	3.7	498	2	Q6XTP8	Q6xtp8 influenza a
739	96.5	3.7	498	2	Q6XTP9	Q6xtp9 influenza a
740	96.5	3.7	498	2	Q6XTQ4	Q6xtq4 influenza a
741	96.5	3.7	498	2	Q6XTQ6	Q6xtq6 influenza a
742	96.5	3.7	498	2	Q6XTQ7	Q6xtq7 influenza a
743	96.5	3.7	498	2	Q6XTQ8	Q6xtq8 influenza a
744	96.5	3.7	498	2	Q6XTR0	Q6xtr0 influenza a
745	96.5	3.7	498	2	Q6XTR1	Q6xtr1 influenza a
746	96.5	3.7	498	2	Q6XTR2	Q6xtr2 influenza a
747	96.5	3.7	498	2	Q6XTR4	Q6xtr4 influenza a
748	96.5	3.7	498	2	Q6XTR5	Q6xtr5 influenza a
749	96.5	3.7	498	2	Q6XTR9	Q6xtr9 influenza a
750	96.5	3.7	498	2	Q6XTS3	Q6xts3 influenza a
751	96.5	3.7	498	2	Q6XTS7	Q6xts7 influenza a
752	96.5	3.7	498	2	Q6XTS8	Q6xts8 influenza a
753	96.5	3.7	498	2	Q6XTT0	Q6xtt0 influenza a
754	96.5	3.7	498	2	Q6XTT5	Q6xtt5 influenza a
755	96.5	3.7	498	2	Q6XTT6	Q6xtt6 influenza a
756	96.5	3.7	498	2	Q701N7	Q701n7 influenza a
757	96.5	3.7	739	2	Q7MYC5	Q7myc5 photorhabdu
758	96.5	3.7	827	2	Q7MF19	Q7mf19 vibrio vuln
759	96.5	3.7	901	1	CPHA_ANAVA	Q86109 anabaena va
760	96.5	3.7	966	2	Q7VGQ2	Q7vgq2 helicobacte
761	96.5	3.7	1400	2	Q63BZ9	Q63bz9 bacillus ce

762	96.5	3.7	1455	2	Q640L5	Q640l5 mus musculu
763	96.5	3.7	1622	2	Q9X7B2	Q9x7b2 mycobacteri
764	96.5	3.7	4613	2	Q9ZG15	Q9zgi5 streptomyce
765	96.5	3.7	4630	2	Q7UWM5	Q7uwm5 rhodopirell
766	96	3.7	286	2	Q7ZG36	Q7zg36 human immun
767	96	3.7	327	1	GUAC_STRA3	Q8e578 streptococc
768	96	3.7	328	2	Q9H0X2	Q9h0x2 homo sapien
769	96	3.7	334	2	P87892	P87892 human endog
770	96	3.7	338	2	Q9H200	Q9h200 homo sapien
771	96	3.7	360	2	Q6NW43	Q6nw43 homo sapien
772	96	3.7	361	2	Q8BJE6	Q8bje6 mus musculu
773	96	3.7	369	2	Q701W2	Q701w2 uncultured
774	96	3.7	369	2	Q8BKH4	Q8bkh4 mus musculu
775	96	3.7	369	2	Q8BK11	Q8bki1 mus musculu
776	96	3.7	370	2	Q8TBK0	Q8tbk0 homo sapien
777	96	3.7	378	2	Q8PTZ8	Q8ptz8 methanosarc
778	96	3.7	381	2	Q733G0	Q733g0 bacillus ce
779	96	3.7	417	2	Q970Q7	Q970q7 sulfolobus
780	96	3.7	477	2	Q8U1L8	Q8uli8 pyrococcus
781	96	3.7	485	2	Q9KE53	Q9ke53 bacillus ha
782	96	3.7	489	2	Q9SMY2	Q9sm y2 arabidopsis
783	96	3.7	633	1	GATE_SULSO	Q97zh6 sulfolobus
784	96	3.7	704	2	Q8P7V1	Q8p7v1 xanthomonas
785	96	3.7	737	2	Q8BJ11	Q8bj11 mus musculu
786	96	3.7	896	2	Q9F2I7	Q9f2i7 synechococc
787	96	3.7	947	2	Q767I1	Q767i1 rattus norv
788	96	3.7	1222	2	Q6AAC2	Q6aac2 propionibac
789	96	3.7	1325	2	Q86UL0	Q86ul0 homo sapien
790	96	3.7	1376	2	Q83W66	Q83w66 escherichia
791	96	3.7	1718	2	Q69ZE8	Q69ze8 mus musculu
792	96	3.7	2516	2	Q84BD6	Q84bd6 myxococcus
793	95.5	3.6	325	1	LYSK_PYRHO	O59402 pyrococcus
794	95.5	3.6	406	1	YNQ5_YEAST	P53891 saccharomyc
795	95.5	3.6	479	2	Q84RI9	Q84ri9 dunaliella
796	95.5	3.6	480	2	Q66450	Q66450 aquifex aeo
797	95.5	3.6	498	1	VNUC_IAGD7	Q09159 influenza a
798	95.5	3.6	498	1	VNUC_IAME5	Q07548 influenza a
799	95.5	3.6	498	1	VNUC_IAMEE	Q08035 influenza a
800	95.5	3.6	498	1	VNUC_IATX7	P18072 influenza a
801	95.5	3.6	498	2	Q92607	Q92607 influenza a
802	95.5	3.6	498	2	Q6XT74	Q6xt74 influenza a
803	95.5	3.6	498	2	Q6XT75	Q6xt75 influenza a
804	95.5	3.6	498	2	Q6XT76	Q6xt76 influenza a
805	95.5	3.6	498	2	Q6XT77	Q6xt77 influenza a
806	95.5	3.6	498	2	Q6XT78	Q6xt78 influenza a
807	95.5	3.6	498	2	Q6XT81	Q6xt81 influenza a
808	95.5	3.6	498	2	Q6XT86	Q6xt86 influenza a
809	95.5	3.6	498	2	Q6XTA4	Q6xta4 influenza a
810	95.5	3.6	498	2	Q6XTA5	Q6xta5 influenza a
811	95.5	3.6	498	2	Q6XTQ0	Q6xtq0 influenza a
812	95.5	3.6	498	2	Q6XTQ5	Q6xtq5 influenza a
813	95.5	3.6	498	2	Q6XTS0	Q6xts0 influenza a
814	95.5	3.6	498	2	Q6XTS1	Q6xts1 influenza a
815	95.5	3.6	506	2	Q9H625	Q9h625 homo sapien
816	95.5	3.6	546	2	Q98PL7	Q98pl7 mycoplasma
817	95.5	3.6	565	2	Q8A406	Q8a406 bacteroides
818	95.5	3.6	585	2	Q73MM6	Q73mm6 treponema d
819	95.5	3.6	605	2	Q709L5	Q709l5 rice yellow
820	95.5	3.6	645	2	Q8RCT8	Q8rct8 thermoaer
821	95.5	3.6	726	2	Q7Q7S8	Q7q7s8 anopheles g
822	95.5	3.6	801	2	Q8ZN48	Q8zn48 salmonella
823	95.5	3.6	809	1	QUIA_ACIAD	Q59086 acinetobact
824	95.5	3.6	877	2	Q84FL0	Q84fl0 pantoea agg
825	95.5	3.6	901	1	CPHA_ANASP	P58572 anabaena sp
826	95.5	3.6	953	2	Q68YI2	Q68yi2 rickettsia
827	95.5	3.6	955	1	UVRA_RICCN	Q92g31 rickettsia
828	95.5	3.6	1029	2	Q9ZT71	Q9zt71 arabidopsis
829	95.5	3.6	1147	1	KMLS_RABIT	P29294 oryctolagus
830	95.5	3.6	1169	2	Q8CMT1	Q8cmt1 staphylococ
831	95.5	3.6	1259	2	Q8KFA9	Q8kfa9 chlorobium
832	95.5	3.6	1285	2	Q9WXU3	Q9wxu3 thermotoga
833	95.5	3.6	1381	2	Q39049	Q39049 arabidopsis
834	95.5	3.6	1610	2	Q6MWA6	Q6mwa6 oryza sativ



835	95.5	3.6	1616	2	Q73XL5	Q73xl5 mycobacteri	908	94.5	3.6	3242	2	Q72X91	Q72x91 bacillus ce
836	95.5	3.6	1727	2	Q7S6A4	Q7s6a4 neurospora	909	94	3.6	342	2	P93153	P93153 gossypium h
837	95.5	3.6	1733	2	O53579	O53579 mycobacteri	910	94	3.6	359	2	Q6AA24	Q6aa24 propionibac
838	95.5	3.6	1733	2	Q7TVM9	Q7tvm9 mycobacteri	911	94	3.6	447	2	O04511	O04511 arabidopsis
839	95.5	3.6	2624	2	Q6RKF3	Q6rkf3 cochllobolu	912	94	3.6	455	2	Q89NT5	Q89nt5 bradyrhizob
840	95	3.6	408	1	ARCA_MYCHO	P41141 mycoplasma	913	94	3.6	479	2	Q67SE1	Q67se1 symbiobacte
841	95	3.6	409	2	Q7NDK4	Q7ndk4 gloeobacter	914	94	3.6	483	2	Q8X170	Q8x170 clostridium
842	95	3.6	454	2	Q91748	Q91748 xenopus lae	915	94	3.6	494	2	Q7W897	Q7w897 bordetella
843	95	3.6	458	2	Q96Y71	Q96y71 sulfolobus	916	94	3.6	494	2	Q7WLVS	Q7wlv5 bordetella
844	95	3.6	468	2	Q67278	Q67278 influenza a	917	94	3.6	498	2	Q6XTT2	Q6xtt2 influenza a
845	95	3.6	468	2	Q89872	Q89872 influenza a	918	94	3.6	579	2	Q8YZR7	Q8yzzr7 anabaena sp
846	95	3.6	474	2	Q8FWS1	Q8fws1 brucella su	919	94	3.6	658	2	Q7VIC1	Q7vic1 helicobacte
847	95	3.6	498	1	VNUC_IASIN	P26072 influenza a	920	94	3.6	730	1	EF2_METTH	Q27131 methanobact
848	95	3.6	498	2	Q6XTT3	Q6xtt3 influenza a	921	94	3.6	777	1	YD81_SCHPO	Q10146 schizosacch
849	95	3.6	498	2	Q6XTT4	Q6xtt4 influenza a	922	94	3.6	785	1	MUS2_LISIN	Q92ch6 listeria in
850	95	3.6	757	1	AMO_ECOLI	P46883 escherichia	923	94	3.6	817	2	Q8CQ88	Q8cq88 staphylococ
851	95	3.6	792	2	Q6ZTT1	Q6ztt1 homo sapien	924	94	3.6	851	1	MUTS_PHOLL	Q7n8k0 photorhabdu
852	95	3.6	851	2	Q99TH2	Q99th2 staphylococ	925	94	3.6	867	2	Q9PYP4	Q9pypp4 xestia c-ni
853	95	3.6	876	2	Q7A565	Q7a565 staphylococ	926	94	3.6	873	1	CPHA_SYNY3	P73833 synechocyst
854	95	3.6	876	2	Q649R1	Q649r1 uncultured	927	94	3.6	876	2	Q7A0N8	Q7a0n8 staphylococ
855	95	3.6	961	2	O17505	Q17505 bombyx mori	928	94	3.6	876	2	Q9RMM6	Q9rmn6 staphylococ
856	95	3.6	1120	2	O17505	Q17505 bacteroides	929	94	3.6	876	2	Q6G8N6	Q6g8n6 staphylococ
857	95	3.6	1125	2	Q8A3E2	Q8a3e2 bombyx mori	930	94	3.6	892	2	Q7VEG5	Q7veg5 prochloroco
858	95	3.6	1335	2	Q17250	Q17250 bombyx mori	931	94	3.6	901	1	PODK_TREPA	O83728 treponema p
859	95	3.6	1335	2	Q95PE2	Q95pe2 dictyosteli	932	94	3.6	960	2	Q8VZF3	Q8vzf3 arabidopsis
860	95	3.6	1369	2	Q8I7W9	Q8i7w9 treponema p	933	94	3.6	1053	1	FAK1_CHICK	Q00944 gallus gall
861	95	3.6	1376	2	Q8FKM0	Q8fkm0 escherichia	934	94	3.6	1058	2	Q8ZS94	Q8zs94 anabaena sp
862	95	3.6	1416	1	RPOC_TREPA	O83270 debaryomyce	935	94	3.6	1060	2	Q64J43	Q64j43 corynebacte
863	95	3.6	1457	2	Q6BI69	Q6bi69 staphylococ	936	94	3.6	1313	2	Q9EQM9	Q9eqm9 rattus norv
864	94.5	3.6	161	1	COAD_STAEP	Q8c8z5 helicobacte	937	94	3.6	1316	2	Q6BZB2	Q6bz22 debaryomyce
865	94.5	3.6	402	1	PGK_HELJPJ	Q9zjpl bacillus ha	938	94	3.6	1330	1	XDH_RAT	P22985 rattus norv
866	94.5	3.6	404	2	Q9KCF8	Q9kcf8 pseudomonas	939	94	3.6	1437	1	DPO3_LACPL	Q88vk2 lactobacill
867	94.5	3.6	434	2	Q9HWS9	Q9hws9 pyrococcus	940	94	3.6	1546	1	RPOC_DEIRA	Q9rvw0 deinococcus
868	94.5	3.6	469	2	Q8U4Q7	Q8u4q7 pyrococcus	941	94	3.6	4077	2	O52820	O52820 amycolatops
869	94.5	3.6	472	2	Q8NKW7	Q8nkw7 pyrococcus	942	93.5	3.6	256	2	Q81BU2	Q81bu2 bacillus ce
870	94.5	3.6	473	2	Q97ZU7	Q97zu7 sulfolobus	943	93.5	3.6	331	2	Q6NAH3	Q6nah3 rhodopseudo
871	94.5	3.6	498	1	VNUC_IAB39	O8028 influenza a	944	93.5	3.6	332	2	Q8P8A8	Q8p8a8 xanthomonas
872	94.5	3.6	498	1	VNUC_IAKIT	Q91743 influenza a	945	93.5	3.6	408	1	RL4_PRUAR	Q9xf97 prunus arme
873	94.5	3.6	498	1	VNUC_IAMEB	Q8034 influenza a	946	93.5	3.6	426	2	Q92DJ2	Q92dj2 listeria in
874	94.5	3.6	498	1	VNUC_IAMEB	Q8036 influenza a	947	93.5	3.6	489	2	Q8WZX9	Q8wzx9 neurospora
875	94.5	3.6	498	1	VNUC_IAMEG	Q8033 influenza a	948	93.5	3.6	493	2	Q08030	Q08030 influenza a
876	94.5	3.6	498	2	Q67224	Q67224 influenza a	949	93.5	3.6	498	1	VNUC_IACAL	P18070 influenza a
877	94.5	3.6	498	2	Q6XT79	Q6xt79 influenza a	950	93.5	3.6	498	1	VNUC_IAMEA	Q08031 influenza a
878	94.5	3.6	498	2	Q6XT80	Q6xt80 influenza a	951	93.5	3.6	498	1	VNUC_IAMEF	Q08041 influenza a
879	94.5	3.6	498	2	Q6XT85	Q6xt85 influenza a	952	93.5	3.6	498	1	VNUC_IASH1	P16986 influenza a
880	94.5	3.6	498	2	Q785R8	Q785r8 influenza a	953	93.5	3.6	498	2	Q6XT87	Q6xt87 influenza a
881	94.5	3.6	498	2	Q785R9	Q785r9 influenza a	954	93.5	3.6	498	2	Q9E5Y8	Q9e5y8 influenza a
882	94.5	3.6	498	2	Q8AZ74	Q8az74 influenza a	955	93.5	3.6	514	2	Q7VIS7	Q7vis7 helicobacte
883	94.5	3.6	498	2	Q8B676	Q8b676 influenza a	956	93.5	3.6	571	2	Q751M2	Q751m2 ashbya goss
884	94.5	3.6	498	2	Q9YIW1	Q9yiw1 influenza a	957	93.5	3.6	595	1	THD1_LYCES	P25306 lycopersico
885	94.5	3.6	498	2	Q9YJRO	Q9yjr0 influenza a	958	93.5	3.6	639	2	O82107	O82107 zea mays (m
886	94.5	3.6	546	2	Q81P24	Q81p24 bacillus an	959	93.5	3.6	655	2	Q8U398	Q8u398 pyrococcus
887	94.5	3.6	546	2	Q6HHB9	Q6hbb9 bacillus th	960	93.5	3.6	666	1	ENV_MLVHO	P21436 homulv muri
888	94.5	3.6	568	2	Q9SXD0	Q9sxd0 arabidopsis	961	93.5	3.6	714	2	Q7QIC5	Q7qic5 anopheles g
889	94.5	3.6	571	2	Q17447	Q17447 caenorhabdi	962	93.5	3.6	766	2	Q8BWZ2	Q8bwz2 m mus muscu
890	94.5	3.6	580	2	Q6C0E8	Q6c0e8 yarrowia li	963	93.5	3.6	777	1	FRZE_MYXXA	P18769 myxococcus
891	94.5	3.6	584	2	Q88JS0	Q88js0 pseudomonas	964	93.5	3.6	871	1	MVP_ICTPU	Q9dgm7 ictalurus p
892	94.5	3.6	590	1	SELN_HUMAN	Q9nzv5 homo sapien	965	93.5	3.6	983	2	O75039	Q75039 homo sapien
893	94.5	3.6	626	2	Q6A0D4	Q6a0d4 mus musculu	966	93.5	3.6	1069	2	Q6BI56	Q6bi56 debaryomyce
894	94.5	3.6	636	2	Q7U1F2	Q7ulf2 mycobacteri	967	93.5	3.6	1263	2	Q7RDV9	Q7rdv9 plasmodium
895	94.5	3.6	651	2	Q94AT5	Q94at5 arabidopsis	968	93.5	3.6	1438	2	Q65JJ0	Q65jj0 bacillus li
896	94.5	3.6	662	1	ACSA_SCHPO	P78773 schizosacch	969	93.5	3.6	1459	1	LHN2_HUMAN	Q95490 homo sapien
897	94.5	3.6	728	2	Q8PX47	Q8px47 methanosarc	970	93.5	3.6	1613	2	Q9KRZ1	Q9krz1 vibrio chol
898	94.5	3.6	757	2	Q7D9E5	Q7d9e5 mycobacteri	971	93.5	3.6	1638	2	Q8IWQ7	Q8iwq7 homo sapien
899	94.5	3.6	787	2	P95059	P95059 mycobacteri	972	93.5	3.6	1638	2	Q86XX2	Q86xx2 homo sapien
900	94.5	3.6	818	2	Q73JH4	Q73jh4 treponema d	973	93.5	3.6	1719	2	Q86XX3	Q86xx3 homo sapien
901	94.5	3.6	888	2	Q6C2Y0	Q6c2y0 yarrowia li	974	93.5	3.6	2358	2	Q9L1V8	Q9l1v8 streptomyce
902	94.5	3.6	953	2	Q7PA36	Q7pa36 rickettsia	975	93	3.5	214	2	Q9HAF4	Q9haf4 homo sapien
903	94.5	3.6	981	2	Q8FLW9	Q8flw9 corynebacte	976	93	3.5	255	2	Q929Q5	Q929q5 listeria in
904	94.5	3.6	1179	2	Q92F61	Q92f61 listeria in	977	93	3.5	377	2	Q93A66	Q93a66 uncultured
905	94.5	3.6	1346	2	Q7XPZ6	Q7xpz6 oryza sativ	978	93	3.5	393	2	Q92EB8	Q92eb8 listeria in
906	94.5	3.6	1457	2	Q6IRM3	Q6irm3 xenopus lae	979	93	3.5	413	2	O50931	O50931 borrelia bu
907	94.5	3.6	2274	2	Q8DZ40	Q8dz40 streptococc	980	93	3.5	414	2	Q9KET8	Q9ket8 bacillus ha



981	93	3.5	441	2	Q93GH6	Q93gh6 bacillus su
982	93	3.5	485	2	Q8A0H6	Q8a0h6 bacteroides
983	93	3.5	487	2	Q82FM2	Q82fm2 streptomyc
984	93	3.5	498	1	VNUC_IABRA	P18069 influenza a
985	93	3.5	498	1	VNUC_IAME4	Q07531 influenza a
986	93	3.5	498	1	VNUC_IAUSS	P18073 influenza a
987	93	3.5	498	2	Q9EMD4	Q9emd4 influenza a
988	93	3.5	541	2	Q6AJ62	Q6aj62 desulfotale
989	93	3.5	554	2	P79026	P79026 emericella
990	93	3.5	588	1	SYD_PASMU	P57895 pasteurella
991	93	3.5	588	2	Q87PW2	Q87pw2 vibrio para
992	93	3.5	623	2	Q98990	Q98990 salmo salar
993	93	3.5	623	2	Q98991	Q98991 salmo salar
994	93	3.5	675	1	RGS9_MOUSE	O54828 mus musculu
995	93	3.5	677	1	RGS9_RAT	P49805 rattus norv
996	93	3.5	734	2	Q6FRI6	Q6fri6 candida gla
997	93	3.5	767	1	YNW4_YEAST	P53866 saccharomyc
998	93	3.5	782	2	Q6LKY8	Q6lky8 photobacter
999	93	3.5	811	2	Q64YR9	Q64yr9 bacteroides
1000	93	3.5	893	1	MVP_HUMAN	Q14764 homo sapien
1001	93	3.5	908	2	Q6FIF6	Q6fif6 mesoplasma
1002	93	3.5	954	2	Q64C96	Q64c96 uncultured
1003	93	3.5	1007	2	Q9F3J0	Q9f3j0 streptomyc
1004	93	3.5	1033	2	Q7S8U3	Q7s8u3 neurospora
1005	93	3.5	1049	2	Q8EKS3	Q8eks3 shewanella
1006	93	3.5	1109	2	Q8FA54	Q8f4s4 leptospira
1007	93	3.5	1110	2	Q72R14	Q72r14 leptospira
1008	93	3.5	1304	2	Q9CMP6	Q9cmp6 pasteurella
1009	93	3.5	1310	1	ACE_RABIT	P12822 coryctolagus
1010	93	3.5	1333	1	RPOC_COREF	Q8fs96 corynebacte
1011	93	3.5	1498	2	Q7YZS4	Q7yzs4 physarum po
1012	93	3.5	1526	2	Q86YZ9	Q86yz9 homo sapien
1013	93	3.5	1544	2	Q86WK2	Q86wk2 homo sapien
1014	93	3.5	1544	2	Q86Z00	Q86z00 homo sapien
1015	93	3.5	1554	2	Q86SH6	Q86sh6 homo sapien
1016	93	3.5	1556	2	Q86WK1	Q86wk1 homo sapien
1017	93	3.5	1566	2	Q86WK3	Q86wk3 homo sapien
1018	93	3.5	1566	2	Q86WK4	Q86wk4 homo sapien
1019	93	3.5	1569	2	Q86Z01	Q86z01 homo sapien
1020	93	3.5	1579	2	Q86SH0	Q86sh0 homo sapien
1021	93	3.5	3049	2	Q7QSI8	Q7qsi8 giardia lam
1022	92.5	3.5	351	2	Q18621	Q18621 caenorhabdi
1023	92.5	3.5	373	2	Q688J4	Q688j4 oryza sativ
1024	92.5	3.5	382	2	Q9CD67	Q9cd67 mycobacteri
1025	92.5	3.5	391	2	Q8NR87	Q8nr87 corynebacte
1026	92.5	3.5	393	2	Q8Y9J0	Q8y9j0 listeria mo
1027	92.5	3.5	399	2	Q6CRH2	Q6crh2 kluyveromyc
1028	92.5	3.5	400	2	Q8GCH2	Q8gch2 xanthomonas
1029	92.5	3.5	456	2	Q7MYW7	Q7myw7 photorhabdu
1030	92.5	3.5	472	2	Q8G0I3	Q8g0i3 brucella su
1031	92.5	3.5	478	2	Q6MPK9	Q6mpk9 bdellovibri
1032	92.5	3.5	489	1	YABN_BACSU	P37556 bacillus su
1033	92.5	3.5	493	2	Q07542	Q07542 influenza a
1034	92.5	3.5	493	2	Q07544	Q07544 influenza a
1035	92.5	3.5	493	2	Q07547	Q07547 influenza a
1036	92.5	3.5	493	2	Q07562	Q07562 influenza a
1037	92.5	3.5	493	2	Q08037	Q08037 influenza a
1038	92.5	3.5	493	2	Q08038	Q08038 influenza a
1039	92.5	3.5	493	2	Q08040	Q08040 influenza a
1040	92.5	3.5	493	2	Q09112	Q09112 influenza a
1041	92.5	3.5	498	1	VNUC_IAB37	Q07539 influenza a
1042	92.5	3.5	498	1	VNUC_IAME6	Q07546 influenza a
1043	92.5	3.5	498	1	VNUC_IANT6	P03467 influenza a
1044	92.5	3.5	498	1	VNUC_IAS11	Q07550 influenza a
1045	92.5	3.5	498	2	Q6XTQ1	Q6xtq1 influenza a
1046	92.5	3.5	520	1	TUL2_HUMAN	Q00295 homo sapien
1047	92.5	3.5	521	2	Q8C4D5	Q8c4d5 mus musculu
1048	92.5	3.5	554	2	Q80US1	Q80us1 mus musculu
1049	92.5	3.5	560	2	Q7NTT6	Q7ntt6 chromobacte
1050	92.5	3.5	605	2	Q6RX29	Q6rx29 arabidopsis
1051	92.5	3.5	641	2	Q7U3P8	Q7u3p8 synechococc
1052	92.5	3.5	656	2	Q9H4S6	Q9h4s6 homo sapien
1053	92.5	3.5	668	1	MTMW_METWO	O59647 methanobact

1054	92.5	3.5	745	1	K6A6_HUMAN	Q9uk32 homo sapien
1055	92.5	3.5	829	2	Q9F9F8	Q9f9f8 helicobacte
1056	92.5	3.5	843	1	MVPA_DICD1	P34118 dictyosteli
1057	92.5	3.5	857	2	Q7W5V3	Q7w5v3 bordetella
1058	92.5	3.5	914	2	Q9FUC2	Q9fuc2 ricinus com
1059	92.5	3.5	953	1	UVRA_RICPR	Q9zcc3 rickettsia
1060	92.5	3.5	961	2	Q6FRK6	Q6frk6 candida gla
1061	92.5	3.5	1067	2	Q8TA72	Q8ta72 asterias am
1062	92.5	3.5	1354	2	Q9LZW9	Q9lzw9 arabidopsis
1063	92.5	3.5	1501	1	SNQ2_YEAST	P32568 saccharomyc
1064	92.5	3.5	1610	2	Q7UVX7	Q7uvx7 rhodopirell
1065	92.5	3.5	1900	2	Q8YN83	Q8yn83 anabaena sp
1066	92.5	3.5	2042	2	Q8TZ07	Q8tz07 methanopyru
1067	92.5	3.5	2312	2	Q7PNQ7	Q7pnq7 anopheles g
1068	92.5	3.5	2373	2	Q8CUZ9	Q8cuz9 oceanobacil
1069	92.5	3.5	2671	2	Q754A3	Q754a3 ashbya goss
1070	92	3.5	327	1	GUAC_STRAS	Q8dzl4 streptococc
1071	92	3.5	331	2	Q6CHQ6	Q6chq6 yarrowia li
1072	92	3.5	354	2	Q6BWX6	Q6bwx6 debaryomyce
1073	92	3.5	411	1	DHE2_ARATH	Q38946 arabidopsis
1074	92	3.5	413	2	O54761	O54761 spermophilu
1075	92	3.5	423	1	MR11_PYRAB	Q9uzc9 pyrococcus
1076	92	3.5	426	2	Q8JS53	Q8js53 phthorimaea
1077	92	3.5	461	2	Q81DV1	Q81dv1 bacillus ce
1078	92	3.5	484	2	Q80ZD1	Q80zd1 tamias stri
1079	92	3.5	546	2	Q639W6	Q639w6 bacillus ce
1080	92	3.5	571	1	HEMA_NDVH3	P35741 newcastle d
1081	92	3.5	576	1	NAE2_THEMEA	Q9x0y0 thermotoga
1082	92	3.5	588	1	SYD_HAEIN	P43817 haemophilus
1083	92	3.5	623	2	Q91197	Q91197 oncorhynchu
1084	92	3.5	623	2	Q98992	Q98992 salmo salar
1085	92	3.5	671	2	Q969R2	Q969r2 homo sapien
1086	92	3.5	686	2	Q833W2	Q833w2 enterococcu
1087	92	3.5	687	2	Q9M2B9	Q9m2b9 arabidopsis
1088	92	3.5	690	1	IF2_THEMEA	Q9wzn3 thermotoga
1089	92	3.5	745	2	Q7X3Y6	Q7x9y6 saccharum h
1090	92	3.5	818	2	Q8NXY8	Q8nxy8 staphylococ
1091	92	3.5	844	2	Q81767	Q81767 arabidopsis
1092	92	3.5	849	2	Q6PF69	Q6pf69 xenopus lae
1093	92	3.5	880	1	DPO1_BACSU	O34996 bacillus su
1094	92	3.5	889	2	Q9SKE7	Q9ske7 arabidopsis
1095	92	3.5	919	2	Q6A037	Q6a037 mus musculu
1096	92	3.5	927	1	IF2_STRAS	Q9zfd2 streptococc
1097	92	3.5	927	1	IF2_STRAS	Q8elh3 streptococc
1098	92	3.5	927	2	Q6T719	Q6t719 streptococc
1099	92	3.5	927	2	Q9K2K6	Q9k2k6 streptococc
1100	92	3.5	927	2	Q9K2M9	Q9k2m9 streptococc
1101	92	3.5	927	2	Q9K507	Q9k507 streptococc
1102	92	3.5	999	2	Q86519	Q86519 rice yellow
1103	92	3.5	1024	2	Q8CCE7	Q8cce7 mus musculu
1104	92	3.5	1026	2	Q6BRI4	Q6bri4 debaryomyce
1105	92	3.5	1036	2	Q86999	Q86999 clostridium
1106	92	3.5	1059	1	SPS_VICFA	Q43876 vicia faba
1107	92	3.5	1117	2	Q53971	Q53971 streptococc
1108	92	3.5	1234	2	Q92K44	Q92k44 rhizobium m
1109	92	3.5	1401	1	DPO3_THETN	Q8ra32 thermoanaer
1110	92	3.5	1568	2	O16858	O16858 microciona
1111	92	3.5	1997	1	OTOF_MOUSE	Q9esf1 mus musculu
1112	92	3.5	2527	2	Q9V7F2	Q9v7f2 drosophila
1113	91.5	3.5	219	2	Q8XJA7	Q8xja7 clostridium
1114	91.5	3.5	246	1	LYTT_BACCR	Q814j1 bacillus ce
1115	91.5	3.5	252	2	Q8P690	Q8p690 xanthomonas
1116	91.5	3.5	256	2	Q6HC57	Q6hc57 bacillus th
1117	91.5	3.5	323	2	Q702F2	Q702f2 uncultured
1118	91.5	3.5	370	1	AMAA_BACST	P37112 bacillus st
1119	91.5	3.5	381	2	Q8NR44	Q8nr44 corynebacte
1120	91.5	3.5	383	2	Q882Q5	Q882q5 pseudomonas
1121	91.5	3.5	391	2	Q9X223	Q9x223 thermotoga
1122	91.5	3.5	423	2	Q7Q4F3	Q7q4f3 anopheles g
1123	91.5	3.5	425	2	Q8P1D3	Q8p1d3 streptococc
1124	91.5	3.5	442	2	Q8FSD4	Q8fsd4 corynebacte
1125	91.5	3.5	492	2	Q7RG47	Q7rg47 plasmodium
1126	91.5	3.5	498	1	VNUC_IAME3	Q07545 influenza a

Q9uk32	homo sapien
Q9f9f8	helicobacte
P34118	dictyosteli
Q7w5v3	bordetella
Q9fuc2	ricinus com
Q9zcc3	rickettsia
Q6frk6	candida gla
Q8ta72	asterias am
Q9lzw9	arabidopsis
P32568	saccharomyc
Q7uvx7	rhodopirell
Q8yn83	anabaena sp
Q8tz07	methanopyru
Q7pnq7	anopheles g
Q8cuz9	oceanobacil
Q754a3	ashbya goss
Q8dzl4	streptococc
Q6chq6	yarrowia li
Q6bwx6	debaryomyce
Q38946	arabidopsis
O54761	spermophilu
Q9uzc9	pyrococcus
Q8js53	phthorimaea
Q81dv1	bacillus ce
Q80zd1	tamias stri
Q639w6	bacillus ce
P35741	newcastle d
Q9x0y0	thermotoga
P43817	haemophilus
Q91197	oncorhynchu
Q98992	salmo salar
Q969r2	homo sapien
Q833w2	enterococcu
Q9m2b9	arabidopsis
Q9wzn3	thermotoga
Q7x9y6	saccharum h
Q8nxy8	staphylococ
Q81767	arabidopsis
Q6pf69	xenopus lae
O34996	bacillus su
Q9ske7	arabidopsis
Q6a037	mus musculu
Q9zfd2	streptococc
Q8elh3	streptococc
Q6t719	streptococc
Q9k2k6	streptococc
Q9k2m9	streptococc
Q9k507	streptococc
Q86519	rice yellow
Q8cce7	mus musculu
Q6bri4	debaryomyce
Q86999	clostridium
Q43876	vicia faba
Q53971	streptococc
Q92k44	rhizobium m
Q8ra32	thermoanaer
O16858	microciona
Q9esf1	mus musculu
Q9v7f2	drosophila
Q8xja7	clostridium
Q814j1	bacillus ce
Q8p690	xanthomonas
Q6hc57	bacillus th
Q702f2	uncultured
P37112	bacillus st
Q8nr44	corynebacte
Q882q5	pseudomonas
Q9x223	thermotoga
Q7q4f3	anopheles g
Q8p1d3	streptococc
Q8fsd4	corynebacte
Q7rg47	plasmodium
Q07545	influenza a

1127	91.5	3.5	498	2	Q91MA3	Q91ma3 influenza a	1200	91	3.5	1956	2	Q6DNE1	Q6dne1 lyngbya maj
1128	91.5	3.5	498	2	Q91MA4	Q91ma4 influenza a	1201	91	3.5	2028	2	Q8CIR4	Q8cir4 mus musculu
1129	91.5	3.5	498	2	Q91MA5	Q91ma5 influenza a	1202	91	3.5	2467	2	O15050	O15050 homo sapien
1130	91.5	3.5	498	2	Q9WLG4	Q9wlg4 influenza a	1203	91	3.5	3680	1	DMD_CANFA	DMD_CANFA canis famil
1131	91.5	3.5	500	1	NUSA_SALTY	P37430 salmonella	1204	91	3.5	4037	2	Q74KU3	Q74ku3 lactobacill
1132	91.5	3.5	505	2	Q6BPJ5	Q6bpj5 debaryomyce	1205	90.5	3.5	337	2	Q7MIT7	Q7mit7 vibrio vuln
1133	91.5	3.5	512	2	Q8R858	Q8r858 thermoanaer	1206	90.5	3.5	339	2	Q65MV5	Q65mv5 bacillus li
1134	91.5	3.5	527	2	Q8VZX0	Q8vzx0 oceanobacil	1207	90.5	3.5	361	2	Q94JD7	Q94jd7 oryza sativ
1135	91.5	3.5	537	2	Q8VZX0	Q8vzx0 vigna ungui	1208	90.5	3.5	382	2	Q9HLJ3	Q9hlj3 thermoplasm
1136	91.5	3.5	553	2	Q8NU15	Q8nu15 corynebacte	1209	90.5	3.5	438	2	Q72JQ4	Q72jq4 thermus the
1137	91.5	3.5	565	2	Q9PBW6	Q9pbw6 xylella fas	1210	90.5	3.5	444	2	Q82HY0	Q82hy0 streptomyc
1138	91.5	3.5	631	2	Q67PV1	Q67pv1 symbiobacte	1211	90.5	3.5	445	2	Q8R693	Q8r693 fusobacteri
1139	91.5	3.5	655	2	Q827F4	Q827f4 streptomyc	1212	90.5	3.5	452	2	Q84TQ8	Q84tq8 phaseolus v
1140	91.5	3.5	702	1	TRP_COPCI	P16578 coprinus ci	1213	90.5	3.5	471	2	Q7WPW6	Q7wpw6 bordetella
1141	91.5	3.5	708	2	Q81R76	Q81r76 bacillus an	1214	90.5	3.5	496	1	DNAA_BRUSU	DNAA_BRUSU brucella su
1142	91.5	3.5	720	2	Q7TPS0	Q7tps0 mus musculu	1215	90.5	3.5	500	2	Q8Z3H6	Q8z3h6 salmonella
1143	91.5	3.5	730	1	IF2_BACHD	Q9ka77 bacillus ha	1216	90.5	3.5	505	2	Q8YHC9	Q8yhc9 brucella me
1144	91.5	3.5	762	1	METE_BACCR	Q819h7 bacillus ce	1217	90.5	3.5	519	2	Q9LF02	Q9lfo2 arabidopsis
1145	91.5	3.5	808	2	Q6BLG3	Q6blg3 debaryomyce	1218	90.5	3.5	529	2	Q73HS5	Q73hs5 wolbachia p
1146	91.5	3.5	856	2	Q9C594	Q9c594 arabidopsis	1219	90.5	3.5	536	2	Q84TQ9	Q84tq9 phaseolus v
1147	91.5	3.5	883	2	Q7Y051	Q7y051 arabidopsis	1220	90.5	3.5	560	1	SYR_METTH	SYR_METTH methanobact
1148	91.5	3.5	901	2	Q6GH55	Q6gh55 staphylococ	1221	90.5	3.5	603	1	UVRC_LISIN	UVRC_LISIN listeria in
1149	91.5	3.5	958	1	GCSP_YERPE	Q8zhi8 yersinia pe	1222	90.5	3.5	620	2	Q84F37	Q84f37 streptomyc
1150	91.5	3.5	959	2	Q666R7	Q666r7 yersinia ps	1223	90.5	3.5	629	2	Q97TK2	Q97tk2 clostridium
1151	91.5	3.5	1116	2	Q6RCR7	Q6rcr7 legionella	1224	90.5	3.5	692	2	Q84TR2	Q84tr2 phaseolus v
1152	91.5	3.5	1130	2	Q9K2K8	Q9k2k8 streptococc	1225	90.5	3.5	711	2	Q84TR0	Q84tr0 phaseolus v
1153	91.5	3.5	1134	2	Q9L908	Q9l908 streptococc	1226	90.5	3.5	713	2	Q7N2I0	Q7n2i0 photorhabdu
1154	91.5	3.5	1354	2	Q9C0G6	Q9c0g6 homo sapien	1227	90.5	3.5	721	2	Q88YQ4	Q88yg4 lactobacill
1155	91.5	3.5	1713	2	Q97B15	Q97b15 thermoplasm	1228	90.5	3.5	729	2	Q84TR1	Q84tr1 phaseolus v
1156	91.5	3.5	1732	2	Q54874	Q54874 rattus norv	1229	90.5	3.5	740	2	Q8VUB0	Q8vub0 lactococcu
1157	91.5	3.5	1776	2	Q6BMI2	Q6bmi2 debaryomyce	1230	90.5	3.5	758	1	YH38_CHRVO	YH38_CHRVO chromobacte
1158	91.5	3.5	3418	1	BRC2_HUMAN	P51587 homo sapien	1231	90.5	3.5	832	2	Q72RN6	Q72rn6 leptospira
1159	91.5	3.5	5106	2	Q9VAV5	Q9vav5 drosophila	1232	90.5	3.5	832	2	Q8F425	Q8f425 leptospira
1160	91	3.5	319	1	YE52_SCHPO	O14169 schizosacch	1233	90.5	3.5	850	2	Q6W1H3	Q6wlh3 rhizobium s
1161	91	3.5	347	2	Q71058	Q71058 human immu	1234	90.5	3.5	857	2	Q7VXL4	Q7vxl4 bordetella
1162	91	3.5	385	2	Q742C7	Q74zc7 ashbya goss	1235	90.5	3.5	861	2	Q76IN4	Q76in4 entamoeba h
1163	91	3.5	395	2	Q8FSP9	Q8fsf9 corynebacte	1236	90.5	3.5	877	2	Q6BZ57	Q6bz57 debaryomyce
1164	91	3.5	414	2	Q97FD5	Q97fd5 clostridium	1237	90.5	3.5	883	2	Q76MR5	Q76mr5 poeophila gu
1165	91	3.5	415	2	Q7VXC4	Q7vxc4 bordetella	1238	90.5	3.5	1033	2	Q6CXA1	Q6cxa1 kluyveromyc
1166	91	3.5	445	2	Q8RB04	Q8rb04 thermoanaer	1239	90.5	3.5	1105	2	Q9VX31	Q9vxx31 drosophila
1167	91	3.5	478	1	VP26_DROME	Q9w552 drosophila	1240	90.5	3.5	1167	1	SCA1_STRPY	SCA1_STRPY streptococc
1168	91	3.5	498	1	VNUC_IAOHI	P23997 influenza a	1241	90.5	3.5	1291	2	Q9ZHU6	Q9zhu6 helicobacte
1169	91	3.5	498	1	VNUC_IAS06	Q08042 influenza a	1242	90.5	3.5	1425	2	Q7P614	Q7p614 fusobacteri
1170	91	3.5	512	1	GUAA_BACAN	Q81ve0 bacillus an	1243	90.5	3.5	1496	2	Q9M2L7	Q9m2l7 arabidopsis
1171	91	3.5	512	1	GUAA_BACAN	Q73er7 bacillus ce	1244	90.5	3.5	1504	2	Q9ZGA6	Q9zga6 streptomyc
1172	91	3.5	515	2	Q63GV4	Q63gv4 bacillus ce	1245	90.5	3.5	1513	2	P96901	P96901 mycobacteri
1173	91	3.5	520	2	Q64VK6	Q64vk6 bacteroides	1246	90.5	3.5	1647	2	Q8P2A0	Q8p2a0 streptococc
1174	91	3.5	536	2	Q6LPS7	Q6lps7 photobacter	1247	90.5	3.5	1679	1	YMF9_YEAST	YMF9_YEAST saccharomyc
1175	91	3.5	551	2	Q8PK65	Q8pk65 xanthomonas	1248	90.5	3.5	1684	2	Q8AYN8	Q8ayn8 cyprinus ca
1176	91	3.5	564	2	Q7QEU6	Q7geu6 anopheles g	1249	90.5	3.5	1963	2	Q9LXT9	Q9lxt9 arabidopsis
1177	91	3.5	599	2	Q6D497	Q6d497 erwinia car	1250	90.5	3.5	2118	2	Q6KAR3	Q6kar3 mus musculu
1178	91	3.5	604	2	Q97YJ0	Q97yj0 sulfolobus	1251	90.5	3.5	2571	2	Q87704	Q87704 bacillus su
1179	91	3.5	617	2	Q87WG3	Q87wg3 pseudomonas	1252	90.5	3.4	240	2	Q65GA9	Q65ga9 bacillus li
1180	91	3.5	621	2	Q92AZ6	Q92az6 listeria in	1253	90	3.4	272	2	Q65Q26	Q65q26 mannheimia
1181	91	3.5	657	2	Q651T5	Q65it5 oryza sativ	1254	90	3.4	295	2	Q67C42	Q67c42 nicotiana t
1182	91	3.5	663	2	Q6FMQ0	Q6fmq0 candida gla	1255	90	3.4	303	2	Q96LV9	Q96lv9 homo sapien
1183	91	3.5	679	2	Q9LDT4	Q9ldt4 avena fatua	1256	90	3.4	316	2	Q9XSC7	Q9xsc7 sus scrofa
1184	91	3.5	694	2	Q831U3	Q83lu3 enterococcu	1257	90	3.4	331	2	Q74HH3	Q74hh3 lactobacill
1185	91	3.5	732	2	O17619	O17619 caenorhabdi	1258	90	3.4	353	2	Q8KHJ5	Q8khj5 clostridium
1186	91	3.5	737	1	ACET_RABIT	P22968 oryctolagus	1259	90	3.4	372	2	O54590	O54590 halobacteri
1187	91	3.5	754	2	Q6G3Z6	Q6g3z6 bartonella	1260	90	3.4	378	2	Q6FLB6	Q6flb6 candida gla
1188	91	3.5	781	1	K6PF_CANFA	P52784 canis famil	1261	90	3.4	387	2	Q82XE5	Q82xe5 nitrosomona
1189	91	3.5	816	2	Q8D3K7	Q8d3k7 vibrio vuln	1262	90	3.4	392	2	Q73PQ1	Q73pq1 treponema d
1190	91	3.5	869	2	Q8Y161	Q8y161 ralstonia s	1263	90	3.4	415	2	Q7WA23	Q7wa23 bordetella
1191	91	3.5	871	2	Q97K23	Q97k23 clostridium	1264	90	3.4	415	2	Q7WJ52	Q7wj52 bordetella
1192	91	3.5	893	2	Q8AGK6	Q8agk6 simian t-ly	1265	90	3.4	415	2	Q8A3I8	Q8a3i8 bacteroides
1193	91	3.5	988	2	Q9X537	Q9x537 corynebacte	1266	90	3.4	426	2	O67155	O67155 aquifex aeo
1194	91	3.5	1010	2	Q9ZPN1	Q9zpn1 avena sativ	1267	90	3.4	432	2	O15324	O15324 homo sapien
1195	91	3.5	1077	2	Q9UKW0	Q9ukw0 homo sapien	1268	90	3.4	435	2	Q7D8K2	Q7d8k2 mycobacteri
1196	91	3.5	1268	2	Q6ZUP9	Q6zup9 homo sapien	1269	90	3.4	435	2	O86315	O86315 mycobacteri
1197	91	3.5	1291	2	Q9ZHT2	Q9zht2 helicobacte	1270	90	3.4	435	2	Q7U0C0	Q7u0c0 mycobacteri
1198	91	3.5	1337	2	Q6ZQD5	Q6zqd5 mus musculu	1271	90	3.4	455	1	SYPC_METJA	SYPC_METJA methanococc
1199	91	3.5	1827	2	Q7ULP1	Q7ulp1 rhodopirell	1272	90	3.4				









QY 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG 360  
QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDSGTPIAKMFQEI VHKS VVLIPLGAVDDGHSQ 480  
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDSGTPIAKMFQEI VHKS VVLIPLGAVDDGHSQ 480  
QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

RESULT 2  
CGL2 HUMAN STANDARD; PRT; 508 AA.  
AC Q96KN2; Q9BT98;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Glutamate carboxypeptidase-like protein 2 precursor (CNDP dipeptidase 1).  
GN Name=CNDP1; Synonyms=CPGL2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN {1}  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Chen J.M., Barrett A.J.;  
RT "Cloning and sequencing of a second human homologue of glutamate carboxypeptidase in peptidase family M20.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN {2}  
RP SEQUENCE OF 199-508 FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- SIMILARITY: Belongs to the peptidase M20A family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AJ417564; CAD10388.1; -.  
DR EMBL; BC004271; -; NOT\_ANNOTATED\_CDS.  
DR MEROPS; M20.006; -.  
DR Genew; HGNC:20675; CNDP1.  
DR InterPro; IPR001261; Arge\_dape.  
DR InterPro; IPR002933; Peptidase\_M20.  
DR pfam; PF01546; Peptidase\_M20; 1.  
DR PROSITE; PS00758; ARGE\_DAPE\_CPG2\_1; FALSE\_NEG.  
DR PROSITE; PS00759; ARGE\_DAPE\_CPG2\_2; FALSE\_NEG.  
KW Carboxypeptidase; Hydrolase; Metalloprotease; Signal.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 508 Glutamate carboxypeptidase-like protein  
FT CHAIN 28 508 2.  
FT CONFLICT 238 238 L -> P (in Ref. 2).  
FT CONFLICT 273 273 L -> P (in Ref. 2).  
FT SEQUENCE 508 AA; 56779 MW; 0FDEA8991FDB495D CRC64;  
SQ  
Query Match 98.6%; Score 2585.5; DB 1; Length 508;  
Best Local Similarity 99.2%; Pred. No. 2.4e-177;  
Matches 504; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 MDPKLGMAASLLAV-LLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 59  
Db 1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60  
Qy 60 ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE 119  
Db 61 ESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE 120  
Qy 120 SDPTKGTVCIFYGHLDVQPADRGDWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 179  
Db 121 SDPTKGTVCIFYGHLDVQPADRGDWLTDPYVLTEVGKLYGRGATDNKGPVLAWINAVSA 180  
Qy 180 FRALEQDLPVNIKFIIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAI 239  
Db 181 FRALEQDLPVNIKFIIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAI 240  
Qy 240 TYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299  
Db 241 TYGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300  
Qy 300 VPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEP 359  
Db 301 VPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEP 360  
Qy 360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 419  
Db 361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWI 420  
Qy 420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTPIAKMFQEI VHKS VVLIPLGAVDDGHS 479  
Db 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDSGTPIAKMFQEI VHKS VVLIPLGAVDDGHS 480  
Qy 480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508

RESULT 3  
Q66HG3  
ID Q66HG3 PRELIMINARY; PRT; 492 AA.  
AC Q66HG3;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN {1}  
RP SEQUENCE FROM N.A.



RC	TISSUE=Kidney;
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RA	Director MGC Project;
RA	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC081877; AAH81877.1; --
DR	InterPro; IPR002933; Peptidase M20.
DR	Pfam; PF01546; Peptidase_M20; 1.
KW	Hypothetical protein.
SQ	SEQUENCE 492 AA; 54927 MW; EF8DAE8C15BF06F5 CRC64;
<p>Query Match 80.1%; Score 2100.5; DB 2; Length 492;            Best Local Similarity 82.3%; Pred. No. 1.8e-142;            Matches 395; Conservative 43; Mismatches 41; Indels 1; Gaps 1</p>	
QY	29 SPP-PALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMVAADTLQR 87
Db	3 SPHSGTLEKLFQYIDLHQDEFVQTLKEWVAIESDSVQPMRRLRQELFRMVAADKLRN 62
QY	88 LGARVASVDMGPQQLPDGQSLPIPPVILAEELGSDPTKGTVCIFYGLHDVQADRGDWLTD 147
Db	63 LGARVDSVDLGSQQMPDGGQSLPTPPIILAEELGNDPKKPSVCFYGLHDVQPAKEDGWLTD 122
QY	148 PYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEGSVALE 207
Db	123 PYTLTEVDGKLYGRGATDNKGPVLAWINAVSTFRALQDDLPNVVKFILEGMEEGSVALE 182
QY	208 ELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFG 267
Db	183 ELVKREKDNFFSGVDYIVISDNLWLSQKKPALTCGTRGNCYFTVEVKCRDQDFHSGTFFG 242
QY	268 ILHEPMADLVALLGSLVDSGHILVPGIYDEVVPLTEEEINTYKAHLDEEYRNSRVE 327
Db	243 ILNEPMADLVALLGSLVDSGHILVPGIYDQMAPITEEEKTMYENIDLDEEYQKSSRVE 302
QY	328 KFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTIVIPGRVIGKFSIRLVPHMNVSAVE 387
Db	303 RFLFDTKKEELLTHLWRYPSLSIHGIEGAFDEPGTKTIVIPGRVLGKFSIRLVPHMTPSVVE 362
QY	388 KQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDDTQYLAACKRAIRTVFGTEPDMIRD 447
Db	363 TQVTOHLEAVFSKRNSFNKMAVSMVLGLQPWTANINGTQYLAARRAIQTIVFGVDPDMIQD 422
QY	448 GSTIPIAKMFOEIVHKSVVLIPLGAVDGGEHSQNEKINRWNYIEGTYKLFAPFAFFLEMAQLH. 507
Db	423 GSTIPIAKIFQDITQKSVNMLPLGAVDGGEHSQNEKINRWNYIQGSKLFAAFFLELSKLH 482
RESULT 4	
Q8BUG2	
ID Q8BUG2	PRELIMINARY; PRT: 492 AA.

Q8BUG2;  
01-MAR-2003 (TrEMBLrel. 23, Created)  
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:DG30009N02 product:similar to GLUTAMATE CARBOXYPEPTIDASE-LIKE PROTEIN 2.  
Name=Cndp1; Synonym=Cnl1;  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Kidney;  
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
Carninci P., Hayashizaki Y.;  
"High-efficiency full-length cDNA cloning.";  
Meth. Enzymol. 303:19-44(1999).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Kidney;  
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RIKEN FANTOM Consortium;  
"Functional annotation of a full-length mouse cDNA collection.";  
Nature 409:685-690(2001).  
[3]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Kidney;  
The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
Nature 420:563-573(2002).  
[4]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Kidney;  
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
Genome Res. 10:1617-1630(2000).  
[5]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Kidney;  
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1757-1771(2000).  
[6]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Kidney;  
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
EMBL: AK085308; BAC39417.1; -.

RESULT 4  
O8BUG2

ID Q8BUG2 PRELIMINARY: PRT: 492 AA.



DR MGD; MGI:2451097; Cndp1.  
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR002933; Peptidase M20.  
DR Pfam; PF01546; Peptidase\_M20; I.  
KW Carboxypeptidase.  
SQ SEQUENCE 492 AA; 55090 MW; 5A3E3F984CBF4567 CRC64;  
  
Query Match 79.9%; Score 2097; DB 2; Length 492;  
Best Local Similarity 81.4%; Pred. No. 3.1e-142;  
Matches 394; Conservative 43; Mismatches 45; Indels 2; Gaps 1;  
  
Qy 24 MFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAAAD 83  
Db 1 MFSSAH--SGLLEKLFHYIDLHQDEFVQTLKEWVAIESDSVQVPVRLRQKLFQMMALAAD 58  
  
Qy 84 TLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFGHLDVQPADRGD 143  
Db 59 KLRNLGAGVESIDLGSQQMPDGQSLPIPPILLAEELGSDPEKPTVCYFGHLDVQPAQKDDG 118  
  
Qy 144 WLTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGS 203  
Db 119 WLTDPTYTLTEVDGKLYGRGATDNKGPVLAWINAVSTFRALQDLPVNIKFIIEGMEEAGS 178  
  
Qy 204 VALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSG 263  
Db 179 IALEELVMREKDHFFSSVDYIVISDNLWLSQRKPAITYGTRGNCYFTVEVKCRDQDFHSG 238  
  
Qy 264 TFGGILHEPMAADLVALLGSLVDSGSHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNS 323  
Db 239 TFGGILNEPMAADLVALLGSLVDSGSHILIPGIYDQMAPITEGEKTMYNIDMDLEEYQNI 298  
  
Qy 324 SRVEKFLFDTKHEELMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 383  
Db 299 NQVEKFLFDTKHEELMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVLGKFSIRLVPTMSP 358  
  
Qy 384 SAVEKQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDTQYLAAKRAIRTVEGTEPD 443  
Db 359 SVVEKQVTQHLEAVFSKRNSFNKMAVSMVLGLHPWTANVNDTQYLAARQRTIKTVFGVNP 418  
  
Qy 444 MIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGKLFAAFFLEM 503  
Db 419 MIRDGSTIPIAKIFQAITOKSVMMPLGAVDDGEHSQNEKINRWNYIQGSKLFAAFFLEL 478  
  
Qy 504 AQLH 507  
Db 479 SKQH 482  
  
RESULT 5  
Q80XP5 PRELIMINARY; PRT; 492 AA.  
ID Q80XP5  
AC Q80XP5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Carnosine dipeptidase 1 (Metallopeptidase M20 family).  
GN Name=Cndp1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Kidney;  
RA Strausberg R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC043305; AAH43305.1; -.  
DR MGD; MGI:2451097; Cndp1.  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR002933; Peptidase M20.  
DR Pfam; PF01546; Peptidase\_M20; I.  
SQ SEQUENCE 492 AA; 55056 MW; 8F5C3AFD859EC804 CRC64;  
  
Query Match 79.7%; Score 2091; DB 2; Length 492;  
Best Local Similarity 81.2%; Pred. No. 8.5e-142;  
Matches 393; Conservative 43; Mismatches 46; Indels 2; Gaps 1;  
  
Qy 24 MFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAAAD 83  
Db 1 MFSSAH--SGLLEKLFHYIDLHQDEFVQTLKEWVAIESDSVQVPVRLRQKLFQMMALAAD 58  
  
Qy 84 TLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEELGSDPTKGTVCYFGHLDVQPADRGD 143  
Db 59 KLRNLGAGVESIDLGSQQMPDGQSLPIPPILLAEELGSDPEKPTVCYFGHLDVQPAQKDDG 118  
  
Qy 144 WLTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGS 203  
Db 119 WLTDPTYTLTEVDGKLYGRGATDNKGPVLAWINAVSTFRALQDLPVNIKFIIEGMEEAGS 178  
  
Qy 204 VALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSG 263  
Db 179 IALEELVMREKDHFFSSVDYIVISDNLWLSQRKPAITYGTRGNCYFTVEVKCRDQDFHSG 238  
  
Qy 264 TFGGILHEPMAADLVALLGSLVDSGSHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNS 323  
Db 239 TFGGILNEPMAADLVALLGSLVDSGSHILIPGIYDQMAPITEGEKTMYNIDMDLEEYQNI 298  
  
Qy 324 SRVEKFLFDTKHEELMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNV 383  
Db 299 NQVEKFLFDTKHEELMHLWRYPYSLSIHGIEGAFDEPGTKTVIPGRVLGKFSIRLVPTMSP 358  
  
Qy 384 SAVEKQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIANIDTQYLAAKRAIRTVEGTEPD 443  
Db 359 SVVEKQVTQHLEAVFSKRNSFNKMAVSMVLGLHPWTANVNDTQYLAARQRTIKTVFGVNP 418  
  
Qy 444 MIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGKLFAAFFLEM 503  
Db 419 MIRDGSTIPIAKIFQAITOKSVMMPLGAVDDGEHSQNEKINRWNYIQGSKLFAAFFLEL 478  
  
Qy 504 AQLH 507  
Db 479 SKQH 482  
  
RESULT 6  
Q6PA54 PRELIMINARY; PRT; 494 AA.  
ID Q6PA54  
AC Q6PA54;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)





Db 4 LPNLFKYVDEHQNEYVERLAQWVAVQ--SVSAWPEKRGGEIKKINEMAGKDIERLGGTVEL 61

QY 95 VDMGPQQLPDCQSLPIPPVILAEALGSDPTKGTVCYFGHLDVQPADRGDGLWLTDPYVLTEV 154

Db 62 VDIGMKLPSEGEIPLPPIVLGRGLSDPGKKTVCYIYGHLDVQPASIEDGWDSPFILEER 121

QY 155 DGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEK 214

Db 122 DGKMYGRGSTDDKGPVLAWFNIIIEAYOKIQGELPINIKFCFEGMEESGSEGLDDLVSFRK 181

QY 215 DRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKCRDODFHSGTGGILHEPMA 274

Db 182 DTFEKDVDYVCISDNWYLGKTKPCITYGLRGICYFFIEMECCDXLHSGVFGGSVHEAMT 241

QY 275 DLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTK 334

Db 242 DLIALMGTLVDNKGKIKVPGIYDQVAKLTDEEKKLYEKIEFDLEEYAKDVGAGKLMHDTX 301

QY 335 EEILMHLWRVPSLSIHGIEGAFDEPGTKVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHL 394

Db 302 EQILMHRWRVPSLSLHGIEGAFSEAGAKTVIPRKVIGKFSIRLVPDMDPKVVEKQVISHL 361

QY 395 EDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIA 454

Db 362 EKTFAELKSNKLKVMYMGHGAWVSDNHPHYMAGRKAMKTVFGVEPDLTREGGSIPTV 421

QY 455 KMFQEIIVHKSVVLIPLGAVDDGESHSONEKNRWNYIEGTKLFAAFFLEMAQL 506

Db 422 LTFQEATQNVMLLPVGSDDGAHSONEKNRNSYIQGTMKLGAFYFEVSQ 473

RESULT 8

Q6P336 PRELIMINARY; PRT; 499 AA.

AC Q6P336;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE LOC394903 protein (Fragment).

GN Name=LOC394903;

OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8364;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Klein S., Gerhard D.S.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC064197; AAH64197.1; -.

DR GO; GO:0008237; F:metallopeptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002933; Peptidase M20.

DR Pfam; PF01546; Peptidase\_M20; 1.

FT NON TER 1

SQ SEQUENCE 499 AA; 55422 MW; DDFD025F1506DE27 CRC64;

Query Match 53.2%; Score 1396.5; DB 2; Length 499;

Best Local Similarity 55.0%; Pred. No. 7.6e-92;

Matches 269; Conservative 84; Mismatches 127; Indels 9; Gaps 4;

QY 16 LLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFQELF 75

Db 16 LIFLLTCQVLLSPVK----DGVFQYIDAHQDEFIQLKDWVAIESDSDPSK--RDLLN 69

QY 76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEALGSDPTKGTVCYGHLDV 135

Db 70 KWMELTKDFILKGNVEMAEIGEQLSSGERIPLPPVILAEALGNDKSKPTVCYGHMDV 129

QY 136 QPADRGDGLTDPYVLTEVDKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Db 130 QPAKQTDGLTDPYTVVEKDNLYGRGTSDDKQGVALLHALESVNVN--GLPVNVKLV 187

QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVEVKC 255

Db 188 EGMEEVGSGLKLVEDKXDTFFSNVDYIVVTDTPWLS-KKPGITYGARGNCYFFLEVQG 246

QY 256 RDQDFHSGTGGILHEPNADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHL 315

Db 247 SRDLHSGGGTGVHEAMSDLIYLLNTLADGKGRILVPGIYEAVPVGENETDLYKNLEF 306

QY 316 DLEEYRNSRVEKFLFDTKBEILMHLWRYPSPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Db 307 SQEQMQADTGVQTQFLHDTKEDLLMHRWRYPSLTIHGIEGAFCGTGTKTVIPAKVIGKFSM 366

QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Db 367 RQVPNMDPVVEKQVTDYLEAKFSERKSPNKIKVMVIGAKPWLADNMNEPQYLAARRAVK 426

QY 436 TVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGESHSONEKNRWNYIEGTKL 495

Db 427 RVFNLEADMIRAGGTIPIAKTLEDVLGKSVMLLGIGGPDADPHGQNEKISKYNYIEGTKL 486

QY 496 FFAAFFLEMA 504

Db 487 YASYLQELS 495

RESULT 9

Q8AWF8 PRELIMINARY; PRT; 489 AA.

AC Q8AWF8;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Glutamate carboxypeptidase (Darmin protein).

GN Name=Darmin; Synonyms=darmin;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22597554; PubMed=12711541; DOI=10.1016/S1567-133X(03)00011-5;

RA Pera E.M., Martinez S.L., Flanagan J.J., Brechner M., Wessely O.,

RA De Robertis E.M.;

RT "Darmin is a novel secreted protein expressed during endoderm

RT development in Xenopus.";

RL Gene Expr. Patterns 3:147-152(2003).





FT NON TER 1 1  
SQ SEQUENCE 494 AA; 54813 MW; 2E349630FCF08147 CRC64;  
Query Match 53.0%; Score 1391.5; DB 2; Length 494;  
Best Local Similarity 54.8%; Pred. No. 1.7e-91;  
Matches 268; Conservative 83; Mismatches 129; Indels 9; Gaps 4;  
QY 16 LLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELF 75  
Db 11 IIFLLTYQVLLSPVPN---NGVFQYIDAHQDEFIQRKDWVAIESDSSDPK--RDLVN 64  
QY 76 RMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCYFGHLDV 135  
Db 65 KMMEMTKDYILKLGGSVEMAEIGEQLSSGEKIPLPVPVILAELGNDKSKPTVCYFGHMDV 124  
QY 136 QPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195  
Db 125 QPAKQTDGWLTEPYTVVEKDDNLYGRGTSDDKGQVLALLHALESVNVN--GLP VNVKLA I 182  
QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255  
Db 183 EGMEEVSGDGLVKLEKVEDKDTFFSNVDYIVVTDTPWLS--KKPGITYGARGNCYFFIEVQG 241  
QY 256 RDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKA IHL 315  
Db 242 ARDLHSGGFGGTVHEAMSDLIYLLNTLADGKGRILVPGIYEAVPVGENETDLYKNLEF 301  
QY 316 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPYSLSIHGIEGAFDEPCTKTVIPGRVIGKFSI 375  
Db 302 SLEEMQADTGKQFLHDTKEDLLMHRWRYPSLSIHGIEGAFSGTGKTVIPAKVIGKFSI 361  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTGLHPWIANIDDTQYLAAKRAIR 435  
Db 362 RQVPNMEPSVNVKQVTDYLEAKFSEKSPNKIKVTMVIGAKPWLADNMNEPQYLAARRAVK 421  
QY 436 TVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGGEHSQNEKINRWNYIEGTKL 495  
Db 422 RVFNLEADMIRAGGTIPIAKTLEDVLGKSVMLLGIGGPDADPHGQNEKISKYNYIEGTKL 481  
QY 496 FFAFFLEMA 504  
Db 482 YASYLQELS 490

RESULT 11  
Q801E4  
ID Q801E4 PRELIMINARY; PRT; 500 AA.  
AC Q801E4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Glutamate carboxypeptidase-like protein 1 (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=83355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22480013; PubMed=12591597; DOI=10.1016/S0925-4773(02)00460-4;  
RA Chen Y., Jurgens K., Hollemann T., Claussen M., Ramadori G.,  
RA Pieler T.;  
RT "Cell-autonomous and signal-dependent expression of liver and  
RT intestine marker genes in pluripotent precursor cells from Xenopus  
RT embryos.";  
RL Mech. Dev. 120:277-288(2003).  
DR EMBL; AY188285; AAC31611.1; --  
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR002933; Peptidase\_M20.  
DR Pfam; PF01546; Peptidase\_M20; 1.  
KW Carboxypeptidase.

FT NON TER 1 1  
SQ SEQUENCE 500 AA; 55479 MW; F2FCB0B3AD4879E4 CRC64;  
Query Match 53.0%; Score 1391.5; DB 2; Length 500;  
Best Local Similarity 54.8%; Pred. No. 1.7e-91;  
Matches 268; Conservative 83; Mismatches 129; Indels 9; Gaps 4;  
QY 16 LLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELF 75  
Db 17 IIFLLTYQVLLSPVPN---NGVFQYIDAHQDEFIQRKDWVAIESDSSDPK--RDLVN 70  
QY 76 RMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCYFGHLDV 135  
Db 71 KMMEMTKDYILKLGGSVEMAEIGEQLSSGEKIPLPVPVILAELGNDKSKPTVCYFGHMDV 130  
QY 136 QPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195  
Db 131 QPAKQTDGWLTEPYTVVEKDDNLYGRGTSDDKGQVLALLHALESVNVN--GLP VNVKLA I 188  
QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255  
Db 189 EGMEEVSGDGLVKLEKVEDKDTFFSNVDYIVVTDTPWLS--KKPGITYGARGNCYFFIEVQG 247  
QY 256 RDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKA IHL 315  
Db 248 ARDLHSGGFGGTVHEAMSDLIYLLNTLADGKGRILVPGIYEAVPVGENETDLYKNLEF 307  
QY 316 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPYSLSIHGIEGAFDEPCTKTVIPGRVIGKFSI 375  
Db 308 SLEEMQADTGKQFLHDTKEDLLMHRWRYPSLSIHGIEGAFSGTGKTVIPAKVIGKFSI 367  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVMVMTGLHPWIANIDDTQYLAAKRAIR 435  
Db 368 RQVPNMEPSVNVKQVTDYLEAKFSEKSPNKIKVTMVIGAKPWLADNMNEPQYLAARRAVK 427  
QY 436 TVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGGEHSQNEKINRWNYIEGTKL 495  
Db 428 RVFNLEADMIRAGGTIPIAKTLEDVLGKSVMLLGIGGPDADPHGQNEKISKYNYIEGTKL 487  
QY 496 FFAFFLEMA 504  
Db 488 YASYLQELS 496

RESULT 12  
Q7TOR7  
ID Q7TOR7 PRELIMINARY; PRT; 474 AA.  
AC Q7TOR7;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cn2-prov protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=83355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,



RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Klein S., Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC056069; AAH56069.1; -;  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR002933; Peptidase\_M20.  
DR Pfam; PF01546; Peptidase\_M20; 1.  
SQ SEQUENCE 474 AA; 52745 MW; 33D9F60F6D375FEF CRC64;

Query Match 52.9%; Score 1388; DB 2; Length 474;  
Best Local Similarity 53.6%; Pred. No. 2.9e-91;  
Matches 254; Conservative 91; Mismatches 127; Indels 2; Gaps 1;

QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV 92  
Db 2 SVLPALFEHIDKNQDLYVKRLAEWVAI--PSVSAWPEKRGKEIKRMMEVAAKEVERLGKGT 59  
QY 93 ASVDMGPPQQLPDGQSLPIPPVILAELGSDPTKGTVCYFVGHLDVQPADRGDGLTDPYVLT 152  
Db 60 ELVDIGKQKLPDGTETPLPILLGLKSDPGKTKVCYVGHLDVQPAALDGDWDSEFPVLD 119  
QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEK 212  
Db 120 ERDGKLYGRGSTDDKGPVLAWLNSIEAYQQIKQEIQVNLNMFCEGMEESSEGLDDLIFA 179  
QY 213 EKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEP 272  
Db 180 RKDTFFKGVDYVCISDNYWLGKPKCITYGLRGICYFFIEVECSKDLHSGVYGGSVHEA 239  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 240 MTDLIALMGSLVDKNGKILIPGINEAVAPVLKEEKDIYEAIEFDLEDFANDIGAELLHE 299  
QY 333 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 300 SKEKILMHRWRFPSPSLHGI EGAFSAAGAKTVIPRKVIGKFSIRLVPMNPDVQKQVED 359  
QY 393 HLEDVFSKRNSSNMVSMVTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 452  
Db 360 YLTCKFKELGSPNKFQVTMGHGKPPWVSDFNHHPYVAGRKAMKTVENVEPDLTREGGSIP 419  
QY 453 IAKMFOEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQL 506  
Db 420 VTLTFQEATGKNVMLLPVGSADDDGAHSQNEKLNRFENYIQGVKLLGAYLYEVSNL 473

RESULT 13  
Q6P358 PRELIMINARY; PRT; 474 AA.  
ID Q6P358  
AC Q6P358;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein MGC75655.  
GN Name=MGC75655;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8364;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC064175; AAH64175.1; -;  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR002933; Peptidase\_M20.  
DR Pfam; PF01546; Peptidase\_M20; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 474 AA; 52722 MW; E0D6F40C7EB7E0E3 CRC64;

Query Match 52.7%; Score 1382; DB 2; Length 474;  
Best Local Similarity 53.8%; Pred. No. 7.8e-91;  
Matches 255; Conservative 86; Mismatches 131; Indels 2; Gaps 1;

QY 33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPRFRQELFRMMAVAADTLQRLGARV 92  
Db 2 SVLQTLFEYIDKNQDLYVKRLAEWVAIQ--SVSAWPEKRGKEIKRMMEVAAKEIERLGTT 59  
QY 93 ASVDMGPPQQLPDGQSLPIPPVILAELGSDPTKGTVCYFVGHLDVQPADRGDGLTDPYVLT 152  
Db 60 ELADIGKQKLPDGTETPLPILLGLKSDPGKTKVCYVGHLDVQPAALDGDWDSEFPVLE 119  
QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLVPNIKFIIEGMEEAGSVALEELVEK 212  
Db 120 ERDGKLYGRGSTDDKGPVLAWLNSIEAYQKTNQDLVNLKFCFEGMEESSEGLDDLIFA 179  
QY 213 EKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEP 272  
Db 180 RKDTFFKGVDYVCISDNYWLGKTKPCITYGLRGICYFFIEVECSKDLHSGVYGGSVHEA 239  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTETEEINTYKAHLDLEEYRNSRVEKFLFD 332  
Db 240 MTDLIALMGSLVDKNGKILIPGINEAVAPVLKEEKDIYEAIEFDLEDFANDIGAELLHE 299  
QY 333 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTR 392  
Db 300 SKEKILMHRWRFPSPSLHGI EGAFSATGAKTVIPRKVIGKFSIRLVPMNPDVQKQVED 359  
QY 393 HLEDVFSKRNSSNMVSMVTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 452



Db 360 YLTKKFKELGSPNKFQVTMGHGKGPWVSDFNHPHYVAGRKAMKTVFNVEPDLTREGGSIP 419  
Qy 453 IAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLPFAAFFLEMAQL 506  
Db 420 VTLTQEQATGKNVMLLPVGSADDAHSGNEKLNRSNYIQGVKLLGALYIEVSNL 473

RESULT 14  
CGL1\_MOUSE  
ID CGL1\_MOUSE STANDARD; PRT; 475 AA.  
AC Q9D1A2; Q99PV1;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like  
DE protein 1) (CNDP dipeptidase 2).  
GN Name=Cndp2; Synonyms=Cn2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yoshikawa T., Nagasugi Y., Sugano S., Hashimoto K., Masuho Y.,  
RA Seki N.;  
RT "Novel mouse gene differentially expressed in kidney.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SIMILARITY: Belongs to the peptidase M20A family.  
CC -----  
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CC -----  
CC EMBL; AB046738; BAB21596.1; -.  
DR EMBL; AK003779; BAB22991.1; -.  
DR EMBL; BC005532; AAH05532.1; -.  
DR MEROPS; M20.005; -.  
DR MGD; MGI:1913304; Cn2.  
DR InterPro; IPR001261; Arge\_dapE.  
DR InterPro; IPR002933; Peptidase M20.  
DR Pfam; PF01546; Peptidase M20; 1.  
DR PROSITE; PS00758; ARGE\_DAPE\_CPG2\_1; FALSE\_NEG.  
DR PROSITE; PS00759; ARGE\_DAPE\_CPG2\_2; FALSE\_NEG.  
KW Carboxypeptidase; Hydrolyase; Metalloprotease.  
FT CONFLICT 357 V -> A (in Ref. 1).  
SQ SEQUENCE 475 AA; 52767 MW; 086950275A698500 CRC64;  
  
Query Match 52.7%; Score 1382; DB 1; Length 475;  
Best Local Similarity 54.2%; Pred. No. 7.8e-91;  
Matches 256; Conservative 81; Mismatches 133; Indels 2; Gaps 1;  
  
Qy 35 LEKVFOYIDLHQDFVQTLKEWVAIESDSVQVPFRERQELFRMMAVAADTLQRLGARVAS 94  
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Db 4 LKAVFQYIDENQDRYVKKLAEWVAIQ--SVSAWPEKRGEIRRMMEVAADVQLGGSVEL 61  
  
Qy 95 VDMGPQLPDGQSLPIPPVILAEGLSDPTKGTVCYFGHLDVQPADRGDWLTDPYVLTEV 154  
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Qy 155 DGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNKFIIEGMEEAGSVALEELVEKEK 214  
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Db 122 EGKLYGRGSTDDKGPVAGWNNALEAYQKTQEIIPVNLRFCEGMEESGSEGLDELIFAQK 181  
  
Qy 215 DRFFSGVDYIVISDNLWISQKPAITYGTRGNSYFMVVEVKCRDQDFHSGTFGGILHEPMA 274  
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Qy 335 EEILMHLWRYPSPLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQVTRHL 394  
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Qy 455 KMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLPFAAFFLEMAQL 506  
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Db 422 LTFQEQATGKNVMLLPVGSADDAHSGNEKLNRLNRYIEGTKMLAAYLYEVSQ 473

Search completed: February 8, 2005, 23:26:40  
Job time : 232 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 8, 2005, 23:09:11 ; Search time 43 Seconds  
(without alignments)  
880.165 Million cell updates/sec

Title: US-10-036-342-57  
Perfect score: 2623  
Sequence: 1 MDPKLGMAASLLAVLLLLL.....NYIEGTKLFAAFLEMAQLH 507

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1174.5	44.8	429	4	US-09-270-767-45937
2	990	37.7	492	4	US-09-248-796A-14755
3	607.5	23.2	148	4	US-09-621-976-3957
4	574.5	21.9	878	4	US-09-538-092-61
5	451.5	17.2	495	4	US-09-438-185A-981
6	432.5	16.5	457	4	US-09-583-110-4829
7	428	16.3	393	4	US-09-198-452A-1054
8	403	15.4	466	4	US-09-902-540-15643
9	395.5	15.1	345	4	US-09-248-796A-14559
10	367	14.0	304	4	US-09-107-433-3644
11	261	10.0	103	4	US-09-621-976-4417
12	248	9.5	98	4	US-09-513-999C-5701
13	248	9.5	98	4	US-09-513-999C-5702
14	242.5	9.2	267	4	US-09-602-777A-192
15	233	8.9	231	4	US-09-602-777A-194
16	230.5	8.8	476	4	US-09-902-540-14806
17	225.5	8.6	406	4	US-09-328-352-5309
18	215	8.2	370	4	US-09-331-568A-30
19	211	8.0	431	3	US-09-134-001C-4338
20	210	8.0	376	4	US-09-489-039A-9125
21	195.5	7.5	632	4	US-09-252-991A-17148
22	188.5	7.2	386	4	US-09-543-681A-8238
23	187	7.1	440	4	US-09-107-532A-4071
24	176	6.7	318	4	US-09-581-005-2
25	175	6.7	402	4	US-09-134-000C-5335
26	174	6.6	439	4	US-09-634-238-412
27	172	6.6	331	4	US-09-724-623-78

28	172	6.6	355	4	US-09-331-568A-28	Sequence 28, Appl
29	172	6.6	425	4	US-09-134-000C-3861	Sequence 3861, Ap
30	172	6.6	465	4	US-09-634-238-411	Sequence 411, App
31	171	6.5	418	3	US-09-134-001C-3552	Sequence 3552, Ap
32	169	6.4	408	4	US-09-902-540-10715	Sequence 10715, A
33	162.5	6.2	450	4	US-09-107-532A-6534	Sequence 6534, Ap
34	158	6.0	402	4	US-09-540-236-2685	Sequence 2685, Ap
35	157.5	6.0	466	4	US-09-583-110-5296	Sequence 5296, Ap
36	157.5	6.0	470	4	US-09-107-433-3616	Sequence 3616, Ap
37	150	5.7	388	4	US-09-331-568A-4	Sequence 4, Appli
38	150	5.7	388	4	US-09-331-568A-29	Sequence 29, Appl
39	149	5.7	396	4	US-09-543-681A-8308	Sequence 8308, Ap
40	144	5.5	380	4	US-09-902-540-10970	Sequence 10970, A
41	141	5.4	408	1	US-08-127-278-4	Sequence 4, Appli
42	141	5.4	408	1	US-08-555-860-4	Sequence 4, Appli
43	141	5.4	408	3	US-09-814-951A-4	Sequence 4, Appli
44	141	5.4	421	4	US-09-949-016-10991	Sequence 10991, A
45	139.5	5.3	443	4	US-09-583-110-4278	Sequence 4278, Ap
46	139.5	5.3	446	4	US-09-107-433-4675	Sequence 4675, Ap
47	137.5	5.2	393	4	US-09-252-991A-22875	Sequence 22875, A
48	137	5.2	370	4	US-09-270-767-33923	Sequence 33923, A
49	137	5.2	370	4	US-09-270-767-49140	Sequence 49140, A
50	136.5	5.2	446	3	US-09-134-001C-5125	Sequence 5125, Ap
51	133.5	5.1	434	4	US-09-252-991A-21048	Sequence 21048, A
52	132	5.0	383	3	US-09-575-602-4	Sequence 4, Appli
53	132	5.0	383	4	US-09-032-086-4	Sequence 4, Appli
54	128.5	4.9	258	4	US-09-134-000C-4891	Sequence 4891, Ap
55	126	4.8	418	4	US-09-710-279-380	Sequence 380, App
56	125.5	4.8	430	3	US-09-134-001C-4302	Sequence 4302, Ap
57	125	4.8	373	3	US-09-814-951A-2	Sequence 2, Appli
58	123.5	4.7	441	4	US-09-489-039A-12164	Sequence 12164, A
59	116	4.4	334	4	US-09-107-532A-6586	Sequence 6586, Ap
60	114	4.3	265	4	US-09-134-000C-6459	Sequence 6459, Ap
61	114	4.3	803	4	US-09-543-681A-4623	Sequence 4623, Ap
62	113.5	4.3	409	4	US-09-564-559B-5	Sequence 5, Appli
63	113.5	4.3	409	4	US-09-564-559B-6	Sequence 6, Appli
64	113	4.3	410	1	US-08-792-283A-7	Sequence 7, Appli
65	113	4.3	410	2	US-09-105-908-7	Sequence 7, Appli
66	113	4.3	410	3	US-09-271-713-7	Sequence 7, Appli
67	113	4.3	410	3	US-09-023-809B-1	Sequence 1, Appli
68	113	4.3	410	4	US-09-723-546-1	Sequence 1, Appli
69	112	4.3	409	4	US-09-564-559B-7	Sequence 7, Appli
70	112	4.3	409	4	US-09-564-559B-8	Sequence 8, Appli
71	112	4.3	409	4	US-09-564-559B-9	Sequence 9, Appli
72	112	4.3	409	4	US-09-564-559B-10	Sequence 10, Appli
73	112	4.3	410	3	US-09-023-809B-2	Sequence 2, Appli
74	112	4.3	410	4	US-09-723-546-2	Sequence 2, Appli
75	111	4.2	422	4	US-09-602-777A-202	Sequence 202, App
76	110.5	4.2	164	4	US-09-270-767-31641	Sequence 31641, A
77	110.5	4.2	164	4	US-09-270-767-46858	Sequence 46858, A
78	110	4.2	615	4	US-09-949-016-11320	Sequence 11320, A
79	110	4.2	1953	4	US-09-917-254-92	Sequence 92, Appl
80	109	4.2	290	4	US-09-252-991A-19355	Sequence 19355, A
81	108	4.1	246	4	US-09-602-777A-206	Sequence 206, App
82	107.5	4.1	379	4	US-09-107-532A-5519	Sequence 5519, Ap
83	105	4.0	141	4	US-09-270-767-33804	Sequence 33804, A
84	104.5	4.0	383	4	US-09-543-681A-7526	Sequence 7526, Ap
85	103	3.9	385	4	US-09-134-000C-4952	Sequence 4952, Ap
86	103	3.9	809	4	US-09-543-681A-6686	Sequence 6686, Ap
87	102.5	3.9	338	4	US-09-270-767-44278	Sequence 44278, A
88	102.5	3.9	1118	4	US-09-585-173B-36	Sequence 36, Appl
89	101	3.9	353	4	US-09-328-352-5230	Sequence 5230, Ap
90	100.5	3.8	826	4	US-09-756-247-41	Sequence 41, Appl
91	100	3.8	471	4	US-09-543-681A-5705	Sequence 5705, Ap
92	99	3.8	1031	4	US-09-585-173B-40	Sequence 40, Appl
93	99	3.8	1704	4	US-09-392-812A-2	Sequence 2, Appli
94	98	3.7	362	4	US-09-902-540-9705	Sequence 9705, Ap
95	98	3.7	895	4	US-09-489-039A-12499	Sequence 12499, A
96	97.5	3.7	462	4	US-09-252-991A-28292	Sequence 28292, A
97	97.5	3.7	981	4	US-09-328-352-4484	Sequence 4484, Ap
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99	96.5	3.7	4551	4	US-09-141-908-2	Sequence 2, Appli
100	96.5	3.7	4551	4	US-09-657-440-1	Sequence 1, Appli

101	96.5	3.7	4613	3	US-09-105-537-31	Sequence 31, Appli	174	90	3.4	495	4	US-09-479-645A-4	Sequence 4, Appli
102	96.5	3.7	11877	3	US-09-105-537-6	Sequence 6, Appli	175	90	3.4	664	4	US-09-328-352-5225	Sequence 5225, Ap
103	96	3.7	2867	4	US-09-902-540-12593	Sequence 12593, A	176	90	3.4	1313	3	US-08-989-299-9	Sequence 9, Appli
104	95.5	3.6	410	1	US-08-792-283A-8	Sequence 8, Appli	177	90	3.4	1313	4	US-09-407-427-9	Sequence 9, Appli
105	95.5	3.6	410	2	US-09-105-908-8	Sequence 8, Appli	178	89.5	3.4	401	4	US-09-462-645C-2	Sequence 2, Appli
106	95.5	3.6	410	3	US-09-271-713-8	Sequence 8, Appli	179	89.5	3.4	401	4	US-09-462-645C-6	Sequence 6, Appli
107	95	3.6	409	3	US-09-023-809B-3	Sequence 3, Appli	180	89.5	3.4	401	4	US-09-462-645C-10	Sequence 10, Appl
108	95	3.6	409	4	US-09-564-559B-1	Sequence 1, Appli	181	89.5	3.4	426	4	US-09-134-000C-6758	Sequence 6758, Ap
109	95	3.6	409	4	US-09-564-559B-2	Sequence 2, Appli	182	89.5	3.4	629	4	US-09-248-796A-19256	Sequence 19256, A
110	95	3.6	409	4	US-09-564-559B-3	Sequence 3, Appli	183	89.5	3.4	1181	3	US-09-206-898-23	Sequence 23, Appl
111	95	3.6	409	4	US-09-564-559B-4	Sequence 4, Appli	184	89.5	3.4	1724	4	US-09-607-510-2	Sequence 2, Appli
112	95	3.6	409	4	US-09-723-546-3	Sequence 3, Appli	185	89	3.4	237	4	US-09-949-016-10565	Sequence 10565, A
113	95	3.6	1256	4	US-09-248-796A-18057	Sequence 18057, A	186	89	3.4	237	4	US-09-949-016-10566	Sequence 10566, A
114	94.5	3.6	172	3	US-09-134-001C-3427	Sequence 3427, Ap	187	89	3.4	353	4	US-09-902-540-10913	Sequence 10913, A
115	94.5	3.6	478	4	US-09-710-279-768	Sequence 768, App	188	89	3.4	665	3	US-08-506-296B-68	Sequence 68, Appl
116	94	3.6	817	4	US-09-710-279-50	Sequence 50, Appl	189	89	3.4	732	3	US-08-989-299-5	Sequence 5, Appli
117	94	3.6	817	4	US-09-710-279-1528	Sequence 1528, Ap	190	89	3.4	732	4	US-09-407-427-5	Sequence 5, Appli
118	94	3.6	823	3	US-09-134-001C-4081	Sequence 4081, Ap	191	89	3.4	1312	3	US-08-989-299-8	Sequence 8, Appli
119	.94	3.6	1053	3	US-08-863-118-3	Sequence 3, Appli	192	89	3.4	1312	4	US-09-407-427-8	Sequence 8, Appli
120	93.5	3.6	412	4	US-09-543-681A-8182	Sequence 8182, Ap	193	89	3.4	15281	2	US-08-471-119A-2	Sequence 2, Appli
121	93.5	3.6	472	4	US-09-252-991A-22807	Sequence 22807, A	194	88.5	3.4	283	4	US-09-425-578-2	Sequence 2, Appli
122	93.5	3.6	535	3	US-09-134-001C-3338	Sequence 3338, Ap	195	88.5	3.4	500	4	US-09-538-092-65	Sequence 65, Appl
123	93.5	3.6	639	3	US-09-347-801-17	Sequence 17, Appl	196	88.5	3.4	563	4	US-09-949-016-6287	Sequence 6287, Ap
124	93.5	3.6	639	4	US-09-854-731-17	Sequence 17, Appl	197	88.5	3.4	759	4	US-09-489-039A-13760	Sequence 13760, A
125	93.5	3.6	777	4	US-09-902-540-15059	Sequence 15059, A	198	88	3.4	75	4	US-09-513-999C-7485	Sequence 7485, Ap
126	93	3.5	373	4	US-09-248-796A-19382	Sequence 19382, A	199	88	3.4	364	4	US-09-328-352-6641	Sequence 6641, Ap
127	93	3.5	398	4	US-08-792-283A-9	Sequence 6418, Ap	200	88	3.4	466	4	US-09-248-796A-16844	Sequence 16844, A
128	93	3.5	410	1	US-08-997-080-194	Sequence 9, Appli	201	88	3.4	483	4	US-09-248-796A-18158	Sequence 18158, A
129	93	3.5	410	2	US-09-105-908-9	Sequence 9, Appli	202	88	3.4	508	4	US-09-858-664A-18	Sequence 18, Appl
130	93	3.5	410	3	US-09-271-713-9	Sequence 9, Appli	203	88	3.4	508	4	US-10-274-978-19	Sequence 19, Appl
131	93	3.5	429	4	US-09-902-540-15549	Sequence 15549, A	204	88	3.4	508	4	US-10-697-263-19	Sequence 19, Appl
132	93	3.5	480	2	US-08-913-477-17	Sequence 17, Appl	205	87.5	3.3	732	1	US-08-481-626-2	Sequence 2, Appli
133	93	3.5	501	2	US-08-913-477-23	Sequence 23, Appl	206	87.5	3.3	732	3	US-08-989-299-4	Sequence 4, Appli
134	93	3.5	900	4	US-09-949-016-7501	Sequence 7501, Ap	207	87.5	3.3	732	4	US-09-407-427-4	Sequence 4, Appli
135	93	3.5	900	4	US-09-949-016-7502	Sequence 7502, Ap	208	87.5	3.3	789	4	US-09-107-532A-6734	Sequence 6734, Ap
136	93	3.5	1310	3	US-08-989-299-10	Sequence 10, Appl	209	87.5	3.3	804	4	US-09-270-767-46750	Sequence 46750, A
137	93	3.5	1310	4	US-09-407-427-10	Sequence 10, Appl	210	87.5	3.3	1052	3	US-08-863-118-1	Sequence 1, Appli
138	92.5	3.5	370	2	US-08-997-080-194	Sequence 194, App	211	87.5	3.3	1052	3	US-09-377-310-2	Sequence 2, Appli
139	92.5	3.5	370	2	US-08-997-362-194	Sequence 194, App	212	87.5	3.3	1306	3	US-08-989-299-7	Sequence 7, Appli
140	92.5	3.5	370	3	US-09-095-855-194	Sequence 194, App	213	87.5	3.3	1306	4	US-09-407-427-7	Sequence 7, Appli
141	92.5	3.5	370	3	US-09-324-542-194	Sequence 194, App	214	87.5	3.3	1481	4	US-09-949-016-8693	Sequence 8693, Ap
142	92.5	3.5	370	4	US-09-205-426-194	Sequence 194, App	215	87.5	3.3	1481	4	US-09-949-016-8694	Sequence 8694, Ap
143	92.5	3.5	520	1	US-08-706-292-2	Sequence 2, Appli	216	87.5	3.3	1481	4	US-09-949-016-8695	Sequence 8695, Ap
144	92.5	3.5	520	3	US-09-032-365A-15	Sequence 15, Appl	217	87.5	3.3	1481	4	US-09-949-016-8696	Sequence 8696, Ap
145	92.5	3.5	623	4	US-09-583-110-3324	Sequence 3324, Ap	218	87.5	3.3	1486	4	US-09-949-016-8675	Sequence 8675, Ap
146	92.5	3.5	633	4	US-09-107-433-4091	Sequence 4091, Ap	219	87.5	3.3	1486	4	US-09-949-016-8676	Sequence 8676, Ap
147	92.5	3.5	968	4	US-09-252-991A-18925	Sequence 18925, A	220	87.5	3.3	1486	4	US-09-949-016-8677	Sequence 8677, Ap
148	92	3.5	228	4	US-09-248-796A-17522	Sequence 17522, A	221	87.5	3.3	1486	4	US-09-949-016-8678	Sequence 8678, Ap
149	92	3.5	686	4	US-09-134-000C-5066	Sequence 5066, Ap	222	87.5	3.3	1486	4	US-09-949-016-8679	Sequence 8679, Ap
150	92	3.5	1059	4	US-09-394-272-5	Sequence 5, Appli	223	87.5	3.3	1486	4	US-09-949-016-8680	Sequence 8680, Ap
151	91.5	3.5	310	4	US-09-724-623-122	Sequence 122, App	224	87.5	3.3	1486	4	US-09-949-016-8681	Sequence 8681, Ap
152	91.5	3.5	3418	2	US-08-639-501-2	Sequence 2, Appli	225	87.5	3.3	1486	4	US-09-949-016-8682	Sequence 8682, Ap
153	91.5	3.5	3418	3	US-09-044-946-2	Sequence 2, Appli	226	87.5	3.3	1499	4	US-09-949-016-8683	Sequence 8683, Ap
154	91.5	3.5	3418	3	US-08-755-587-44	Sequence 44, Appl	227	87.5	3.3	1499	4	US-09-949-016-8684	Sequence 8684, Ap
155	91.5	3.5	3418	3	US-09-044-908-2	Sequence 2, Appli	228	87.5	3.3	1499	4	US-09-949-016-8685	Sequence 8685, Ap
156	91	3.5	656	4	US-09-252-991A-25135	Sequence 25135, A	229	87.5	3.3	1499	4	US-09-949-016-8686	Sequence 8686, Ap
157	91	3.5	706	4	US-09-134-000C-5534	Sequence 5534, Ap	230	87.5	3.3	1499	4	US-09-949-016-8687	Sequence 8687, Ap
158	91	3.5	737	3	US-08-989-299-6	Sequence 6, Appli	231	87.5	3.3	1499	4	US-09-949-016-8688	Sequence 8688, Ap
159	91	3.5	737	4	US-09-407-427-6	Sequence 6, Appli	232	87.5	3.3	1499	4	US-09-949-016-8689	Sequence 8689, Ap
160	90.5	3.5	616	4	US-09-248-796A-17521	Sequence 17521, A	233	87.5	3.3	1499	4	US-09-949-016-8690	Sequence 8690, Ap
161	90.5	3.5	921	3	US-09-206-800-10	Sequence 10, Appl	234	87.5	3.3	1499	4	US-09-949-016-8691	Sequence 8691, Ap
162	90.5	3.5	1167	2	US-08-589-756-2	Sequence 2, Appli	235	87.5	3.3	1858	4	US-09-489-039A-11380	Sequence 11380, A
163	90.5	3.5	1167	3	US-09-206-800-2	Sequence 2, Appli	236	87.5	3.3	7831	4	US-09-902-540-12902	Sequence 12902, A
164	90.5	3.5	1167	3	US-09-206-898-2	Sequence 2, Appli	237	87	3.3	139	4	US-09-328-352-7327	Sequence 7327, Ap
165	90.5	3.5	3418	2	US-08-603-753D-4	Sequence 4, Appli	238	87	3.3	559	4	US-09-902-540-14492	Sequence 14492, A
166	90.5	3.5	3418	3	US-09-099-753-4	Sequence 4, Appli	239	87	3.3	602	4	US-09-569-037-6	Sequence 6, Appli
167	90.5	3.5	3418	3	US-08-986-106-4	Sequence 4, Appli	240	87	3.3	631	4	US-09-569-037-5	Sequence 5, Appli
168	90	3.4	195	4	US-09-270-767-32113	Sequence 32113, A	241	87	3.3	663	4	US-09-543-681A-4450	Sequence 4450, Ap
169	90	3.4	195	4	US-09-270-767-47330	Sequence 47330, A	242	87	3.3	1456	4	US-09-134-000C-6427	Sequence 6427, Ap
170	90	3.4	432	4	US-09-917-254-80	Sequence 80, Appl	243	86.5	3.3	471	4	US-09-107-532A-4629	Sequence 4629, Ap
171	90	3.4	432	4	US-09-949-016-6467	Sequence 6467, Ap	244	86.5	3.3	529	1	US-08-548-509-2	Sequence 2, Appli
172	90	3.4	447	4	US-09-949-016-11453	Sequence 11453, A	245	86.5	3.3	605	4	US-09-902-540-14269	Sequence 14269, A
173	90	3.4	495	4	US-09-479-645A-2	Sequence 2, Appli	246	86.5	3.3	734	4	US-09-438-185A-125	Sequence 125, App



247	86.5	3.3	826	4	US-09-328-352-7515	Sequence 7515, Ap	320	83	3.2	407	4	US-09-902-540-15171	Sequence 15171, A
248	86.5	3.3	1627	4	US-09-252-991A-28863	Sequence 28863, A	321	83	3.2	501	4	US-09-489-039A-12663	Sequence 12663, A
249	86.5	3.3	2141	4	US-09-949-016-10918	Sequence 10918, A	322	83	3.2	506	1	US-07-612-673-2	Sequence 2, Appli
250	86	3.3	222	4	US-09-134-000C-4293	Sequence 4293, Ap	323	83	3.2	576	4	US-09-578-921A-2	Sequence 2, Appli
251	86	3.3	459	4	US-09-950-772-4	Sequence 4, Appli	324	83	3.2	967	4	US-09-543-681A-6407	Sequence 6407, Ap
252	86	3.3	574	3	US-09-385-028-4	Sequence 4, Appli	325	83	3.2	988	4	US-09-382-552-233	Sequence 233, App
253	86	3.3	574	4	US-09-726-614-4	Sequence 4, Appli	326	83	3.2	2080	4	US-09-382-552-2	Sequence 2, Appli
254	86	3.3	574	4	US-09-385-040-4	Sequence 4, Appli	327	83	3.2	2285	4	US-09-252-991A-17790	Sequence 17790, A
255	86	3.3	618	4	US-09-934-901-18	Sequence 18, Appl	328	83	3.2	2366	1	US-08-480-604A-10	Sequence 10, Appl
256	86	3.3	618	4	US-09-934-868-8	Sequence 8, Appli	329	83	3.2	2366	2	US-08-405-496A-10	Sequence 10, Appl
257	86	3.3	618	4	US-10-321-210-18	Sequence 18, Appl	330	83	3.2	2366	3	US-08-915-136-10	Sequence 10, Appl
258	86	3.3	618	4	US-10-320-874-18	Sequence 18, Appl	331	83	3.2	2366	3	US-08-957-310-10	Sequence 10, Appl
259	86	3.3	788	4	US-09-270-767-44611	Sequence 44611, A	332	83	3.2	2366	4	US-10-011-366-10	Sequence 10, Appl
260	86	3.3	795	3	US-09-370-807-6	Sequence 6, Appli	333	83	3.2	2366	4	US-09-084-517-10	Sequence 10, Appl
261	86	3.3	795	4	US-09-921-259-6	Sequence 6, Appli	334	82.5	3.1	347	4	US-09-540-236-2130	Sequence 2130, Ap
262	86	3.3	1287	4	US-09-949-016-7826	Sequence 7826, Ap	335	82.5	3.1	521	1	US-07-796-361A-11	Sequence 11, Appl
263	85.5	3.3	268	4	US-09-949-016-7216	Sequence 7216, Ap	336	82.5	3.1	521	1	US-08-539-666-2	Sequence 2, Appli
264	85.5	3.3	388	4	US-09-489-039A-9214	Sequence 9214, Ap	337	82.5	3.1	532	4	US-09-792-024-70	Sequence 70, Appl
265	85.5	3.3	498	4	US-09-248-796A-25517	Sequence 25517, A	338	82.5	3.1	772	4	US-09-252-991A-31855	Sequence 31855, A
266	85.5	3.3	849	4	US-09-543-681A-5761	Sequence 5761, Ap	339	82.5	3.1	815	4	US-09-914-259-18	Sequence 18, Appl
267	85.5	3.3	1026	4	US-09-248-796A-16128	Sequence 16128, A	340	82.5	3.1	1132	4	US-09-248-796A-15026	Sequence 15026, A
268	85.5	3.3	1179	4	US-09-252-991A-17895	Sequence 17895, A	341	82.5	3.1	1493	4	US-09-713-273A-20	Sequence 20, Appl
269	85	3.2	195	4	US-09-270-767-32953	Sequence 32953, A	342	82.5	3.1	2165	1	US-08-514-975B-2	Sequence 2, Appli
270	85	3.2	195	4	US-09-270-767-48170	Sequence 48170, A	343	82.5	3.1	2165	4	US-09-368-076-29	Sequence 29, Appl
271	85	3.2	389	4	US-09-949-016-9488	Sequence 9488, Ap	344	82.5	3.1	2165	4	US-09-368-076-30	Sequence 30, Appl
272	85	3.2	420	4	US-09-902-540-12220	Sequence 12220, A	345	82.5	3.1	2165	5	PCT-US95-12507-2	Sequence 2, Appli
273	85	3.2	426	4	US-09-489-039A-7944	Sequence 7944, Ap	346	82	3.1	334	4	US-09-538-092-894	Sequence 894, App
274	85	3.2	498	4	US-09-489-039A-13707	Sequence 13707, A	347	82	3.1	417	4	US-09-107-532A-6148	Sequence 6148, Ap
275	85	3.2	547	3	US-09-555-000-2	Sequence 2, Appli	348	82	3.1	465	4	US-09-489-039A-13461	Sequence 13461, A
276	85	3.2	672	3	US-09-040-843-4	Sequence 4, Appli	349	82	3.1	498	4	US-09-252-991A-28182	Sequence 28182, A
277	85	3.2	672	3	US-09-621-855-4	Sequence 4, Appli	350	82	3.1	543	3	US-08-426-509A-14	Sequence 14, Appl
278	85	3.2	713	2	US-08-849-212-4	Sequence 2, Appli	351	82	3.1	543	4	US-08-232-545-14	Sequence 8, Appli
279	85	3.2	866	3	US-09-040-843-2	Sequence 2, Appli	352	82	3.1	543	4	US-09-470-881-8	Sequence 8, Appli
280	85	3.2	866	3	US-09-621-855-2	Sequence 2, Appli	353	82	3.1	543	4	US-09-538-092-870	Sequence 870, App
281	85	3.2	1464	4	US-10-038-224-2	Sequence 2, Appli	354	82	3.1	543	5	PCT-US95-05008-14	Sequence 14, Appl
282	85	3.2	1755	4	US-09-724-126A-4	Sequence 4, Appli	355	82	3.1	581	3	US-09-323-872A-46	Sequence 46, Appl
283	84.5	3.2	208	4	US-09-902-540-15342	Sequence 15342, A	356	82	3.1	647	1	US-07-894-212A-8	Sequence 8, Appli
284	84.5	3.2	332	4	US-09-583-110-4063	Sequence 4063, Ap	357	82	3.1	649	1	US-07-894-212A-2	Sequence 2, Appli
285	84.5	3.2	526	4	US-09-248-796A-14807	Sequence 14807, A	358	82	3.1	650	1	US-07-893-928A-1	Sequence 1, Appli
286	84.5	3.2	575	4	US-09-543-681A-6584	Sequence 6584, Ap	359	82	3.1	743	4	US-09-585-858-13	Sequence 13, Appl
287	84.5	3.2	1259	4	US-09-489-039A-8840	Sequence 8840, Ap	360	82	3.1	743	4	US-10-270-878-13	Sequence 13, Appl
288	84.5	3.2	4861	4	US-09-919-497-70	Sequence 70, Appl	361	82	3.1	897	4	US-09-543-681A-4915	Sequence 4915, Ap
289	84	3.2	397	1	US-08-415-823-2	Sequence 2, Appli	362	82	3.1	910	4	US-09-623-326-7	Sequence 7, Appli
290	84	3.2	397	2	US-09-086-662-2	Sequence 2, Appli	363	82	3.1	910	4	US-09-623-326-8	Sequence 8, Appli
291	84	3.2	504	1	US-08-135-511-30	Sequence 30, Appl	364	82	3.1	2368	1	US-08-198-446B-15	Sequence 15, Appl
292	84	3.2	504	1	US-08-187-453-30	Sequence 30, Appl	365	82	3.1	2368	2	US-08-870-693-15	Sequence 15, Appl
293	84	3.2	668	4	US-09-248-796A-17495	Sequence 17495, A	366	81.5	3.1	335	4	US-09-902-540-12406	Sequence 12406, A
294	84	3.2	724	4	US-09-543-681A-4745	Sequence 4745, Ap	367	81.5	3.1	440	6	5310667-9	Patent No. 5310667
295	84	3.2	735	3	US-09-147-236-7	Sequence 7, Appli	368	81.5	3.1	440	6	5310667-9	Patent No. 5310667
296	84	3.2	735	4	US-09-522-474-7	Sequence 7, Appli	369	81.5	3.1	442	1	US-08-476-008-64	Sequence 64, Appl
297	84	3.2	754	4	US-09-543-681A-5416	Sequence 5416, Ap	370	81.5	3.1	442	1	US-08-306-063-64	Sequence 64, Appl
298	84	3.2	823	4	US-09-107-532A-6343	Sequence 6343, Ap	371	81.5	3.1	442	1	US-08-833-485-64	Sequence 64, Appl
299	84	3.2	953	2	US-08-500-857A-2	Sequence 2, Appli	372	81.5	3.1	442	3	US-09-137-440-64	Sequence 64, Appl
300	84	3.2	1125	4	US-09-900-920-60	Sequence 60, Appl	373	81.5	3.1	476	2	US-08-541-033A-26	Sequence 26, Appl
301	84	3.2	1501	4	US-09-252-991A-20266	Sequence 20266, A	374	81.5	3.1	476	2	US-08-828-451-26	Sequence 26, Appl
302	84	3.2	1734	4	US-09-724-126A-19	Sequence 19, Appl	375	81.5	3.1	487	2	US-08-541-033A-24	Sequence 24, Appl
303	84	3.2	1749	4	US-09-724-126A-2	Sequence 2, Appli	376	81.5	3.1	487	2	US-08-451-033A-4	Sequence 4, Appli
304	84	3.2	1881	3	US-09-233-086-3	Sequence 3, Appli	377	81.5	3.1	512	2	US-08-541-033A-4	Sequence 4, Appli
305	83.5	3.2	344	4	US-09-328-352-7987	Sequence 7987, Ap	378	81.5	3.1	512	2	US-08-828-451-4	Sequence 4, Appli
306	83.5	3.2	464	4	US-09-489-039A-8157	Sequence 8157, Ap	379	81.5	3.1	514	3	US-09-717-432-2	Sequence 2, Appli
307	83.5	3.2	496	4	US-08-622-191-1	Sequence 1, Appli	380	81.5	3.1	514	3	US-09-912-484-2	Sequence 2, Appli
308	83.5	3.2	510	4	US-09-710-279-2860	Sequence 2860, Ap	381	81.5	3.1	526	2	US-08-541-033A-2	Sequence 2, Appli
309	83.5	3.2	545	3	US-08-974-180-15	Sequence 15, Appl	382	81.5	3.1	526	2	US-08-828-451-2	Sequence 2, Appli
310	83.5	3.2	583	4	US-09-710-279-1358	Sequence 1358, Ap	383	81.5	3.1	539	3	US-08-687-590-27	Sequence 27, Appl
311	83.5	3.2	778	4	US-09-328-352-7907	Sequence 7907, Ap	384	81.5	3.1	539	4	US-09-702-705-326	Sequence 326, App
312	83.5	3.2	927	3	US-09-134-001C-4831	Sequence 4831, Ap	385	81.5	3.1	539	4	US-09-736-457-326	Sequence 326, App
313	83.5	3.2	1010	3	US-09-134-001C-5178	Sequence 5178, Ap	386	81.5	3.1	539	4	US-09-671-325-326	Sequence 326, App
314	83.5	3.2	2322	4	US-09-976-594-15	Sequence 15, Appl	387	81.5	3.1	539	4	US-09-589-184-326	Sequence 326, App
315	83.5	3.2	2322	4	US-09-919-039-15	Sequence 15, Appl	388	81.5	3.1	539	4	US-09-589-184-326	Sequence 326, App
316	83.5	3.2	3169	3	US-09-453-702B-257	Sequence 257, App	389	81.5	3.1	539	4	US-09-658-824-326	Sequence 326, App
317	83.5	3.2	3666	2	US-08-222-617A-12	Sequence 12, Appl	390	81.5	3.1	573	3	US-09-134-001C-5026	Sequence 5026, Ap
318	83.5	3.2	3727	2	US-08-222-617A-27	Sequence 27, Appl	391	81.5	3.1	624	4	US-09-198-452A-1089	Sequence 1089, Ap
319	83.5	3.2	3778	2	US-08-222-617A-2	Sequence 2, Appli	392	81.5	3.1	624	4	US-09-438-185A-1017	Sequence 1017, Ap



393	81.5	3.1	635	3	US-08-506-296B-71	Sequence 71, Appl	466	80.5	3.1	1150	2	US-08-589-756-3	Sequence 3, Appli
394	81.5	3.1	702	4	US-09-107-532A-6866	Sequence 6866, Ap	467	80.5	3.1	1150	3	US-09-206-800-3	Sequence 3, Appli
395	81.5	3.1	704	4	US-09-902-540-10479	Sequence 10479, A	468	80.5	3.1	1150	3	US-09-206-898-3	Sequence 3, Appli
396	81.5	3.1	800	3	US-08-776-265-3	Sequence 3, Appli	469	80.5	3.1	3739	3	US-09-320-878-2	Sequence 2, Appli
397	81.5	3.1	800	4	US-09-398-184-3	Sequence 3, Appli	470	80.5	3.1	3739	3	US-09-105-537-33	Sequence 33, Appli
398	81.5	3.1	819	4	US-09-902-540-13635	Sequence 13635, A	471	80.5	3.1	3739	4	US-09-141-908-3	Sequence 3, Appli
399	81.5	3.1	837	3	US-09-012-710-12	Sequence 12, Appl	472	80.5	3.1	3739	4	US-09-657-440-2	Sequence 2, Appli
400	81.5	3.1	837	3	US-09-556-273-12	Sequence 12, Appl	473	80	3.0	304	4	US-09-543-681A-8069	Sequence 8069, Ap
401	81.5	3.1	977	4	US-09-248-796A-15579	Sequence 15579, A	474	80	3.0	314	4	US-09-248-796A-20373	Sequence 20373, A
402	81.5	3.1	1755	3	US-09-724-126A-6	Sequence 6, Appli	475	80	3.0	327	4	US-09-248-796A-17148	Sequence 17148, A
403	81.5	3.1	2138	4	US-09-583-110-5274	Sequence 5274, Ap	476	80	3.0	330	4	US-09-540-236-2714	Sequence 2714, Ap
404	81	3.1	319	4	US-09-489-039A-8872	Sequence 8872, Ap	477	80	3.0	399	6	5474928-2	Patent No. 5474928
405	81	3.1	340	3	US-09-134-001C-3258	Sequence 3258, Ap	478	80	3.0	399	6	5474928-2	Patent No. 5474928
406	81	3.1	413	4	US-09-252-991A-21766	Sequence 21766, A	479	80	3.0	401	4	US-09-949-016-7956	Sequence 7956, Ap
407	81	3.1	421	4	US-09-949-016-5872	Sequence 5872, Ap	480	80	3.0	445	4	US-09-489-039A-11173	Sequence 11173, A
408	81	3.1	425	1	US-08-615-170-17	Sequence 17, Appl	481	80	3.0	459	4	US-09-949-016-11641	Sequence 11641, A
409	81	3.1	475	4	US-09-438-185A-835	Sequence 835, App	482	80	3.0	485	4	US-10-138-701-28	Sequence 28, Appl
410	81	3.1	485	3	US-09-009-494-2	Sequence 2, Appli	483	80	3.0	544	4	US-09-328-352-6896	Sequence 6896, Ap
411	81	3.1	485	3	US-09-010-233-8	Sequence 8, Appli	484	80	3.0	550	4	US-09-328-352-5727	Sequence 5727, Ap
412	81	3.1	485	3	US-09-010-232-4	Sequence 4, Appli	485	80	3.0	552	1	US-08-116-098-2	Sequence 2, Appli
413	81	3.1	485	4	US-09-710-279-1346	Sequence 1346, Ap	486	80	3.0	552	3	US-08-687-590-32	Sequence 32, Appl
414	81	3.1	491	3	US-09-134-001C-4677	Sequence 4677, Ap	487	80	3.0	582	4	US-09-107-433-5141	Sequence 5141, Ap
415	81	3.1	498	3	US-08-686-968C-231	Sequence 231, App	488	80	3.0	587	4	US-09-583-110-4237	Sequence 4237, Ap
416	81	3.1	500	4	US-09-949-016-7131	Sequence 7131, Ap	489	80	3.0	592	4	US-09-813-453B-43	Sequence 43, Appl
417	81	3.1	550	4	US-09-328-352-5333	Sequence 5333, Ap	490	80	3.0	703	4	US-09-248-796A-14529	Sequence 14529, A
418	81	3.1	558	4	US-09-538-092-832	Sequence 832, App	491	80	3.0	758	3	US-09-134-001C-4588	Sequence 4588, Ap
419	81	3.1	575	4	US-09-949-016-7622	Sequence 7622, Ap	492	80	3.0	812	4	US-09-166-350-12	Sequence 12, Appl
420	81	3.1	575	4	US-09-949-016-7623	Sequence 7623, Ap	493	80	3.0	868	4	US-09-830-433A-73	Sequence 73, Appl
421	81	3.1	585	4	US-09-248-796A-14925	Sequence 14925, A	494	80	3.0	893	3	US-08-484-661A-2	Sequence 2, Appli
422	81	3.1	592	2	US-08-599-171A-30	Sequence 30, Appl	495	80	3.0	893	3	US-08-656-664-2	Sequence 2, Appli
423	81	3.1	592	2	US-08-646-590B-30	Sequence 30, Appl	496	80	3.0	893	5	PCT-US96-09641-2	Sequence 2, Appli
424	81	3.1	592	3	US-09-069-226-30	Sequence 30, Appl	497	80	3.0	1123	4	US-09-262-537-4	Sequence 4, Appli
425	81	3.1	592	3	US-09-412-184-30	Sequence 30, Appl	498	80	3.0	1161	3	US-09-327-536-2	Sequence 2, Appli
426	81	3.1	609	4	US-09-396-149-6	Sequence 6, Appli	499	80	3.0	1204	4	US-09-583-110-4083	Sequence 4083, Ap
427	81	3.1	610	4	US-09-949-016-7708	Sequence 7708, Ap	500	80	3.0	1262	4	US-09-107-433-5067	Sequence 5067, Ap
428	81	3.1	677	3	US-09-019-160-3	Sequence 3, Appli	501	80	3.0	1289	2	US-08-542-003-2	Sequence 2, Appli
429	81	3.1	706	4	US-09-538-092-649	Sequence 649, App	502	80	3.0	1289	2	US-08-322-760A-2	Sequence 2, Appli
430	81	3.1	708	3	US-09-019-160-5	Sequence 5, Appli	503	80	3.0	1289	4	US-09-236-949-2	Sequence 2, Appli
431	81	3.1	740	3	US-09-323-872A-25	Sequence 25, Appl	504	80	3.0	1313	2	US-08-244-537-2	Sequence 2, Appli
432	81	3.1	740	4	US-09-072-433-30	Sequence 30, Appl	505	80	3.0	2325	3	US-08-417-089-6	Sequence 6, Appli
433	81	3.1	744	4	US-09-328-352-7920	Sequence 7920, Ap	506	80	3.0	2325	3	US-08-695-651-6	Sequence 6, Appli
434	81	3.1	873	4	US-09-710-279-3036	Sequence 3036, Ap	507	80	3.0	2325	3	US-08-930-285-6	Sequence 6, Appli
435	81	3.1	893	3	US-09-019-160-6	Sequence 6, Appli	508	80	3.0	2325	3	US-08-695-421-6	Sequence 6, Appli
436	81	3.1	893	3	US-09-019-160-7	Sequence 7, Appli	509	80	3.0	2325	4	US-08-697-826A-10	Sequence 10, Appl
437	81	3.1	893	3	US-09-019-160-8	Sequence 8, Appli	510	79.5	3.0	205	6	5175383-6	Patent No. 5175383
438	81	3.1	893	3	US-09-019-160-9	Sequence 9, Appli	511	79.5	3.0	205	6	5175383-6	Patent No. 5175383
439	81	3.1	897	3	US-09-134-001C-3600	Sequence 3600, Ap	512	79.5	3.0	329	2	US-08-913-477-4	Sequence 4, Appli
440	81	3.1	1047	4	US-09-198-452A-1058	Sequence 1058, Ap	513	79.5	3.0	406	4	US-09-107-532A-5410	Sequence 5410, Ap
441	81	3.1	1047	4	US-09-438-185A-985	Sequence 985, App	514	79.5	3.0	415	4	US-09-898-461-7	Sequence 7, Appli
442	81	3.1	1203	4	US-09-583-110-3634	Sequence 3634, Ap	515	79.5	3.0	493	4	US-09-710-279-1832	Sequence 1832, Ap
443	81	3.1	1216	4	US-09-107-433-4255	Sequence 4255, Ap	516	79.5	3.0	511	4	US-09-902-540-10893	Sequence 10893, A
444	80.5	3.1	273	2	US-08-997-080-75	Sequence 75, Appl	517	79.5	3.0	513	3	US-09-134-001C-4490	Sequence 4490, Ap
445	80.5	3.1	273	2	US-08-997-362-75	Sequence 75, Appl	518	79.5	3.0	524	4	US-09-549-519-27	Sequence 27, Appl
446	80.5	3.1	273	3	US-08-873-970-75	Sequence 75, Appl	519	79.5	3.0	524	4	US-09-549-519-28	Sequence 28, Appl
447	80.5	3.1	273	3	US-09-095-855-75	Sequence 75, Appl	520	79.5	3.0	593	3	US-09-134-001C-3991	Sequence 3991, Ap
448	80.5	3.1	273	3	US-09-324-542-75	Sequence 75, Appl	521	79.5	3.0	629	4	US-09-569-037-9	Sequence 9, Appli
449	80.5	3.1	273	4	US-09-205-426-75	Sequence 75, Appl	522	79.5	3.0	729	1	US-08-417-276-2	Sequence 2, Appli
450	80.5	3.1	300	4	US-09-248-796A-17946	Sequence 17946, A	523	79.5	3.0	735	4	US-09-585-858-10	Sequence 10, Appl
451	80.5	3.1	371	4	US-09-134-000C-5173	Sequence 5173, Ap	524	79.5	3.0	735	4	US-10-270-878-10	Sequence 10, Appl
452	80.5	3.1	464	4	US-09-583-110-3968	Sequence 3968, Ap	525	79.5	3.0	773	2	US-08-484-101B-42	Sequence 42, Appl
453	80.5	3.1	468	4	US-09-107-433-4005	Sequence 4005, Ap	526	79.5	3.0	773	2	US-08-484-101B-44	Sequence 44, Appl
454	80.5	3.1	478	4	US-09-489-039A-10194	Sequence 10194, A	527	79.5	3.0	773	3	US-08-714-524D-42	Sequence 42, Appl
455	80.5	3.1	500	3	US-08-926-842B-16	Sequence 16, Appl	528	79.5	3.0	773	3	US-08-714-524D-44	Sequence 44, Appl
456	80.5	3.1	571	4	US-09-710-279-118	Sequence 118, App	529	79.5	3.0	793	2	US-08-468-558-5	Sequence 5, Appli
457	80.5	3.1	707	4	US-09-902-540-16063	Sequence 16063, A	530	79.5	3.0	793	3	US-08-676-444-5	Sequence 5, Appli
458	80.5	3.1	921	3	US-09-206-800-11	Sequence 11, Appl	531	79.5	3.0	1052	2	US-08-863-118-2	Sequence 2, Appli
459	80.5	3.1	924	4	US-09-267-311-2	Sequence 2, Appli	532	79.5	3.0	1055	2	US-08-659-251-5	Sequence 5, Appli
460	80.5	3.1	942	4	US-09-171-937C-40	Sequence 40, Appl	533	79.5	3.0	1055	3	US-09-256-490-5	Sequence 5, Appli
461	80.5	3.1	1057	3	US-08-853-948B-2	Sequence 2, Appli	534	79.5	3.0	1055	5	PCT-US96-11445-5	Sequence 5, Appli
462	80.5	3.1	1057	3	US-09-697-367-23	Sequence 23, Appl	535	79.5	3.0	1129	4	US-09-252-991A-22330	Sequence 22330, A
463	80.5	3.1	1057	4	US-09-394-272-2	Sequence 2, Appli	536	79.5	3.0	1178	4	US-09-489-039A-9944	Sequence 9944, Ap
464	80.5	3.1	1057	4	US-09-918-909A-29	Sequence 29, Appl	537	79.5	3.0	1201	4	US-09-252-991A-32259	Sequence 32259, A
465	80.5	3.1	1146	3	US-08-914-999-6	Sequence 6, Appli	538	79.5	3.0	1422	4	US-09-540-236-3021	Sequence 3021, Ap

539	79.5	3.0	1447	3	US-09-376-330-17	Sequence 17, Appl	612	78.5	3.0	519	4	US-09-107-532A-6778	Sequence 6778, Ap
540	79.5	3.0	1627	1	US-07-665-792E-9	Sequence 9, Appli	613	78.5	3.0	520	4	US-09-949-016-8026	Sequence 8026, Ap
541	79	3.0	284	1	US-09-949-016-9557	Sequence 9557, Ap	614	78.5	3.0	668	4	US-09-902-540-14244	Sequence 14244, A
542	79	3.0	323	1	US-07-992-827D-1	Sequence 1, Appli	615	78.5	3.0	672	4	US-09-949-016-8895	Sequence 8895, Ap
543	79	3.0	323	1	US-08-216-593-1	Sequence 1, Appli	616	78.5	3.0	682	4	US-08-836-687B-37	Sequence 37, Appl
544	79	3.0	323	5	PCT-US93-12380-1	Sequence 1, Appli	617	78.5	3.0	700	1	US-08-726-525-7	Sequence 7, Appli
545	79	3.0	329	2	US-08-913-477-2	Sequence 2, Appli	618	78.5	3.0	700	2	US-08-487-942-7	Sequence 7, Appli
546	79	3.0	372	4	US-09-107-433-3106	Sequence 3106, Ap	619	78.5	3.0	700	2	US-08-726-036A-7	Sequence 7, Appli
547	79	3.0	374	4	US-09-134-000C-5319	Sequence 5319, Ap	620	78.5	3.0	700	3	US-09-422-869-23	Sequence 23, Appl
548	79	3.0	400	3	US-08-961-083-190	Sequence 190, App	621	78.5	3.0	700	3	US-09-083-516-7	Sequence 7, Appli
549	79	3.0	400	4	US-09-536-784-190	Sequence 190, App	622	78.5	3.0	700	4	US-09-538-092-947	Sequence 947, App
550	79	3.0	404	4	US-09-252-991A-19166	Sequence 19166, A	623	78.5	3.0	804	3	US-09-134-001C-5218	Sequence 5218, Ap
551	79	3.0	404	4	US-09-489-039A-13783	Sequence 13783, A	624	78.5	3.0	862	3	US-09-346-237-1	Sequence 1, Appli
552	79	3.0	408	4	US-09-540-236-2740	Sequence 2740, Ap	625	78.5	3.0	956	4	US-09-914-259-17	Sequence 17, Appl
553	79	3.0	423	3	US-08-923-454A-6	Sequence 6, Appli	626	78.5	3.0	1020	2	US-08-070-301-3	Sequence 3, Appli
554	79	3.0	432	1	US-08-615-170-3	Sequence 3, Appli	627	78.5	3.0	1618	1	US-07-853-913-4	Sequence 4, Appli
555	79	3.0	436	3	US-08-923-454A-29	Sequence 29, Appl	628	78.5	3.0	1618	4	US-09-538-092-1143	Sequence 1143, Ap
556	79	3.0	445	1	US-08-615-170-5	Sequence 5, Appli	629	78.5	3.0	4302	3	US-08-658-136-5	Sequence 5, Appli
557	79	3.0	446	3	US-09-081-686-2	Sequence 2, Appli	630	78.5	3.0	4302	3	US-09-052-469-8	Sequence 8, Appli
558	79	3.0	460	4	US-09-266-965-126	Sequence 126, App	631	78.5	3.0	4302	4	US-08-422-582-8	Sequence 8, Appli
559	79	3.0	478	4	US-09-134-000C-5543	Sequence 5543, Ap	632	78.5	3.0	4302	4	US-09-052-262-8	Sequence 2, Appli
560	79	3.0	478	4	US-09-902-540-14070	Sequence 14070, A	633	78.5	3.0	4303	2	US-08-460-751-2	Sequence 2, Appli
561	79	3.0	486	4	US-09-949-016-10286	Sequence 10286, A	634	78.5	3.0	4303	4	US-09-479-467A-2	Sequence 6, Appli
562	79	3.0	525	3	US-09-212-247C-11	Sequence 11, Appl	635	78.5	3.0	4339	3	US-09-052-469-6	Sequence 6, Appli
563	79	3.0	533	4	US-09-549-519-31	Sequence 31, Appl	636	78.5	3.0	4339	4	US-08-422-582-6	Sequence 6, Appli
564	79	3.0	578	4	US-09-134-000C-3811	Sequence 3811, Ap	637	78.5	3.0	4339	4	US-09-052-262-6	Sequence 3866, Ap
565	79	3.0	583	4	US-09-583-110-3571	Sequence 3571, Ap	638	78	3.0	272	4	US-09-583-110-3866	Sequence 4601, Ap
566	79	3.0	610	3	US-08-484-661A-16	Sequence 16, Appl	639	78	3.0	310	4	US-09-107-433-4601	Sequence 5669, Ap
567	79	3.0	610	3	US-08-484-661A-29	Sequence 29, Appl	640	78	3.0	317	4	US-09-134-000C-5669	Sequence 4544, Ap
568	79	3.0	610	3	US-08-484-661A-35	Sequence 35, Appl	641	78	3.0	345	4	US-09-107-433-3960	Sequence 3960, Ap
569	79	3.0	610	3	US-08-656-664-16	Sequence 16, Appl	642	78	3.0	351	4	US-09-928-847B-13	Sequence 13, Appl
570	79	3.0	610	3	US-08-656-664-29	Sequence 29, Appl	643	78	3.0	389	4	US-09-248-796A-17588	Sequence 17588, A
571	79	3.0	610	3	US-08-656-664-35	Sequence 35, Appl	644	78	3.0	390	4	US-09-252-991A-19899	Sequence 19899, A
572	79	3.0	610	3	US-08-656-664-54	Sequence 54, Appl	645	78	3.0	401	4	US-09-800-170-15	Sequence 15, Appl
573	79	3.0	610	5	PCT-US96-09641-16	Sequence 16, Appl	646	78	3.0	456	4	US-07-754-918A-13	Sequence 13, Appl
574	79	3.0	610	5	PCT-US96-09641-29	Sequence 29, Appl	647	78	3.0	481	1	US-08-186-811-2	Sequence 2, Appli
575	79	3.0	610	5	PCT-US96-09641-35	Sequence 35, Appl	648	78	3.0	481	1	US-08-311-611A-98	Sequence 98, Appl
576	79	3.0	610	5	PCT-US96-09641-54	Sequence 54, Appl	649	78	3.0	481	1	US-08-372-783-98	Sequence 98, Appl
577	79	3.0	636	4	US-09-270-767-45810	Sequence 45810, A	650	78	3.0	481	1	US-08-372-105-98	Sequence 98, Appl
578	79	3.0	643	4	US-09-538-092-389	Sequence 389, App	651	78	3.0	481	1	US-08-306-473A-98	Sequence 98, Appl
579	79	3.0	656	4	US-09-538-092-654	Sequence 654, App	652	78	3.0	481	1	US-08-261-660A-4	Sequence 4, Appli
580	79	3.0	666	4	US-09-252-991A-17462	Sequence 17462, A	653	78	3.0	481	1	US-08-209-762-98	Sequence 98, Appl
581	79	3.0	740	1	US-08-309-512-10	Sequence 10, Appl	654	78	3.0	481	1	US-08-473-344-98	Sequence 6, Appli
582	79	3.0	740	5	PCT-US92-08756A-10	Sequence 10, Appl	655	78	3.0	481	1	US-08-377-391A-2	Sequence 2, Appli
583	79	3.0	780	4	US-09-262-537-10	Sequence 10, Appl	656	78	3.0	481	2	US-08-485-445A-98	Sequence 98, Appl
584	79	3.0	823	4	US-09-252-991A-31026	Sequence 31026, A	657	78	3.0	481	2	US-08-779-400-2	Sequence 2, Appli
585	79	3.0	841	3	US-09-546-990-2	Sequence 2, Appli	658	78	3.0	481	2	US-08-955-660-2	Sequence 2, Appli
586	79	3.0	1114	4	US-09-262-537-34	Sequence 34, Appl	659	78	3.0	481	2	US-09-119-263-98	Sequence 98, Appl
587	79	3.0	1177	4	US-09-262-537-2	Sequence 2, Appli	660	78	3.0	481	3	US-08-657-162-98	Sequence 98, Appl
588	79	3.0	1336	2	US-08-231-193A-58	Sequence 58, Appl	661	78	3.0	481	3	US-09-224-480-98	Sequence 98, Appl
589	79	3.0	1336	2	US-08-486-273A-58	Sequence 58, Appl	662	78	3.0	481	3	US-09-093-539-98	Sequence 98, Appl
590	79	3.0	1336	3	US-08-940-086A-58	Sequence 58, Appl	663	78	3.0	481	3	US-09-146-620-2	Sequence 2, Appli
591	79	3.0	1336	3	US-08-940-035A-58	Sequence 58, Appl	664	78	3.0	481	3	US-09-280-909A-4	Sequence 4, Appli
592	79	3.0	1336	3	US-08-935-105A-58	Sequence 58, Appl	665	78	3.0	481	4	US-09-949-016-6459	Sequence 6459, Ap
593	79	3.0	1336	4	US-09-648-797-58	Sequence 58, Appl	672	78	3.0	481	5	PCT-US94-02465-98	Sequence 98, Appl
594	79	3.0	1336	4	US-09-386-123-58	Sequence 58, Appl	673	78	3.0	481	5	PCT-US94-06931-4	Sequence 4, Appli
595	79	3.0	1336	4	US-10-038-937-58	Sequence 58, Appl	674	78	3.0	481	5	PCT-US95-00498-98	Sequence 98, Appl
596	79	3.0	1403	4	US-09-262-537-6	Sequence 6, Appli	675	78	3.0	481	5	PCT-US95-00656-98	Sequence 17413, A
597	79	3.0	1404	4	US-09-345-473E-24	Sequence 24, Appl	676	78	3.0	481	4	US-09-508-370A-3	Sequence 3, Appli
598	79	3.0	1735	4	US-09-902-540-14547	Sequence 14547, A	677	78	3.0	481	4	US-09-538-092-1153	Sequence 1153, Ap
599	79	3.0	3074	4	US-09-543-681A-5508	Sequence 5508, Ap	679	78	3.0	481	5	US-09-595-682B-28	Sequence 28, Appl
600	78.5	3.0	271	4	US-09-489-039A-8280	Sequence 8280, Ap	680	78	3.0	481	4	US-09-949-016-9670	Sequence 9670, Ap
601	78.5	3.0	385	4	US-09-984-334-1	Sequence 1, Appli	681	78	3.0	481	3	US-08-818-112-75	Sequence 75, Appl
602	78.5	3.0	402	2	US-08-403-852D-19	Sequence 19, Appl	682	78	3.0	481	3	US-08-818-111-76	Sequence 76, Appl
603	78.5	3.0	402	3	US-08-510-646B-20	Sequence 20, Appl	683	78	3.0	580	3	US-09-056-556-75	Sequence 75, Appl
604	78.5	3.0	402	3	US-09-231-818-19	Sequence 19, Appl	684	78	3.0	580	4	US-09-072-596-76	Sequence 76, Appl
605	78.5	3.0	402	4	US-09-635-359B-19	Sequence 19, Appl							
606	78.5	3.0	436	4	US-09-252-991A-18821	Sequence 18821, A							
607	78.5	3.0	446	4	US-09-583-110-4349	Sequence 4349, Ap							
608	78.5	3.0	450	4	US-09-492-709A-398	Sequence 398, App							
609	78.5	3.0	513	3	US-08-369-822C-28	Sequence 28, Appl							
610	78.5	3.0	513	3	US-08-582-776C-43	Sequence 43, Appl							
611	78.5	3.0	513	3	US-08-434-831B-40	Sequence 40, Appl							



685	78	3.0	580	4	US-09-072-967-75	Sequence 75, Appl	758	77.5	3.0	889	4	US-09-252-991A-30096	Sequence 30096, A
686	78	3.0	595	4	US-09-270-767-43484	Sequence 43484, A	759	77.5	3.0	908	1	US-08-356-354-6	Sequence 6, Appli
687	78	3.0	636	3	US-09-564-805-237	Sequence 237, App	760	77.5	3.0	908	2	US-08-778-656-6	Sequence 6, Appli
688	78	3.0	647	3	US-08-483-577A-148	Sequence 148, App	761	77.5	3.0	908	3	US-09-376-045-6	Sequence 6, Appli
689	78	3.0	647	3	US-08-897-438-148	Sequence 148, App	762	77.5	3.0	1091	3	US-09-306-595C-7	Sequence 7, Appli
690	78	3.0	647	3	US-08-649-518-148	Sequence 148, App	763	77.5	3.0	1091	4	US-09-925-388-7	Sequence 7, Appli
691	78	3.0	660	1	US-08-487-890A-8	Sequence 8, Appli	764	77.5	3.0	1091	4	US-09-925-388-7	Sequence 7, Appli
692	78	3.0	660	1	US-08-487-890A-10	Sequence 10, Appl	765	77.5	3.0	1114	4	US-09-252-991A-24965	Sequence 24965, A
693	78	3.0	660	2	US-08-478-435-8	Sequence 8, Appli	766	77.5	3.0	1246	4	US-09-252-991A-23140	Sequence 23140, A
694	78	3.0	660	2	US-08-478-435-10	Sequence 10, Appl	767	77.5	3.0	2046	4	US-09-949-016-9365	Sequence 9365, Ap
695	78	3.0	660	2	US-08-337-483-8	Sequence 8, Appli	767	77.5	3.0	2482	4	US-09-252-991A-16967	Sequence 16967, A
696	78	3.0	660	2	US-08-337-483-10	Sequence 10, Appl	768	77.5	3.0	4019	4	US-09-854-133-425	Sequence 425, App
697	78	3.0	660	2	US-08-478-373-8	Sequence 8, Appli	769	77	2.9	173	4	US-09-453-976-16	Sequence 16, Appl
698	78	3.0	660	2	US-08-478-373-10	Sequence 10, Appl	770	77	2.9	206	4	US-09-205-258-463	Sequence 463, App
699	78	3.0	660	3	US-08-474-671-8	Sequence 8, Appli	771	77	2.9	291	4	US-09-134-000C-3787	Sequence 3787, Ap
700	78	3.0	660	3	US-08-474-671-10	Sequence 10, Appl	772	77	2.9	335	4	US-09-134-000C-5784	Sequence 5784, Ap
701	78	3.0	660	3	US-08-483-577A-8	Sequence 8, Appli	773	77	2.9	357	3	US-09-134-001C-4405	Sequence 4405, Ap
702	78	3.0	660	3	US-08-483-577A-10	Sequence 10, Appl	774	77	2.9	378	4	US-09-134-000C-5593	Sequence 5593, Ap
703	78	3.0	660	3	US-08-897-438-8	Sequence 8, Appli	775	77	2.9	379	4	US-09-692-570-15	Sequence 15, Appl
704	78	3.0	660	3	US-08-897-438-10	Sequence 10, Appl	776	77	2.9	418	4	US-09-538-092-1122	Sequence 1122, Ap
705	78	3.0	660	3	US-08-637-654-8	Sequence 8, Appli	777	77	2.9	462	4	US-09-248-796A-17149	Sequence 17149, A
706	78	3.0	660	3	US-08-637-654-10	Sequence 10, Appl	778	77	2.9	476	3	US-09-188-579-114	Sequence 114, App
707	78	3.0	660	3	US-08-649-518-8	Sequence 8, Appli	779	77	2.9	476	4	US-09-315-444-114	Sequence 114, App
708	78	3.0	660	3	US-08-649-518-10	Sequence 10, Appl	780	77	2.9	502	4	US-09-949-016-7837	Sequence 7837, Ap
709	78	3.0	772	4	US-09-252-991A-30121	Sequence 30121, A	781	77	2.9	512	4	US-09-543-681A-7997	Sequence 7997, Ap
710	78	3.0	789	4	US-09-949-016-7237	Sequence 7237, Ap	782	77	2.9	515	4	US-09-543-681A-5651	Sequence 5651, Ap
711	78	3.0	816	1	US-07-731-157A-4	Sequence 4, Appli	783	77	2.9	517	4	US-09-902-540-10229	Sequence 10229, A
712	78	3.0	816	1	US-08-229-444B-2	Sequence 4, Appli	784	77	2.9	521	4	US-09-107-532A-3961	Sequence 3961, Ap
713	78	3.0	816	2	US-08-541-780-4	Sequence 4, Appli	785	77	2.9	587	1	US-08-844-280-2	Sequence 2, Appli
714	78	3.0	827	4	US-09-543-681A-6425	Sequence 6425, Ap	786	77	2.9	587	3	US-09-006-726-2	Sequence 2, Appli
715	78	3.0	829	3	US-09-514-599-6	Sequence 6, Appli	787	77	2.9	610	3	US-09-019-160-4	Sequence 4, Appli
716	78	3.0	829	3	US-09-996-024-6	Sequence 6, Appli	788	77	2.9	625	2	US-08-532-547-7	Sequence 7, Appli
717	78	3.0	879	4	US-09-107-532A-4679	Sequence 4679, Ap	789	77	2.9	625	2	US-08-532-547-9	Sequence 9, Appli
718	78	3.0	883	4	US-09-583-110-2900	Sequence 2900, Ap	790	77	2.9	625	3	US-09-019-809-7	Sequence 7, Appli
719	78	3.0	888	4	US-09-107-433-2964	Sequence 2964, Ap	791	77	2.9	625	3	US-09-019-809-9	Sequence 9, Appli
720	78	3.0	893	3	US-09-019-160-2	Sequence 2, Appli	792	77	2.9	625	3	US-09-471-177-7	Sequence 7, Appli
721	78	3.0	927	4	US-09-107-532A-4335	Sequence 4335, Ap	793	77	2.9	625	4	US-09-471-177-9	Sequence 9, Appli
722	78	3.0	1259	3	US-09-045-360-2	Sequence 13, Appl	794	77	2.9	637	4	US-09-134-000C-4594	Sequence 4594, Ap
723	78	3.0	1464	3	US-09-045-360-2	Sequence 2, Appli	795	77	2.9	751	4	US-09-252-991A-22770	Sequence 22770, A
724	78	3.0	1464	4	US-09-713-273A-21	Sequence 21, Appl	796	77	2.9	773	2	US-08-966-389-4	Sequence 4, Appli
725	78	3.0	1464	3	US-09-746-390-2	Sequence 2, Appli	797	77	2.9	773	2	US-09-103-509-4	Sequence 4, Appli
726	78	3.0	1698	3	US-09-315-793-12	Sequence 12, Appl	798	77	2.9	773	2	US-09-102-644-4	Sequence 4, Appli
727	78	3.0	1896	4	US-09-949-016-9508	Sequence 9508, Ap	799	77	2.9	773	2	US-09-218-032-4	Sequence 4, Appli
728	78	3.0	2324	4	US-09-902-540-9732	Sequence 9732, Ap	800	77	2.9	850	4	US-09-904-389-2	Sequence 2, Appli
729	78	3.0	3519	3	US-09-428-517-4	Sequence 4, Appli	801	77	2.9	858	4	US-09-134-000C-5428	Sequence 5428, Ap
730	77.5	3.0	285	4	US-09-252-991A-29780	Sequence 29780, A	802	77	2.9	900	4	US-09-252-991A-25011	Sequence 25011, A
731	77.5	3.0	315	4	US-09-902-540-11852	Sequence 11852, A	803	77	2.9	964	3	US-08-484-791-2	Sequence 2, Appli
732	77.5	3.0	345	4	US-09-328-352-4841	Sequence 4841, Ap	804	77	2.9	1156	3	US-09-002-285-72	Sequence 72, Appl
733	77.5	3.0	357	4	US-09-910-174B-14	Sequence 14, Appl	805	77	2.9	1156	4	US-09-589-477-72	Sequence 72, Appl
734	77.5	3.0	357	4	US-09-620-461-14	Sequence 14, Appl	806	77	2.9	1156	4	US-09-661-322A-28	Sequence 28, Appl
735	77.5	3.0	361	3	US-09-032-372-12	Sequence 12, Appl	807	77	2.9	1156	4	US-10-099-285A-72	Sequence 72, Appl
736	77.5	3.0	386	3	US-08-972-902-3	Sequence 3, Appli	808	77	2.9	1157	2	US-08-532-547-5	Sequence 5, Appli
737	77.5	3.0	386	4	US-09-520-207-3	Sequence 3, Appli	809	77	2.9	1157	2	US-08-379-656B-5	Sequence 5, Appli
738	77.5	3.0	386	4	US-10-136-253-3	Sequence 3, Appli	810	77	2.9	1157	3	US-08-455-838-5	Sequence 5, Appli
739	77.5	3.0	394	4	US-09-252-991A-24485	Sequence 24485, A	811	77	2.9	1157	3	US-09-019-809-5	Sequence 5, Appli
740	77.5	3.0	447	4	US-09-107-433-3528	Sequence 3528, Ap	812	77	2.9	1157	4	US-09-471-177-5	Sequence 5, Appli
741	77.5	3.0	499	4	US-09-543-681A-6892	Sequence 6892, Ap	813	77	2.9	1157	4	US-09-220-806-5	Sequence 8, Appli
742	77.5	3.0	511	1	US-08-220-151-17	Sequence 17, Appl	814	77	2.9	2257	4	US-09-839-477-8	Sequence 302, App
743	77.5	3.0	511	3	US-08-413-118-17	Sequence 17, Appl	815	77	2.9	2383	4	US-09-492-709A-302	Sequence 302, App
744	77.5	3.0	511	3	US-08-473-446-17	Sequence 17, Appl	816	77	2.9	227	4	US-09-489-039A-13495	Sequence 13495, A
745	77.5	3.0	527	4	US-09-248-796A-20846	Sequence 20846, A	817	76.5	2.9	293	4	US-09-101-307D-6	Sequence 6, Appli
746	77.5	3.0	528	2	US-08-793-229-35	Sequence 35, Appl	818	76.5	2.9	314	4	US-09-583-110-3992	Sequence 3992, Ap
747	77.5	3.0	528	3	US-09-285-957-35	Sequence 35, Appl	819	76.5	2.9	315	4	US-09-107-433-4625	Sequence 4625, Ap
748	77.5	3.0	552	3	US-09-295-186-10	Sequence 10, Appl	820	76.5	2.9	328	4	US-09-489-847-310	Sequence 310, App
749	77.5	3.0	573	3	US-09-295-186-11	Sequence 11, Appl	821	76.5	2.9	374	4	US-09-710-279-2162	Sequence 2162, Ap
750	77.5	3.0	614	4	US-09-328-352-4256	Sequence 4256, Ap	822	76.5	2.9	391	4	US-09-543-681A-5575	Sequence 5575, Ap
751	77.5	3.0	669	4	US-09-134-000C-6185	Sequence 6185, Ap	823	76.5	2.9	398	3	US-09-242-859A-4	Sequence 4, Appli
752	77.5	3.0	710	1	US-08-162-809-22	Sequence 22, Appl	824	76.5	2.9	398	3	US-09-242-859A-8	Sequence 8, Appli
753	77.5	3.0	722	1	US-08-162-809-4	Sequence 4, Appli	825	76.5	2.9	406	3	US-09-134-001C-3202	Sequence 3202, Ap
754	77.5	3.0	788	4	US-09-538-092-567	Sequence 567, App	826	76.5	2.9	407	3	US-08-955-957A-2	Sequence 2, Appli
755	77.5	3.0	802	4	US-09-134-000C-5150	Sequence 5150, Ap	827	76.5	2.9	420	3	US-09-134-001C-3103	Sequence 3103, Ap
756	77.5	3.0	821	1	US-09-377-465A-2	Sequence 2, Appli	828	76.5	2.9	447	4	US-09-724-623-100	Sequence 100, App
757	77.5	3.0	825	4	US-09-645-835A-2	Sequence 2, Appli	830	76.5	2.9	467	4	US-09-489-039A-14156	Sequence 14156, A



831	76.5	2.9	494	3	US-08-484-661A-39	Sequence 39, Appl	904	76	2.9	398	4	US-09-583-110-3408	Sequence 3408, Ap
832	76.5	2.9	494	3	US-08-656-664-39	Sequence 39, Appl	905	76	2.9	413	4	US-09-248-796A-14455	Sequence 14455, A
833	76.5	2.9	494	5	PCT-US96-09641-39	Sequence 39, Appl	906	76	2.9	422	4	US-09-949-016-11004	Sequence 11004, A
834	76.5	2.9	511	4	US-09-538-092-606	Sequence 606, App	907	76	2.9	447	4	US-10-082-272-2	Sequence 2, Appli
835	76.5	2.9	523	4	US-09-489-039A-14269	Sequence 14269, A	908	76	2.9	481	3	US-08-431-517F-2	Sequence 2, Appli
836	76.5	2.9	541	4	US-09-949-016-11454	Sequence 11454, A	909	76	2.9	497	4	US-09-710-279-2812	Sequence 2812, Ap
837	76.5	2.9	571	3	US-08-484-661A-37	Sequence 37, Appl	910	76	2.9	532	2	US-08-899-324-33	Sequence 33, Appl
838	76.5	2.9	571	3	US-08-656-664-37	Sequence 37, Appl	911	76	2.9	532	3	US-08-329-892B-33	Sequence 33, Appl
839	76.5	2.9	571	5	PCT-US96-09641-37	Sequence 37, Appl	912	76	2.9	538	4	US-09-252-991A-17359	Sequence 17359, A
840	76.5	2.9	572	4	US-09-107-433-3479	Sequence 3479, Ap	913	76	2.9	576	4	US-09-248-796A-20180	Sequence 20180, A
841	76.5	2.9	578	3	US-08-484-661A-11	Sequence 11, Appl	914	76	2.9	597	4	US-09-489-039A-12394	Sequence 12394, A
842	76.5	2.9	578	3	US-08-656-664-11	Sequence 11, Appl	915	76	2.9	617	4	US-09-107-433-4596	Sequence 4596, Ap
843	76.5	2.9	578	4	US-09-949-016-9799	Sequence 9799, Ap	916	76	2.9	648	3	US-09-183-706-43	Sequence 43, Appl
844	76.5	2.9	578	5	PCT-US96-09641-11	Sequence 11, Appl	917	76	2.9	648	3	US-09-567-995-43	Sequence 43, Appl
845	76.5	2.9	596	4	US-09-345-473E-21	Sequence 21, Appl	918	76	2.9	657	4	US-09-252-991A-27358	Sequence 27358, A
846	76.5	2.9	607	4	US-09-949-016-6293	Sequence 6293, Ap	919	76	2.9	658	4	US-09-583-110-4743	Sequence 4743, Ap
847	76.5	2.9	610	3	US-08-484-661A-8	Sequence 8, Appli	920	76	2.9	727	4	US-09-543-681A-6701	Sequence 6701, Ap
848	76.5	2.9	610	3	US-08-484-661A-19	Sequence 19, Appl	921	76	2.9	749	4	US-09-562-737-91	Sequence 91, Appl
849	76.5	2.9	610	3	US-08-484-661A-23	Sequence 23, Appl	922	76	2.9	824	4	US-09-134-000C-4908	Sequence 4908, Ap
850	76.5	2.9	610	3	US-08-484-661A-26	Sequence 26, Appl	923	76	2.9	915	4	US-09-949-016-7628	Sequence 7628, Ap
851	76.5	2.9	610	3	US-08-484-661A-33	Sequence 33, Appl	924	76	2.9	955	2	US-08-500-857A-10	Sequence 10, Appl
852	76.5	2.9	610	3	US-08-656-664-8	Sequence 8, Appli	925	76	2.9	1028	4	US-09-328-352-5749	Sequence 5749, Ap
853	76.5	2.9	610	3	US-08-656-664-19	Sequence 19, Appl	926	76	2.9	1089	4	US-09-902-540-14239	Sequence 14239, A
854	76.5	2.9	610	3	US-08-656-664-23	Sequence 23, Appl	927	76	2.9	1120	4	US-09-792-024-86	Sequence 86, Appl
855	76.5	2.9	610	3	US-08-656-664-26	Sequence 26, Appl	928	76	2.9	1151	3	US-08-840-006-6	Sequence 6, Appli
856	76.5	2.9	610	3	US-08-656-664-33	Sequence 33, Appl	929	76	2.9	1200	3	US-08-840-006-5	Sequence 5, Appli
857	76.5	2.9	610	5	PCT-US96-09641-8	Sequence 8, Appli	930	76	2.9	1349	4	US-08-943-144-4	Sequence 4, Appli
858	76.5	2.9	610	5	PCT-US96-09641-19	Sequence 19, Appl	931	76	2.9	2254	2	US-08-677-010-3	Sequence 3, Appli
859	76.5	2.9	610	5	PCT-US96-09641-23	Sequence 23, Appl	932	76	2.9	2254	2	US-08-790-519-3	Sequence 3, Appli
860	76.5	2.9	610	5	PCT-US96-09641-26	Sequence 26, Appl	933	76	2.9	2472	4	US-09-538-092-1312	Sequence 1312, Ap
861	76.5	2.9	610	5	PCT-US96-09641-33	Sequence 33, Appl	934	76	2.9	2749	4	US-09-385-222A-4	Sequence 4, Appli
862	76.5	2.9	732	4	US-09-107-532A-6192	Sequence 6192, Ap	935	75.5	2.9	301	4	US-09-134-000C-6225	Sequence 6225, Ap
863	76.5	2.9	745	4	US-09-543-681A-4267	Sequence 4267, Ap	936	75.5	2.9	313	4	US-09-148-545-236	Sequence 236, App
864	76.5	2.9	750	4	US-09-248-796A-14886	Sequence 14886, A	937	75.5	2.9	313	4	US-09-248-796A-15393	Sequence 15393, A
865	76.5	2.9	775	4	US-09-107-532A-6639	Sequence 6639, Ap	938	75.5	2.9	327	4	US-09-585-858-53	Sequence 53, Appl
866	76.5	2.9	800	4	US-09-489-039A-10358	Sequence 10358, A	939	75.5	2.9	327	4	US-10-270-878-53	Sequence 53, Appl
867	76.5	2.9	857	4	US-09-902-540-12312	Sequence 12312, A	940	75.5	2.9	362	4	US-09-134-000C-6241	Sequence 6241, Ap
868	76.5	2.9	883	4	US-09-248-796A-14418	Sequence 14418, A	941	75.5	2.9	375	4	US-09-248-796A-18358	Sequence 18358, A
869	76.5	2.9	887	3	US-08-472-240A-5	Sequence 5, Appli	942	75.5	2.9	389	4	US-09-134-000C-5942	Sequence 5942, Ap
870	76.5	2.9	944	4	US-09-328-352-4401	Sequence 4401, Ap	943	75.5	2.9	410	1	US-08-792-283A-2	Sequence 2, Appli
871	76.5	2.9	959	4	US-09-949-016-6904	Sequence 6904, Ap	944	75.5	2.9	410	2	US-09-105-908-2	Sequence 2, Appli
872	76.5	2.9	974	4	US-09-540-236-2913	Sequence 2913, Ap	945	75.5	2.9	410	3	US-09-271-713-2	Sequence 2, Appli
873	76.5	2.9	981	4	US-09-949-016-11647	Sequence 11647, A	946	75.5	2.9	412	4	US-09-950-772-6	Sequence 6, Appli
874	76.5	2.9	981	4	US-09-949-016-11648	Sequence 11648, A	947	75.5	2.9	444	4	US-09-248-796A-23448	Sequence 23448, A
875	76.5	2.9	1010	4	US-09-654-449-2	Sequence 2, Appli	948	75.5	2.9	447	4	US-09-610-104C-2	Sequence 2, Appli
876	76.5	2.9	1010	4	US-09-759-152A-2	Sequence 2, Appli	949	75.5	2.9	476	3	US-09-134-218-6	Sequence 6, Appli
877	76.5	2.9	1121	1	US-07-789-915A-2	Sequence 2, Appli	950	75.5	2.9	493	4	US-09-543-681A-8173	Sequence 8173, Ap
878	76.5	2.9	1121	1	US-08-005-002C-2	Sequence 2, Appli	951	75.5	2.9	504	4	US-09-489-039A-14248	Sequence 14248, A
879	76.5	2.9	1121	1	US-08-487-203A-2	Sequence 2, Appli	952	75.5	2.9	518	4	US-09-328-352-7332	Sequence 7332, Ap
880	76.5	2.9	1190	4	US-09-107-532A-7146	Sequence 7146, Ap	953	75.5	2.9	520	4	US-09-328-352-7451	Sequence 7451, Ap
881	76.5	2.9	1334	6	5476657-1	Patent No. 5476657	954	75.5	2.9	523	4	US-09-198-452A-1101	Sequence 1101, Ap
882	76.5	2.9	1334	6	5476657-1	Patent No. 5476657	955	75.5	2.9	528	4	US-09-438-185A-1028	Sequence 1028, Ap
883	76.5	2.9	1338	4	US-09-949-016-6029	Sequence 6029, Ap	956	75.5	2.9	575	1	US-08-348-920-1	Sequence 1, Appli
884	76.5	2.9	1403	1	US-07-908-253-3	Sequence 3, Appli	957	75.5	2.9	603	4	US-09-732-615-2	Sequence 2, Appli
885	76.5	2.9	1403	2	US-08-694-865-17	Sequence 17, Appl	958	75.5	2.9	603	4	US-10-273-051-2	Sequence 2, Appli
886	76.5	2.9	1403	2	US-08-535-837-3	Sequence 3, Appli	959	75.5	2.9	625	4	US-08-759-436-3	Sequence 3, Appli
887	76.5	2.9	1403	3	US-09-124-491-17	Sequence 17, Appl	960	75.5	2.9	625	4	US-08-759-436-5	Sequence 5, Appli
888	76.5	2.9	1403	4	US-09-383-912-17	Sequence 17, Appl	961	75.5	2.9	730	4	US-09-328-352-4442	Sequence 4442, Ap
889	76.5	2.9	2549	4	US-08-265-967C-1	Sequence 1, Appli	962	75.5	2.9	739	4	US-09-543-681A-6437	Sequence 6437, Ap
890	76.5	2.9	2549	4	US-08-305-790B-2	Sequence 2, Appli	963	75.5	2.9	742	4	US-09-107-532A-6890	Sequence 6890, Ap
891	76.5	2.9	2616	6	5206163-3	Patent No. 5206163	964	75.5	2.9	747	4	US-09-902-540-16170	Sequence 16170, A
892	76.5	2.9	2616	6	5206163-3	Patent No. 5206163	965	75.5	2.9	749	4	US-09-562-737-93	Sequence 93, Appl
893	76.5	2.9	3135	1	US-08-323-170B-2	Sequence 2, Appli	966	75.5	2.9	818	4	US-09-328-352-5208	Sequence 5208, Ap
894	76.5	2.9	3135	3	US-08-954-441-2	Sequence 2, Appli	967	75.5	2.9	857	4	US-09-275-252A-11	Sequence 11, Appl
895	76	2.9	245	4	US-08-836-687B-33	Sequence 33, Appl	968	75.5	2.9	868	4	US-09-949-016-11723	Sequence 11723, A
896	76	2.9	304	4	US-09-248-796A-14813	Sequence 14813, A	969	75.5	2.9	931	4	US-09-949-016-10552	Sequence 10552, A
897	76	2.9	315	4	US-09-492-709A-306	Sequence 306, App	970	75.5	2.9	1063	4	US-09-595-857B-29	Sequence 29, Appl
898	76	2.9	333	4	US-09-710-279-1960	Sequence 1960, Ap	971	75.5	2.9	1077	3	US-09-390-234-12	Sequence 12, Appl
899	76	2.9	360	4	US-09-489-039A-13634	Sequence 13634, A	972	75.5	2.9	1077	4	US-09-603-311-12	Sequence 12, Appl
900	76	2.9	369	3	US-09-134-001C-5149	Sequence 5149, Ap	973	75.5	2.9	1138	1	US-07-973-320-2	Sequence 2, Appli
901	76	2.9	382	4	US-09-328-352-7586	Sequence 7586, Ap	974	75.5	2.9	1138	1	US-07-973-320-4	Sequence 4, Appli
902	76	2.9	383	4	US-09-252-991A-18162	Sequence 18162, A	975	75.5	2.9	1164	4	US-09-949-016-11682	Sequence 11682, A
903	76	2.9	391	4	US-09-543-681A-6610	Sequence 6610, Ap	976	75.5	2.9	1185	3	US-09-134-001C-5276	Sequence 5276, Ap

977	75.5	2.9	1202	4	US-09-328-352-6889	Sequence 6889, Ap	1050	74.5	2.8	177	4	US-09-489-039A-10826	Sequence 10826, A
978	75.5	2.9	1255	4	US-09-248-796A-14158	Sequence 14158, A	1051	74.5	2.8	236	1	US-08-307-499-28	Sequence 28, Appl
979	75.5	2.9	1275	4	US-08-426-630-49	Sequence 49, Appl	1052	74.5	2.8	236	3	US-09-299-268-28	Sequence 28, Appl
980	75.5	2.9	1323	4	US-09-949-016-6553	Sequence 6553, Ap	1053	74.5	2.8	243	4	US-09-252-991A-32483	Sequence 32483, A
981	75.5	2.9	1330	4	US-09-543-681A-8057	Sequence 8057, Ap	1054	74.5	2.8	326	4	US-09-902-540-15158	Sequence 15158, A
982	75.5	2.9	1435	4	US-09-949-016-9942	Sequence 9942, Ap	1055	74.5	2.8	336	4	US-09-252-991A-24121	Sequence 24121, A
983	75.5	2.9	1435	4	US-09-949-016-9943	Sequence 9943, Ap	1056	74.5	2.8	396	4	US-09-252-991A-23803	Sequence 23803, A
984	75.5	2.9	1435	4	US-09-949-016-9944	Sequence 9944, Ap	1057	74.5	2.8	403	1	US-07-672-304-6	Sequence 6, Appli
985	75.5	2.9	1529	4	US-09-107-433-4771	Sequence 4771, Ap	1058	74.5	2.8	403	3	US-08-776-246-4	Sequence 4, Appli
986	75.5	2.9	2237	1	US-08-354-973-1	Sequence 1, Appli	1059	74.5	2.8	432	4	US-09-902-540-12060	Sequence 12060, A
987	75.5	2.9	2364	4	US-09-538-092-1243	Sequence 1243, Ap	1060	74.5	2.8	439	3	US-09-134-001C-4903	Sequence 4903, Ap
988	75	2.9	190	4	US-09-252-991A-19148	Sequence 19148, A	1061	74.5	2.8	448	4	US-09-489-039A-8657	Sequence 8657, Ap
989	75	2.9	201	1	US-08-236-427-3	Sequence 3, Appli	1062	74.5	2.8	464	4	US-09-540-236-3564	Sequence 3564, Ap
990	75	2.9	285	4	US-09-270-767-42260	Sequence 42260, A	1063	74.5	2.8	473	3	US-09-134-001C-4773	Sequence 4773, Ap
991	75	2.9	314	3	US-08-981-957D-13	Sequence 13, Appl	1064	74.5	2.8	473	4	US-09-540-236-2543	Sequence 2543, Ap
992	75	2.9	314	4	US-09-982-704-13	Sequence 13, Appl	1065	74.5	2.8	473	4	US-09-949-016-9820	Sequence 9820, Ap
993	75	2.9	315	3	US-08-793-035-9	Sequence 9, Appli	1066	74.5	2.8	480	3	US-09-171-482-2	Sequence 2, Appli
994	75	2.9	315	3	US-08-793-035-10	Sequence 10, Appl	1067	74.5	2.8	489	4	US-09-949-016-10775	Sequence 10775, A
995	75	2.9	353	4	US-09-543-681A-6054	Sequence 6054, Ap	1068	74.5	2.8	507	4	US-09-248-796A-15920	Sequence 15920, A
996	75	2.9	357	4	US-09-489-039A-13443	Sequence 13443, A	1069	74.5	2.8	509	3	US-09-134-078-18	Sequence 18, Appl
997	75	2.9	358	4	US-09-543-681A-7838	Sequence 7838, Ap	1070	74.5	2.8	529	4	US-09-252-991A-27659	Sequence 27659, A
998	75	2.9	367	4	US-09-248-796A-18155	Sequence 18155, A	1071	74.5	2.8	541	3	US-08-687-590-28	Sequence 28, Appl
999	75	2.9	374	4	US-09-710-279-1664	Sequence 1664, Ap	1072	74.5	2.8	541	3	US-09-311-311C-25	Sequence 25, Appl
1000	75	2.9	389	3	US-09-134-001C-3161	Sequence 4, Appli	1073	74.5	2.8	554	4	US-09-902-540-15061	Sequence 15061, A
1001	75	2.9	400	4	US-09-797-464A-4	Sequence 4, Appli	1074	74.5	2.8	565	4	US-09-248-796A-15341	Sequence 15341, A
1002	75	2.9	423	4	US-09-328-352-5224	Sequence 5224, Ap	1075	74.5	2.8	591	4	US-09-248-796A-18374	Sequence 18374, A
1003	75	2.9	477	1	US-07-847-562-2	Sequence 2, Appli	1076	74.5	2.8	601	4	US-09-270-767-42194	Sequence 42194, A
1004	75	2.9	477	1	US-08-240-328-2	Sequence 2, Appli	1077	74.5	2.8	607	4	US-09-198-452A-374	Sequence 374, App
1005	75	2.9	477	2	US-08-990-849-2	Sequence 2, Appli	1078	74.5	2.8	608	4	US-09-438-185A-361	Sequence 361, App
1006	75	2.9	481	2	US-08-215-089-9	Sequence 9, Appli	1079	74.5	2.8	623	4	US-09-902-540-10027	Sequence 10027, A
1007	75	2.9	481	3	US-08-431-517F-11	Sequence 11, Appl	1080	74.5	2.8	625	3	US-08-581-148C-18	Sequence 18, Appl
1008	75	2.9	481	5	PCT-US95-03384-9	Sequence 9, Appli	1081	74.5	2.8	630	3	US-08-973-462-9	Sequence 9, Appli
1009	75	2.9	498	3	US-09-232-468A-18	Sequence 18, Appl	1082	74.5	2.8	637	4	US-09-360-545-6	Sequence 6, Appli
1010	75	2.9	498	4	US-09-784-984B-52	Sequence 52, Appl	1083	74.5	2.8	637	4	US-09-398-395A-58	Sequence 58, Appl
1011	75	2.9	501	4	US-09-934-901-20	Sequence 20, Appl	1084	74.5	2.8	637	4	US-09-887-586A-58	Sequence 58, Appl
1012	75	2.9	501	4	US-09-934-868-10	Sequence 10, Appl	1085	74.5	2.8	637	4	US-09-895-752-58	Sequence 58, Appl
1013	75	2.9	501	4	US-10-321-210-20	Sequence 20, Appl	1086	74.5	2.8	637	4	US-09-903-012B-58	Sequence 58, Appl
1014	75	2.9	501	4	US-10-320-874-20	Sequence 20, Appl	1087	74.5	2.8	637	4	US-09-900-797-58	Sequence 58, Appl
1015	75	2.9	502	4	US-09-328-352-5891	Sequence 5891, Ap	1088	74.5	2.8	698	4	US-09-107-532A-5685	Sequence 5685, Ap
1016	75	2.9	557	4	US-09-538-092-242	Sequence 242, App	1089	74.5	2.8	722	3	US-09-433-043B-125	Sequence 125, App
1017	75	2.9	558	4	US-09-540-236-2943	Sequence 2943, Ap	1090	74.5	2.8	824	4	US-09-252-991A-32329	Sequence 32329, A
1018	75	2.9	566	4	US-09-949-016-8505	Sequence 8505, Ap	1091	74.5	2.8	905	3	US-09-134-001C-3782	Sequence 3782, Ap
1019	75	2.9	600	4	US-09-252-991A-28916	Sequence 28916, A	1092	74.5	2.8	943	4	US-09-902-540-10641	Sequence 10641, A
1020	75	2.9	603	4	US-09-396-149-8	Sequence 8, Appli	1093	74.5	2.8	968	3	US-09-228-986-76	Sequence 76, Appl
1021	75	2.9	639	4	US-09-248-796A-20583	Sequence 20583, A	1094	74.5	2.8	968	4	US-10-101-464A-76	Sequence 76, Appl
1022	75	2.9	714	4	US-09-492-709A-253	Sequence 253, App	1095	74.5	2.8	989	2	US-08-070-301-14	Sequence 14, Appl
1023	75	2.9	745	4	US-09-902-540-10275	Sequence 10275, A	1096	74.5	2.8	990	4	US-09-540-236-3360	Sequence 3360, Ap
1024	75	2.9	820	4	US-09-583-110-4219	Sequence 4219, Ap	1097	74.5	2.8	1037	3	US-09-134-001C-4794	Sequence 4794, Ap
1025	75	2.9	822	4	US-09-824-734-3	Sequence 3, Appli	1098	74.5	2.8	1363	4	US-09-252-991A-21342	Sequence 21342, A
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1027	75	2.9	836	4	US-09-252-991A-23513	Sequence 23513, A	1100	74.5	2.8	1809	3	US-09-012-515A-12	Sequence 12, Appl
1028	75	2.9	848	4	US-09-902-540-14707	Sequence 14707, A	1101	74.5	2.8	1809	3	US-08-360-144A-12	Sequence 12, Appl
1029	75	2.9	853	2	US-08-468-558-3	Sequence 3, Appli	1102	74.5	2.8	1809	4	US-09-012-504A-12	Sequence 12, Appl
1030	75	2.9	853	3	US-09-354-129-10	Sequence 10, Appl	1103	74.5	2.8	1809	4	US-09-012-399A-12	Sequence 12, Appl
1031	75	2.9	853	3	US-08-676-444-3	Sequence 3, Appli	1104	74.5	2.8	1822	4	US-09-949-016-7999	Sequence 7999, Ap
1032	75	2.9	853	4	US-09-504-357-10	Sequence 10, Appl	1105	74.5	2.8	2172	1	US-08-611-107-31	Sequence 31, Appl
1033	75	2.9	878	4	US-09-489-039A-13174	Sequence 13174, A	1106	74.5	2.8	2549	3	US-08-471-112A-3	Sequence 3, Appli
1034	75	2.9	882	4	US-09-252-991A-24619	Sequence 24619, A	1107	74.5	2.8	2549	4	US-09-950-634-3	Sequence 3, Appli
1035	75	2.9	926	4	US-09-252-991A-31053	Sequence 31053, A	1108	74.5	2.8	2549	4	US-09-538-092-1112	Sequence 1112, Ap
1036	75	2.9	942	1	US-08-141-324-14	Sequence 14, Appl	1109	74.5	2.8	2549	5	PCT-US95-06722-12	Sequence 12, Appl
1037	75	2.9	942	1	US-08-541-902-14	Sequence 14, Appl	1110	74.5	2.8	4866	4	US-09-424-783-2	Sequence 2, Appli
1038	75	2.9	944	4	US-09-949-016-6650	Sequence 6650, Ap	1111	74	2.8	173	4	US-09-853-832-16	Sequence 16, Appl
1039	75	2.9	987	4	US-09-540-236-3017	Sequence 3017, Ap	1112	74	2.8	173	4	US-10-300-818-16	Sequence 16, Appl
1040	75	2.9	988	4	US-09-252-991A-29699	Sequence 29699, A	1113	74	2.8	181	4	US-09-710-279-86	Sequence 86, Appl
1041	75	2.9	1044	4	US-09-893-371A-1	Sequence 1, Appli	1114	74	2.8	182	3	US-09-134-001C-3742	Sequence 3742, Ap
1042	75	2.9	1112	2	US-08-714-402-2	Sequence 2, Appli	1115	74	2.8	201	4	US-09-710-279-1514	Sequence 1514, Ap
1043	75	2.9	1160	4	US-09-328-352-6457	Sequence 6457, Ap	1116	74	2.8	206	3	US-08-705-245-13	Sequence 13, Appl
1044	75	2.9	1211	4	US-09-491-522-5	Sequence 5, Appli	1117	74	2.8	206	4	US-09-490-714-13	Sequence 13, Appl
1045	75	2.9	1211	4	US-09-949-016-11401	Sequence 11401, A	1118	74	2.8	243	4	US-09-902-540-15036	Sequence 15036, A
1046	75	2.9	1711	3	US-08-369-822C-10	Sequence 10, Appl	1119	74	2.8	246	4	US-09-902-540-15999	Sequence 15999, A
1047	75	2.9	1711	3	US-08-582-776C-10	Sequence 10, Appl	1120	74	2.8	295	4	US-09-461-325-193	Sequence 193, App
1048	75	2.9	1711	3	US-08-434-831B-10	Sequence 10, Appl	1121	74	2.8	295	4	US-10-012-542-193	Sequence 193, App
1049	75	2.9	3072	3	US-09-413-814-93	Sequence 93, Appl	1122	74	2.8	295	4	US-10-115-123-193	Sequence 193, App



1123	74	2.8	325	3	US-09-194-905-11	Sequence 11, Appl	1196	74	2.8	2470	4	US-08-305-790B-3	Sequence 3, Appli
1124	74	2.8	325	4	US-09-922-683-11	Sequence 11, Appl	1197	74	2.8	3290	4	US-09-328-352-5486	Sequence 5486, Ap
1125	74	2.8	328	4	US-09-583-110-4551	Sequence 4551, Ap	1198	73.5	2.8	133	1	US-07-846-992-3	Sequence 3, Appli
1126	74	2.8	339	4	US-09-252-991A-20854	Sequence 20854, A	1199	73.5	2.8	133	1	US-08-469-555-3	Sequence 3, Appli
1127	74	2.8	358	4	US-09-328-352-7641	Sequence 7641, Ap	1200	73.5	2.8	225	4	US-09-134-000C-6465	Sequence 6465, Ap
1128	74	2.8	361	4	US-09-543-681A-7025	Sequence 7025, Ap	1201	73.5	2.8	274	4	US-09-252-991A-23361	Sequence 23361, A
1129	74	2.8	367	3	US-08-860-368B-2	Sequence 2, Appli	1202	73.5	2.8	313	4	US-09-902-540-14967	Sequence 14967, A
1130	74	2.8	394	4	US-09-252-991A-19674	Sequence 19674, A	1203	73.5	2.8	333	4	US-09-120-051D-41	Sequence 41, Appl
1131	74	2.8	395	3	US-09-134-001C-3723	Sequence 3723, Ap	1204	73.5	2.8	333	4	US-09-120-051D-59	Sequence 59, Appl
1132	74	2.8	418	4	US-09-328-352-4525	Sequence 4525, Ap	1205	73.5	2.8	334	4	US-09-252-991A-22395	Sequence 22395, A
1133	74	2.8	428	4	US-09-949-016-9739	Sequence 9739, Ap	1206	73.5	2.8	353	4	US-09-120-051D-2	Sequence 2, Appli
1134	74	2.8	430	4	US-09-792-420-2	Sequence 2, Appli	1207	73.5	2.8	367	2	US-08-515-251A-4	Sequence 4, Appli
1135	74	2.8	432	4	US-09-902-540-15774	Sequence 15774, A	1208	73.5	2.8	372	3	US-08-998-416-4	Sequence 4, Appli
1136	74	2.8	441	3	US-09-052-778-14	Sequence 14, Appl	1209	73.5	2.8	375	3	US-09-171-337A-7	Sequence 7, Appli
1137	74	2.8	443	4	US-09-949-016-6420	Sequence 6420, Ap	1210	73.5	2.8	375	4	US-09-631-022-7	Sequence 7, Appli
1138	74	2.8	444	3	US-09-271-608-8	Sequence 8, Appli	1211	73.5	2.8	379	4	US-09-724-797-54	Sequence 54, Appl
1139	74	2.8	444	3	US-09-695-950-8	Sequence 8, Appli	1212	73.5	2.8	389	4	US-09-902-540-12890	Sequence 12890, A
1140	74	2.8	444	3	US-09-696-147-8	Sequence 8, Appli	1213	73.5	2.8	393	3	US-09-242-859A-13	Sequence 13, Appl
1141	74	2.8	444	3	US-09-696-364-8	Sequence 8, Appli	1214	73.5	2.8	393	3	US-09-583-110-3040	Sequence 3040, Ap
1142	74	2.8	449	4	US-09-270-767-57465	Sequence 57465, A	1215	73.5	2.8	407	4	US-09-107-433-3199	Sequence 3199, Ap
1143	74	2.8	455	4	US-09-134-000C-6074	Sequence 6074, Ap	1216	73.5	2.8	408	4	US-09-423-439-10	Sequence 10, Appl
1144	74	2.8	458	4	US-09-407-062-9	Sequence 9, Appli	1217	73.5	2.8	412	3	US-09-958-548-1	Sequence 1, Appli
1145	74	2.8	478	4	US-09-489-039A-7300	Sequence 7300, Ap	1218	73.5	2.8	437	4	US-09-248-796A-18684	Sequence 18684, A
1146	74	2.8	490	4	US-09-902-540-10306	Sequence 10306, A	1219	73.5	2.8	441	4	US-09-107-532A-5054	Sequence 5054, Ap
1147	74	2.8	493	4	US-08-657-749D-2	Sequence 2, Appli	1220	73.5	2.8	442	4	US-09-489-039A-10439	Sequence 10439, A
1148	74	2.8	495	4	US-09-991-552-20	Sequence 20, Appl	1221	73.5	2.8	446	4	US-09-902-540-12791	Sequence 12791, A
1149	74	2.8	498	3	US-09-232-468A-24	Sequence 24, Appl	1222	73.5	2.8	451	4	US-09-417-251A-18	Sequence 18, Appl
1150	74	2.8	498	4	US-09-784-984B-54	Sequence 54, Appl	1223	73.5	2.8	455	3	US-09-036-987A-17	Sequence 17, Appl
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1152	74	2.8	541	4	US-09-328-352-7237	Sequence 7237, Ap	1225	73.5	2.8	455	4	US-09-603-207-17	Sequence 17, Appl
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1154	74	2.8	566	4	US-09-491-522-7	Sequence 7, Appli	1227	73.5	2.8	493	4	US-09-949-016-5911	Sequence 5911, Ap
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1157	74	2.8	591	4	US-09-252-991A-26716	Sequence 26716, A	1230	73.5	2.8	515	3	US-08-582-776C-38	Sequence 38, Appl
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US-09-438-185A-981  
; Sequence 981, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 981  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPn0980  
US-09-438-185A-981

Query Match 17.2%; Score 451.5; DB 4; Length 495;  
Best Local Similarity 27.0%; Pred. No. 2.1e-35;  
Matches 137; Conservative 91; Mismatches 203; Indels 77; Gaps 15;  
QY 24 MFSSPSPPPALLEKVQYIDLHQDEFVQTLKEWVAI-----ESDSVQVPVPRFQELFRMM 78  
Db 31 IFNCSGKPMNLD--KHFDINSANFLEEFKFIFFPSISADSDDLQDCENCAHFL---- 84

QY 79 AVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEELGS-DPTKGTVCYGHLDVQP 137  
Db 85 ---VDHVNKI-----FDVELWETPGH-----PPIIYASYKSEDLPTSLMLYNYHDVQP 130  
QY 138 ADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKPIIEG 197  
Db 131 AQLSDGWKGDPPFILREENGNLARGASDNKGQCFTYTKALQHYYESQGNFPLNIWLIEG 190  
QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD 257  
Db 191 EEESGSLALFTWLEKKKEAL--RADYLLIVDGGFLSEKHYPYVSIGARGIVSMKISLEEGN 248  
QY 258 QDFHSGTGGILHEPMAIDLALLGSLVDSSGHILVPGIYDEV-VPLTEEEINTYKAHLD 316  
Db 249 KDMHSGVLGGIAYNTNRALSEILSSLHHPDNSIAIEGFYDDIALPSDSDRPDLPKSDTLR 308  
QY 317 LEEYRNSSRVEKF--LFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS 374  
Db 309 ECEENLGFRPQGYEASYSPEESALR-----PTVEINGISGGYTGPGFKTVIPYRATAYLS 363  
QY 375 IRLVPHMNVSAVEKQVTRHLED-----VFSK-----RNSSNMVVSMTLGLHPW 418  
Db 364 CRLVPNQDPDKAAHQVHHHLKQQVPSSLKFSYEILPGGSRGWRSSANLPIVKVLQEIYSD 423  
QY 419 IANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDGGEH 478  
Db 424 LYN-----EECLRLVM-----PATIPIGLLGEAAQTSPICGTSYLSDDIH 465  
QY 479 SQNEKINRWNYIEGTKLFAAFFLEMAQL 506  
Db 466 AAEHFMSMDQLKKG-----FLSICQL 486

RESULT 6  
US-09-583-110-4829  
; Sequence 4829, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 4829  
; LENGTH: 457  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-4829

Query Match 16.5%; Score 432.5; DB 4; Length 457;  
Best Local Similarity 29.2%; Pred. No. 1.4e-33;  
Matches 138; Conservative 75; Mismatches 181; Indels 79; Gaps 17;  
QY 45 HQDEFVQTL--KEWVAIESDSVQVPVPRFQELFRMMAVAADTLQRLGARVASVDMGPPQL 102  
Db 21 HYFEVLRTLISKSVFAQQVGLKEVANYLGEIFK-----RVGAEV-EID----- 63

QY 103 PDGQSLPIPPVILAEELGS-DPTKGTVCYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGRG 162  
Db 64 ---ESYTAPFVMAHFKSSRPDAKTLIFYNHYDVTVPADGDQVWTEDPFTLSVRNGFMYGRG 120  
QY 163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKPIIEGMEEAGSVALEELVEKEKDRFFSGVD 222  
Db 121 VDDDKGHITARLSALRKYMQHDDLPVNISFIMEGAEESASTDLDKYLEKHADK-LHGAD 179

QY 223 YIVISDNLWISQRKPA-----ITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLV 277  
Db 180 LLV-----WEQGTKNALEQLEISGNGKGI VTFDAKVKSAADVDIHS-SYGGVVESAPWYLL 233  
QY 278 ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEY--RNSSRVEKF-----LF 331  
Db 234 QALQSLRAADGRILVEGLYEEVHEPNEREMAL-----LETYQORNPEEVSRIYGLELP 286  
QY 332 DTKEEILMHLWRY---PSLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEK 388  
Db 287 LLQEERMAFLKRFFFEPALNIEGIQSGYQGQGVKTLPAEASAKLEVRLVPGLEPHDVLE 346  
QY 389 QVTRHLEDVFSKRNSNMVVSMTLG-----LHPWIANIDDTQ---YLAAKRAIRTV 437  
Db 347 KIRKQLD-----KNGFDKVELYVTLGEMSYRSDMSAPAILNVIELAKKFYPQGVSVLPTT 401  
QY 438 FGTEP-DMIRDGSTIPIAKMFQEIIVHKSVMVLIPLGAVDDGEHSQNEKINRWNY 489  
Db 402 AGTGMHTVFDALVP-----MVAFLGNANSRDRDHGGENVRIADY 442

RESULT 7  
US-09-198-452A-1054  
; Sequence 1054, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection and treatment of infection  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1054  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-1054

Query Match 16.3%; Score 428; DB 4; Length 393;  
Best Local Similarity 29.9%; Pred. No. 2.9e-33;  
Matches 114; Conservative 73; Mismatches 158; Indels 36; Gaps 10;  
QY 24 MFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI-----ESDSVQVPVPRFRQELFRMM 78  
Db 29 IFNCSGKPMNLDs--KHFDINSANFLBEFAKFSIFSPSISADSDHLQDCENCAHFL---- 82  
QY 79 AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS-DPTKGTVCYFGHLDVQP 137  
Db 83 ---VDHVNKI-----FDVELWETPGH-----PPIIYASYKSEDP LSLTMLNYHYDVQP 128  
QY 138 ADRGDGWLTDPPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLFPVNIKFIIEG 197  
Db 129 AQLSDGWKGDPPFILREENGNYARGASDNKGQC FYTLKALQHYYESQGNFPLNIILWIEG 188  
QY 198 MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD 257  
Db 189 EEESGSLALFTWLEKKKEAL--RADYLLIVDGGFLSEKHPYVSGARGIVSMKISLEEGN 246  
QY 258 QDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV-VPLTEEEINTYKAHLD 316  
Db 247 KDMHSGVLGGIAYNTNRALSEILSSLHHPDNSAIEGFYDDLALPSDSDRPDLPKSDTLR 306  
QY 317 LEEYRNSSRVEKF--LFDTKEEILMHLWRYP SLSIHGIEGAFDEPGTKTVPGRVIGKFS 374  
Db 307 ECEENLGRFPQGYEASYSPEESALR-----PTVEINGISGGYTGPGFKTVIPYRATAYLS 361  
QY 375 IRLVPHMNVSAVEKQVTRHLE 395  
Db 362 CRLVPNQDPDKAAHQVTHHLK 382

RESULT 8  
US-09-902-540-15643  
; Sequence 15643, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 15643  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-15643

Query Match 15.4%; Score 403; DB 4; Length 466;  
Best Local Similarity 27.5%; Pred. No. 1.1e-30;  
Matches 134; Conservative 85; Mismatches 219; Indels 50; Gaps 13;  
QY 36 EKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTIQRLGARVASV 95  
Db 4 DNALSHFESKKQTVLEDLKSLVRIPSVS---PFGF DATQVRRSAEATARLLK----- 52  
QY 96 DMGPQQLPDGQSLPIP---PVILAE LGS DPTKGTVCYFGHLDVQPADRGDWLTDPYVLT 152  
Db 53 DRGFENV---QLLEIEGTHPYVYGEVLKAPGKPTLLLYAHHDVQAPAGDEAAWKSPPFEPV 109  
QY 153 EVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLFPVNIKFIIEGMEEAGSVALEELVEK 212  
Db 110 ERDGRLYGRGSADDKAGIVVHTSAVESWLKGAGALPLNVKVIIEGEEIEGSGFLGAFLOE 169  
QY 213 EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEP 272  
Db 170 H--AALLKADAIVLTDTSNFD TGLPSIT TALLRGLVTVDVEVRALRQAVHSGMWGGPVDPD 227  
QY 273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSRV---EKF 329  
Db 228 VMALCRMLATLTHADGSAIEGIRERVKPLTDGERQSIESLPGDEAHFRAQSGLLPGAQV 287  
QY 330 LFDTKEEILMHLWRYP SLSIHGIEGAFDEPGTKTVPGRVIGKFSIRLVPHMNVSAVEKQ 389  
Db 288 LGGAHPWEMN-WRQPSIAINAIQ-ASSRKOARNIICDSAWARVGIRIVPDL EARDVEQR 345  
QY 390 VTRHLEDV-----FSKRNSNMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTE 441  
Db 346 LKEHLRKVCPWGLEVHFDTEGASGW-----WYDPSHPAFQAFAFRALEKGYGTK 394  
QY 442 PDMIRDGSTIPIAKMF-QEIVHKSVMVLIPLGAVDDG---EHSQNEKINRWNYIEGTKLFA 497  
Db 395 AVAICCGASIPFVEPFAKELGGVPALLI---GVEDPYTYAHSENESLHLDGWEKSIRSAI 451  
QY 498 AFFLEMAQ 505  
Db 452 HLYAELAE 459

RESULT 9  
US-09-248-796A-14559  
; Sequence 14559, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A





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; Patent NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5702
; LENGTH: 98
; TYPE: PRT

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;	PRIOR FILING DATE:	1999-06-25	
;	PRIOR APPLICATION NUMBER:	DE 19931636.8	
;	PRIOR FILING DATE:	1999-07-08	
;	PRIOR APPLICATION NUMBER:	DE 19932125.6	
;	PRIOR FILING DATE:	1999-07-09	
;	PRIOR APPLICATION NUMBER:	DE 19932126.4	
;	PRIOR FILING DATE:	1999-07-09	
;	PRIOR APPLICATION NUMBER:	DE 19932127.2	
;	PRIOR FILING DATE:	1999-07-09	
;	PRIOR APPLICATION NUMBER:	DE 19932128.0	
;	PRIOR FILING DATE:	1999-07-09	
;	PRIOR APPLICATION NUMBER:	DE 19932129.9	
;	PRIOR FILING DATE:	1999-07-19	
;	PRIOR APPLICATION NUMBER:	DE 19932226.0	
;	PRIOR FILING DATE:	1999-07-09	
;	PRIOR APPLICATION NUMBER:	DE 19932920.6	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932922.2	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932924.9	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932928.1	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932930.3	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932933.8	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932935.4	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19932973.7	
;	PRIOR FILING DATE:	1999-07-14	
;	PRIOR APPLICATION NUMBER:	DE 19933002.6	
;	PRIOR FILING DATE:	1999-07-14	

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; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 192
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-192

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Query Match	9.2%	Score 242.5;	DB 4;	Length 267;
Best Local Similarity	29.7%;	Pred. No. 2.7e-15;		
Matches 79;	Conservative 37;	Mismatches 113;	Indels 37;	Gaps 7;
QY 42	IDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPOQ	101		
Db	14 IENQREQIFTQLKEIVSF--NSVHSDPNLLEDYAGAKEWKETLTNAGLTVSE-----64			
QY 102	LPDGQSLPIPPVILAEGLSDPTKGT-----VCFYGHLDVQPADRGDGLTDPYVLT	152		
Db 65	-----FAAEDGTNFIGTRKSGEAPKVLLYSHFDVVPSPGLDLWDTNPFELT	112		
QY 153	EVDG----KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNKIFIIEGMEEAGSVALEE	208		
Db 113	ERDAGHGTRWYGRGAADCKGNLVMHLAALRAVEA-SGDTTLNLTYYVEGSEEMGGGALSA	171		
QY 209	LVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI	268		
Db 172	LI-KDKPELFD-ADVILIADSGNASVGTPTLTTLTLLRGGGQVTVTDTLEGAVHSGQNGGA	229		
QY 269	LHEPMADLVALLGSLVDSSGHILVPG	294		
Db 230	APDAVAALVRVLDTLFDEHGRTVIDG	255		

RESULT 15  
 US-09-602-777A-194  
 ; Sequence 194, Application US/09602777A  
 ; Patent No. 6831165  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 ; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION  
 ; FILE REFERENCE: BGI-128CP  
 ; CURRENT APPLICATION NUMBER: US/09/602,777A  
 ; CURRENT FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: US 60/141031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: DE 19931636.8  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19932125.6  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932126.4  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932127.2  
 ; PRIOR FILING DATE: 1999-07-09

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; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
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; PRIOR FILING DATE: 1999-07-14
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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 194
; LENGTH: 231
; TYPE: prt
; ORGANISM: Corynebacterium glutamicum
; US-09-602-777A-194

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	Query Match	8.9%;	Score 233;	DB 4;	Length 231;
	Best Local Similarity	34.9%;	Pred. No. 1.8e-14;		
	Matches 67;	Conservative 27;	Mismatches 82;	Indels 16;	Gaps 5;
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Db	31 AEDGTTNFIGTRKGSEGA PKVLLYSHFDVVPSGPLDLWDTNPFELTERDAGHGTRWYGRG	90			
QY	163 ATDNKGPVLAWINAVSAFRALEQDLPVN KFIIEGMEEAGSVALEELVEKEKD RFFSGVD	222			
Db	91 AADCKGNLVHMLAALRAVEA-SGD TTTLNLTYVVGSEEMGGALSALI-KDKPEI,FD-AD	147			
QY	223 YIVISDNLWTISQRKPATITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGS	282			
Db	148 VILIADSGNASVGTPTLTTLT LRRGGGVQTVTVTILEGAVHSGONGGAAPDAVALVRVLD T	207			
QY	283 LVDSSGHILVPG	294			
Db	208 LRDEHGRTVIDG	219			

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OM protein - protein search, using sw model

Run on: February 8, 2005, 23:26:50 ; Search time 56 Seconds  
(without alignments)  
2948.770 Million cell updates/sec

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Perfect score: 507  
Sequence: 1 MDPKLGMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 507

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1373511 seqs, 325702437 residues

Word size : 6

Total number of hits satisfying chosen parameters: 16357

Minimum DB seq length: 0  
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Post-processing: Listing first 1500 summaries

Database : Published Applications AA:\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	507	100.0	507	9	US-09-963-290-2 Sequence 2, Appli
2	507	100.0	507	10	US-09-931-836-57 Sequence 57, Appl
3	507	100.0	507	13	US-10-036-342-57 Sequence 57, Appl
4	507	100.0	507	13	US-10-036-041-57 Sequence 57, Appl
5	507	100.0	507	14	US-10-035-855-57 Sequence 57, Appl
6	507	100.0	507	14	US-10-036-214-57 Sequence 57, Appl
7	507	100.0	507	14	US-10-035-719-57 Sequence 57, Appl
8	507	100.0	507	14	US-10-036-160-57 Sequence 57, Appl
9	507	100.0	507	14	US-10-035-958-57 Sequence 57, Appl
10	507	100.0	507	14	US-10-036-150-57 Sequence 57, Appl
11	507	100.0	507	14	US-10-036-063-57 Sequence 57, Appl
12	507	100.0	507	14	US-10-035-977-57 Sequence 57, Appl
13	507	100.0	507	15	US-10-275-107-68 Sequence 68, Appl

14	492	97.0	508	9	US-09-731-872-242	Sequence 242, App
15	492	97.0	508	10	US-09-948-783-139	Sequence 139, App
16	492	97.0	508	10	US-09-876-997-242	Sequence 242, App
17	492	97.0	509	10	US-09-892-877-137	Sequence 137, App
18	429	84.6	501	9	US-09-791-378-674	Sequence 674, App
19	429	84.6	501	10	US-09-791-393-2	Sequence 2, Appli
20	429	84.6	501	10	US-09-791-389-2	Sequence 2, Appli
21	429	84.6	501	11	US-09-791-377-674	Sequence 674, App
22	235	46.4	508	15	US-10-369-022-54	Sequence 54, Appl
23	110	21.7	133	15	US-10-296-115-1427	Sequence 1427, Ap
24	100	19.7	316	15	US-10-264-237-2057	Sequence 2057, Ap
25	15	3.0	15	9	US-09-791-378-199	Sequence 199, App
26	15	3.0	15	9	US-09-791-378-657	Sequence 657, App
27	15	3.0	15	10	US-09-791-393-297	Sequence 297, App
28	15	3.0	15	10	US-09-791-389-297	Sequence 297, App
29	15	3.0	15	11	US-09-791-377-199	Sequence 199, App
30	15	3.0	15	11	US-09-791-377-657	Sequence 657, App
31	14	2.8	14	9	US-09-791-378-201	Sequence 201, App
32	14	2.8	14	9	US-09-791-378-665	Sequence 665, App
33	14	2.8	14	11	US-09-791-377-201	Sequence 201, App
34	14	2.8	14	11	US-09-791-377-665	Sequence 665, App
35	11	2.2	11	9	US-09-791-378-200	Sequence 200, App
36	11	2.2	11	9	US-09-791-378-202	Sequence 202, App
37	11	2.2	11	9	US-09-791-378-206	Sequence 206, App
38	11	2.2	11	11	US-09-791-377-200	Sequence 200, App
39	11	2.2	11	11	US-09-791-377-202	Sequence 202, App
40	11	2.2	11	11	US-09-791-377-206	Sequence 206, App
41	10	2.0	10	9	US-09-791-378-203	Sequence 203, App
42	10	2.0	10	9	US-09-791-378-667	Sequence 667, App
43	10	2.0	10	10	US-09-791-393-308	Sequence 308, App
44	10	2.0	10	10	US-09-791-389-308	Sequence 308, App
45	10	2.0	10	11	US-09-791-377-203	Sequence 203, App
46	10	2.0	10	11	US-09-791-377-667	Sequence 667, App
47	9	1.8	9	9	US-09-791-378-204	Sequence 204, App
48	9	1.8	9	11	US-09-791-377-204	Sequence 204, App
49	9	1.8	150	15	US-10-243-552-646	Sequence 646, App
50	9	1.8	194	14	US-10-227-884-32	Sequence 32, Appl
51	9	1.8	194	14	US-10-230-163-32	Sequence 32, Appl
52	9	1.8	194	14	US-10-230-338-32	Sequence 32, Appl
53	9	1.8	194	14	US-10-218-631-32	Sequence 32, Appl
54	9	1.8	194	14	US-10-230-414-32	Sequence 32, Appl
55	9	1.8	194	14	US-10-232-224-32	Sequence 32, Appl
56	9	1.8	194	14	US-10-216-159A-32	Sequence 32, Appl
57	9	1.8	194	14	US-10-218-849-32	Sequence 32, Appl
58	9	1.8	194	14	US-10-227-873-32	Sequence 32, Appl
59	9	1.8	194	14	US-10-227-883-32	Sequence 32, Appl
60	9	1.8	194	14	US-10-219-076-32	Sequence 32, Appl
61	9	1.8	194	14	US-10-230-434-32	Sequence 32, Appl
62	9	1.8	194	14	US-10-219-003-32	Sequence 32, Appl
63	9	1.8	194	14	US-10-219-075-32	Sequence 32, Appl
64	9	1.8	194	14	US-10-219-464-32	Sequence 32, Appl
65	9	1.8	194	14	US-10-219-466-32	Sequence 32, Appl
66	9	1.8	194	14	US-10-219-479-32	Sequence 32, Appl
67	9	1.8	194	14	US-10-219-481-32	Sequence 32, Appl
68	9	1.8	194	14	US-10-230-260-32	Sequence 32, Appl
69	9	1.8	194	14	US-10-232-231-32	Sequence 32, Appl
70	9	1.8	194	14	US-10-232-233-32	Sequence 32, Appl
71	9	1.8	194	14	US-10-216-165-32	Sequence 32, Appl
72	9	1.8	194	14	US-10-218-956-32	Sequence 32, Appl
73	9	1.8	194	14	US-10-219-468-32	Sequence 32, Appl
74	9	1.8	194	14	US-10-219-478-32	Sequence 32, Appl
75	9	1.8	194	14	US-10-219-536-32	Sequence 32, Appl
76	9	1.8	194	14	US-10-233-205-32	Sequence 32, Appl
77	9	1.8	194	14	US-10-219-072-32	Sequence 32, Appl
78	9	1.8	194	14	US-10-219-470-32	Sequence 32, Appl
79	9	1.8	194	14	US-10-219-474-32	Sequence 32, Appl
80	9	1.8	194	14	US-10-219-524-32	Sequence 32, Appl
81	9	1.8	194	14	US-10-219-528-32	Sequence 32, Appl
82	9	1.8	194	14	US-10-227-880-32	Sequence 32, Appl
83	9	1.8	194	14	US-10-227-881-32	Sequence 32, Appl
84	9	1.8	194	14	US-10-227-882-32	Sequence 32, Appl
85	9	1.8	194	14	US-10-230-436-32	Sequence 32, Appl
86	9	1.8	194	14	US-10-232-223-32	Sequence 32, Appl

87	9	1.8	194	14	US-10-232-225-32	Sequence 32, Appl	160	9	1.8	476	14	US-10-073-885-103	Sequence 103, App
88	9	1.8	194	14	US-10-232-227-32	Sequence 32, Appl	161	8	1.6	8	9	US-09-791-378-205	Sequence 205, App
89	9	1.8	194	14	US-10-232-229-32	Sequence 32, Appl	162	8	1.6	8	9	US-09-791-378-207	Sequence 207, App
90	9	1.8	194	14	US-10-232-234-32	Sequence 32, Appl	163	8	1.6	8	9	US-09-791-378-208	Sequence 208, App
91	9	1.8	194	14	US-10-219-060-32	Sequence 32, Appl	164	8	1.6	8	10	US-09-791-393-298	Sequence 298, App
92	9	1.8	194	14	US-10-216-160-32	Sequence 32, Appl	165	8	1.6	8	10	US-09-791-389-298	Sequence 298, App
93	9	1.8	194	14	US-10-216-162-32	Sequence 32, Appl	166	8	1.6	8	11	US-09-791-377-205	Sequence 205, App
94	9	1.8	194	14	US-10-216-164-32	Sequence 32, Appl	167	8	1.6	8	11	US-09-791-377-207	Sequence 207, App
95	9	1.8	194	14	US-10-216-167-32	Sequence 32, Appl	168	8	1.6	8	11	US-09-791-377-208	Sequence 208, App
96	9	1.8	194	14	US-10-216-168-32	Sequence 32, Appl	169	8	1.6	16	14	US-10-350-470-4	Sequence 4, Appli
97	9	1.8	194	14	US-10-219-065-32	Sequence 32, Appl	170	8	1.6	22	10	US-09-876-904A-6	Sequence 6, Appli
98	9	1.8	194	14	US-10-219-071-32	Sequence 32, Appl	171	8	1.6	90	16	US-10-437-963-108300	Sequence 108300,
99	9	1.8	194	14	US-10-219-074-32	Sequence 32, Appl	172	8	1.6	95	16	US-10-437-963-173348	Sequence 173348,
100	9	1.8	194	14	US-10-219-077-32	Sequence 32, Appl	173	8	1.6	103	16	US-10-437-963-178801	Sequence 178801,
101	9	1.8	194	14	US-10-219-465-32	Sequence 32, Appl	174	8	1.6	103	15	US-10-424-599-220596	Sequence 220596,
102	9	1.8	194	14	US-10-219-467-32	Sequence 32, Appl	175	8	1.6	135	16	US-10-437-963-193036	Sequence 193036,
103	9	1.8	194	14	US-10-219-469-32	Sequence 32, Appl	176	8	1.6	166	9	US-09-745-003-8	Sequence 8, Appli
104	9	1.8	194	14	US-10-219-471-32	Sequence 32, Appl	177	8	1.6	175	16	US-10-437-963-131258	Sequence 131258,
105	9	1.8	194	14	US-10-219-473-32	Sequence 32, Appl	178	8	1.6	180	16	US-10-437-963-189526	Sequence 189526,
106	9	1.8	194	14	US-10-219-476-32	Sequence 32, Appl	179	8	1.6	204	16	US-10-767-701-37239	Sequence 37239, A
107	9	1.8	194	14	US-10-219-482-32	Sequence 32, Appl	180	8	1.6	229	15	US-10-425-114-51019	Sequence 51019, A
108	9	1.8	194	14	US-10-227-874-32	Sequence 32, Appl	181	8	1.6	234	15	US-10-282-122A-68549	Sequence 68549, A
109	9	1.8	194	14	US-10-227-876-32	Sequence 32, Appl	182	8	1.6	239	15	US-10-425-114-63663	Sequence 63663, A
110	9	1.8	194	14	US-10-227-878-32	Sequence 32, Appl	183	8	1.6	239	15	US-10-425-114-65677	Sequence 65677, A
111	9	1.8	194	14	US-10-229-974-32	Sequence 32, Appl	184	8	1.6	240	16	US-10-437-963-144973	Sequence 144973,
112	9	1.8	194	14	US-10-230-024-32	Sequence 32, Appl	185	8	1.6	246	16	US-10-767-701-43184	Sequence 43184, A
113	9	1.8	194	14	US-10-230-113-32	Sequence 32, Appl	186	8	1.6	270	16	US-10-437-963-149279	Sequence 149279,
114	9	1.8	194	14	US-10-230-183-32	Sequence 32, Appl	187	8	1.6	273	15	US-10-346-190-86	Sequence 86, Appl
115	9	1.8	194	14	US-10-230-234-32	Sequence 32, Appl	188	8	1.6	273	15	US-10-425-114-55081	Sequence 55081, A
116	9	1.8	194	14	US-10-230-306-32	Sequence 32, Appl	189	8	1.6	274	16	US-10-437-963-199008	Sequence 199008,
117	9	1.8	194	14	US-10-230-426-32	Sequence 32, Appl	190	8	1.6	277	14	US-10-304-630-34	Sequence 34, Appl
118	9	1.8	194	14	US-10-230-427-32	Sequence 32, Appl	191	8	1.6	285	16	US-10-437-963-153979	Sequence 153979,
119	9	1.8	194	14	US-10-230-433-32	Sequence 32, Appl	192	8	1.6	307	16	US-10-437-963-135131	Sequence 135131,
120	9	1.8	194	14	US-10-230-435-32	Sequence 32, Appl	193	8	1.6	317	15	US-10-301-533-50	Sequence 50, Appl
121	9	1.8	194	14	US-10-230-438-32	Sequence 32, Appl	194	8	1.6	317	15	US-10-301-533-51	Sequence 51, Appl
122	9	1.8	194	14	US-10-232-222-32	Sequence 32, Appl	195	8	1.6	317	15	US-10-282-122A-74871	Sequence 74871, A
123	9	1.8	194	14	US-10-219-070-32	Sequence 32, Appl	196	8	1.6	317	15	US-10-282-122A-75433	Sequence 75433, A
124	9	1.8	194	14	US-10-219-472-32	Sequence 32, Appl	197	8	1.6	327	15	US-10-301-533-8	Sequence 8, Appli
125	9	1.8	194	14	US-10-219-527-32	Sequence 32, Appl	198	8	1.6	340	15	US-10-301-533-4	Sequence 4, Appli
126	9	1.8	194	14	US-10-227-877-32	Sequence 32, Appl	199	8	1.6	340	15	US-10-301-533-10	Sequence 10, Appl
127	9	1.8	194	14	US-10-216-166-32	Sequence 32, Appl	200	8	1.6	340	16	US-10-437-963-139474	Sequence 139474,
128	9	1.8	194	14	US-10-218-612-32	Sequence 32, Appl	201	8	1.6	346	16	US-10-437-963-184670	Sequence 184670,
129	9	1.8	194	14	US-10-216-163-32	Sequence 32, Appl	202	8	1.6	373	16	US-10-437-963-149274	Sequence 149274,
130	9	1.8	194	14	US-10-218-765-32	Sequence 32, Appl	203	8	1.6	377	16	US-10-437-963-189528	Sequence 189528,
131	9	1.8	194	14	US-10-219-063-32	Sequence 32, Appl	204	8	1.6	384	15	US-10-365-620-44	Sequence 44, Appl
132	9	1.8	194	14	US-10-219-066-32	Sequence 32, Appl	205	8	1.6	384	17	US-10-912-969-50	Sequence 50, Appl
133	9	1.8	194	14	US-10-219-067-32	Sequence 32, Appl	206	8	1.6	418	16	US-10-437-963-114991	Sequence 114991,
134	9	1.8	194	14	US-10-219-068-32	Sequence 32, Appl	207	8	1.6	420	17	US-10-18-939-64	Sequence 64, Appl
135	9	1.8	194	14	US-10-219-069-32	Sequence 32, Appl	208	8	1.6	453	15	US-10-282-122A-53370	Sequence 53370, A
136	9	1.8	194	14	US-10-219-073-32	Sequence 32, Appl	209	8	1.6	463	15	US-10-369-493-675	Sequence 675, App
137	9	1.8	194	14	US-10-219-475-32	Sequence 32, Appl	210	8	1.6	488	15	US-10-424-599-254994	Sequence 254994,
138	9	1.8	194	14	US-10-219-480-32	Sequence 32, Appl	211	8	1.6	516	15	US-10-369-493-12366	Sequence 12366, A
139	9	1.8	194	14	US-10-219-483-32	Sequence 32, Appl	212	8	1.6	522	15	US-10-369-493-6177	Sequence 6177, Ap
140	9	1.8	194	14	US-10-219-525-32	Sequence 32, Appl	213	8	1.6	556	17	US-10-473-451-5	Sequence 5, Appli
141	9	1.8	194	14	US-10-219-526-32	Sequence 32, Appl	214	8	1.6	557	15	US-10-399-645-12	Sequence 12, Appl
142	9	1.8	194	14	US-10-219-530-32	Sequence 32, Appl	215	8	1.6	578	9	US-09-888-615-100	Sequence 100, App
143	9	1.8	194	14	US-10-219-531-32	Sequence 32, Appl	216	8	1.6	608	17	US-10-912-969-48	Sequence 48, Appl
144	9	1.8	194	14	US-10-219-532-32	Sequence 32, Appl	217	8	1.6	635	14	US-10-302-840A-6	Sequence 6, Appli
145	9	1.8	194	14	US-10-219-533-32	Sequence 32, Appl	218	8	1.6	762	16	US-10-437-963-119029	Sequence 119029,
146	9	1.8	194	14	US-10-230-437-32	Sequence 32, Appl	219	8	1.6	762	16	US-10-437-963-122020	Sequence 122020,
147	9	1.8	194	14	US-10-232-228-32	Sequence 32, Appl	220	8	1.6	768	16	US-10-437-963-118770	Sequence 118770,
148	9	1.8	194	15	US-10-232-226-32	Sequence 32, Appl	221	8	1.6	776	16	US-10-437-963-115826	Sequence 115826,
149	9	1.8	194	15	US-10-230-130-32	Sequence 32, Appl	222	8	1.6	782	15	US-10-258-951-57	Sequence 57, Appl
150	9	1.8	194	15	US-10-230-130-32	Sequence 32, Appl	223	8	1.6	844	15	US-10-258-951-56	Sequence 56, Appl
151	9	1.8	194	15	US-10-232-230-32	Sequence 32, Appl	224	8	1.6	855	16	US-10-437-963-160767	Sequence 160767,
152	9	1.8	194	15	US-10-119-480-32	Sequence 32, Appl	225	8	1.6	878	10	US-09-826-509-347	Sequence 347, App
153	9	1.8	203	15	US-10-138-588-92	Sequence 32, Appl	226	8	1.6	878	17	US-10-925-095-347	Sequence 347, App
154	9	1.8	286	14	US-10-073-885-78	Sequence 78, Appl	227	8	1.6	881	15	US-10-085-198-14	Sequence 14, Appl
155	9	1.8	293	9	US-09-764-864-920	Sequence 920, App	228	8	1.6	906	16	US-10-408-765A-2342	Sequence 2342, Ap
156	9	1.8	308	15	US-10-425-114-64882	Sequence 64882, A	229	8	1.6	1194	14	US-10-225-567A-170	Sequence 170, App
157	9	1.8	475	15	US-10-220-381-18	Sequence 18, Appl	230	8	1.6	1194	16	US-10-722-357-14	Sequence 14, Appl
158	9	1.8	475	15	US-10-275-107-70	Sequence 70, Appl	231	8	1.6	1356	15	US-10-440-464-101	Sequence 101, App
159	9	1.8	476	9	US-09-925-301-1397	Sequence 1397, Ap	232	7	1.4	15	14	US-10-161-791-428	Sequence 428, App



233	7	1.4	15	14	US-10-161-791-429	Sequence 429, App	306	7	1.4	115	9	US-09-989-735-95	Sequence 95, Appl
234	7	1.4	20	15	US-10-352-272-5	Sequence 5, Appli	307	7	1.4	115	9	US-09-990-444-95	Sequence 95, Appl
235	7	1.4	20	16	US-10-398-932-50	Sequence 50, Appl	308	7	1.4	115	9	US-09-991-181-95	Sequence 95, Appl
236	7	1.4	24	14	US-10-159-339-13	Sequence 13, Appl	309	7	1.4	115	9	US-09-989-730-95	Sequence 95, Appl
237	7	1.4	25	15	US-10-649-413-1	Sequence 1, Appli	310	7	1.4	115	9	US-09-990-436-95	Sequence 95, Appl
238	7	1.4	25	15	US-10-649-413-2	Sequence 2, Appli	311	7	1.4	115	9	US-09-993-687-95	Sequence 95, Appl
239	7	1.4	44	15	US-10-424-599-266734	Sequence 266734,	312	7	1.4	115	10	US-09-989-734-95	Sequence 95, Appl
240	7	1.4	50	10	US-09-933-767-498	Sequence 498, App	313	7	1.4	115	10	US-09-997-653-95	Sequence 95, Appl
241	7	1.4	50	14	US-10-004-860-498	Sequence 498, App	314	7	1.4	115	10	US-09-989-724-95	Sequence 95, Appl
242	7	1.4	50	14	US-10-023-282-498	Sequence 498, App	315	7	1.4	115	10	US-09-989-728-95	Sequence 95, Appl
243	7	1.4	51	16	US-10-437-963-162798	Sequence 162798,	316	7	1.4	115	10	US-09-990-441-95	Sequence 95, Appl
244	7	1.4	55	15	US-10-653-595-116	Sequence 116, App	317	7	1.4	115	10	US-09-993-667-95	Sequence 95, Appl
245	7	1.4	56	10	US-09-397-945-116	Sequence 116, App	318	7	1.4	115	10	US-09-997-428-95	Sequence 95, Appl
246	7	1.4	59	15	US-10-424-599-209780	Sequence 209780,	319	7	1.4	115	10	US-09-997-666-95	Sequence 95, Appl
247	7	1.4	60	15	US-10-424-599-168465	Sequence 168465,	320	7	1.4	115	10	US-09-990-438-95	Sequence 95, Appl
248	7	1.4	65	15	US-10-424-599-179475	Sequence 179475,	321	7	1.4	115	10	US-09-990-562-95	Sequence 95, Appl
249	7	1.4	68	9	US-09-738-626-6024	Sequence 6024, Ap	322	7	1.4	115	10	US-09-990-711-95	Sequence 95, Appl
250	7	1.4	70	15	US-10-424-599-260359	Sequence 260359,	323	7	1.4	115	10	US-09-989-726-95	Sequence 95, Appl
251	7	1.4	72	15	US-10-424-599-231670	Sequence 231670,	324	7	1.4	115	10	US-09-998-156-95	Sequence 95, Appl
252	7	1.4	74	16	US-10-767-701-43250	Sequence 43250, A	325	7	1.4	115	10	US-09-990-437-95	Sequence 95, Appl
253	7	1.4	75	8	US-08-424-550B-407	Sequence 407, App	326	7	1.4	115	10	US-09-991-157-95	Sequence 95, Appl
254	7	1.4	78	14	US-10-178-213-278	Sequence 278, App	327	7	1.4	115	10	US-09-997-514-95	Sequence 95, Appl
255	7	1.4	78	16	US-10-767-701-46238	Sequence 46238, A	328	7	1.4	115	10	US-09-997-573-95	Sequence 95, Appl
256	7	1.4	78	16	US-10-767-701-46241	Sequence 46241, A	329	7	1.4	115	10	US-09-991-172-95	Sequence 95, Appl
257	7	1.4	79	14	US-10-178-213-468	Sequence 468, App	330	7	1.4	115	10	US-09-990-726-95	Sequence 95, Appl
258	7	1.4	79	16	US-10-767-701-46239	Sequence 46239, A	331	7	1.4	115	10	US-09-997-559-95	Sequence 95, Appl
259	7	1.4	79	16	US-10-767-701-46240	Sequence 46240, A	332	7	1.4	115	10	US-09-997-601-95	Sequence 95, Appl
260	7	1.4	82	14	US-10-178-213-56	Sequence 56, Appl	333	7	1.4	115	10	US-09-990-443-95	Sequence 95, Appl
261	7	1.4	82	14	US-10-029-386-29385	Sequence 29385, A	334	7	1.4	115	10	US-09-991-854-95	Sequence 95, Appl
262	7	1.4	82	15	US-10-424-599-218055	Sequence 218055,	335	7	1.4	115	10	US-09-997-628-95	Sequence 95, Appl
263	7	1.4	82	16	US-10-437-963-112842	Sequence 112842,	336	7	1.4	115	10	US-09-997-683-95	Sequence 95, Appl
264	7	1.4	82	16	US-10-437-963-162080	Sequence 162080,	337	7	1.4	115	10	US-09-989-729A-95	Sequence 95, Appl
265	7	1.4	83	16	US-10-437-963-193058	Sequence 193058,	338	7	1.4	115	10	US-09-997-349-95	Sequence 95, Appl
266	7	1.4	86	15	US-10-424-599-258080	Sequence 258080,	339	7	1.4	115	10	US-09-997-440-95	Sequence 95, Appl
267	7	1.4	88	15	US-10-424-599-143825	Sequence 143825,	340	7	1.4	115	10	US-09-997-857-95	Sequence 95, Appl
268	7	1.4	93	16	US-10-437-963-142709	Sequence 142709,	341	7	1.4	115	10	US-09-993-469-95	Sequence 95, Appl
269	7	1.4	94	15	US-10-424-599-284246	Sequence 284246,	342	7	1.4	115	10	US-09-997-349-95	Sequence 95, Appl
270	7	1.4	96	16	US-10-398-932-33	Sequence 33, Appl	343	7	1.4	115	10	US-09-997-542-95	Sequence 95, Appl
271	7	1.4	97	14	US-10-080-170-394	Sequence 394, App	344	7	1.4	115	10	US-09-993-748-95	Sequence 95, Appl
272	7	1.4	97	16	US-10-080-170-394	Sequence 394, App	345	7	1.4	115	10	US-09-990-439-95	Sequence 95, Appl
273	7	1.4	97	16	US-10-398-932-38	Sequence 38, Appl	346	7	1.4	115	10	US-09-990-427-95	Sequence 95, Appl
274	7	1.4	97	16	US-10-468-356-394	Sequence 394, App	347	7	1.4	115	10	US-09-989-328-95	Sequence 95, Appl
275	7	1.4	98	15	US-10-425-114-62072	Sequence 62072, A	348	7	1.4	115	10	US-09-993-583-95	Sequence 95, Appl
276	7	1.4	98	16	US-10-437-963-136302	Sequence 136302,	349	7	1.4	115	10	US-09-941-992-95	Sequence 95, Appl
277	7	1.4	100	9	US-09-950-933A-40	Sequence 40, Appl	350	7	1.4	115	10	US-09-992-521-95	Sequence 95, Appl
278	7	1.4	101	14	US-10-106-698-5158	Sequence 5158, Ap	351	7	1.4	115	10	US-09-997-333-95	Sequence 95, Appl
279	7	1.4	101	15	US-10-630-590-157	Sequence 157, App	352	7	1.4	115	10	US-09-997-384-95	Sequence 95, Appl
280	7	1.4	103	16	US-10-437-963-131026	Sequence 131026,	353	7	1.4	115	10	US-09-998-041-95	Sequence 95, Appl
281	7	1.4	105	15	US-10-424-599-272705	Sequence 272705,	354	7	1.4	115	10	US-09-997-585-95	Sequence 95, Appl
282	7	1.4	106	16	US-10-767-701-50716	Sequence 50716, A	355	7	1.4	115	10	US-09-997-614-95	Sequence 95, Appl
283	7	1.4	108	16	US-10-437-963-141417	Sequence 141417,	356	7	1.4	115	10	US-09-989-862-95	Sequence 95, Appl
284	7	1.4	109	16	US-10-437-963-154123	Sequence 154123,	357	7	1.4	115	10	US-09-997-529-95	Sequence 95, Appl
285	7	1.4	111	14	US-10-106-698-6281	Sequence 6281, Ap	358	7	1.4	115	10	US-09-989-725-95	Sequence 95, Appl
286	7	1.4	111	14	US-10-291-851-44	Sequence 44, Appl	359	7	1.4	115	10	US-09-991-150-95	Sequence 95, Appl
287	7	1.4	112	15	US-10-424-599-162392	Sequence 162392,	360	7	1.4	115	10	US-09-997-641-95	Sequence 95, Appl
288	7	1.4	112	16	US-10-437-963-110023	Sequence 110023,	361	7	1.4	115	10	US-09-989-733-95	Sequence 95, Appl
289	7	1.4	112	16	US-10-437-963-158058	Sequence 158058,	362	7	1.4	115	10	US-09-992-643-95	Sequence 95, Appl
290	7	1.4	112	16	US-10-437-963-203082	Sequence 203082,	363	7	1.4	115	13	US-10-052-586-86	Sequence 86, Appl
291	7	1.4	115	9	US-09-864-761-35902	Sequence 35902, A	364	7	1.4	115	14	US-10-174-590-86	Sequence 86, Appl
292	7	1.4	115	9	US-09-989-722-95	Sequence 95, Appl	365	7	1.4	115	14	US-10-176-758-86	Sequence 86, Appl
293	7	1.4	115	9	US-09-989-723-95	Sequence 95, Appl	366	7	1.4	115	14	US-10-175-737-86	Sequence 86, Appl
294	7	1.4	115	9	US-09-989-279-95	Sequence 95, Appl	367	7	1.4	115	14	US-10-174-581-86	Sequence 86, Appl
295	7	1.4	115	9	US-09-989-727-95	Sequence 95, Appl	368	7	1.4	115	14	US-10-176-483-86	Sequence 86, Appl
296	7	1.4	115	9	US-09-989-731-95	Sequence 95, Appl	369	7	1.4	115	14	US-10-176-749-86	Sequence 86, Appl
297	7	1.4	115	9	US-09-989-732-95	Sequence 95, Appl	370	7	1.4	115	14	US-10-176-914-86	Sequence 86, Appl
298	7	1.4	115	9	US-09-991-073-95	Sequence 95, Appl	371	7	1.4	115	14	US-10-176-915-86	Sequence 86, Appl
299	7	1.4	115	9	US-09-990-442-95	Sequence 95, Appl	372	7	1.4	115	14	US-10-173-706-86	Sequence 86, Appl
300	7	1.4	115	9	US-09-991-163-95	Sequence 95, Appl	373	7	1.4	115	14	US-10-175-738-86	Sequence 86, Appl
301	7	1.4	115	9	US-09-993-604-95	Sequence 95, Appl	374	7	1.4	115	14	US-10-175-752-86	Sequence 86, Appl
302	7	1.4	115	9	US-09-990-456-95	Sequence 95, Appl	375	7	1.4	115	14	US-10-176-482-86	Sequence 86, Appl
303	7	1.4	115	9	US-09-989-721-95	Sequence 95, Appl	376	7	1.4	115	14	US-10-176-757-86	Sequence 86, Appl
304	7	1.4	115	9	US-09-992-598-95	Sequence 95, Appl	377	7	1.4	115	14	US-10-176-913-86	Sequence 86, Appl
305	7	1.4	115	9	US-09-989-293A-95	Sequence 95, Appl	378	7	1.4	115	14	US-10-180-552-86	Sequence 86, Appl













817	7	1.4	115	14	US-10-184-642-86	Sequence 86, Appl	890	7	1.4	117	15	US-10-424-599-158835	Sequence 158835,
818	7	1.4	115	14	US-10-196-747-86	Sequence 86, Appl	891	7	1.4	118	16	US-10-437-963-175252	Sequence 175252,
819	7	1.4	115	14	US-10-173-689-86	Sequence 86, Appl	892	7	1.4	119	16	US-10-437-963-159484	Sequence 159484,
820	7	1.4	115	14	US-10-173-690-86	Sequence 86, Appl	893	7	1.4	119	16	US-10-437-963-188072	Sequence 188072,
821	7	1.4	115	14	US-10-173-691-86	Sequence 86, Appl	894	7	1.4	119	16	US-10-767-701-52606	Sequence 52606, A
822	7	1.4	115	14	US-10-173-694-86	Sequence 86, Appl	895	7	1.4	120	15	US-10-424-599-240756	Sequence 240756,
823	7	1.4	115	14	US-10-173-698-86	Sequence 86, Appl	896	7	1.4	120	16	US-10-437-963-115498	Sequence 115498,
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827	7	1.4	115	14	US-10-174-583-86	Sequence 86, Appl	900	7	1.4	125	11	US-09-833-245-1979	Sequence 1979, Ap
828	7	1.4	115	14	US-10-174-587-86	Sequence 86, Appl	901	7	1.4	127	16	US-10-437-963-174804	Sequence 174804,
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830	7	1.4	115	14	US-10-174-591-86	Sequence 86, Appl	903	7	1.4	129	10	US-09-992-600A-74	Sequence 74, Appl
831	7	1.4	115	14	US-10-175-736-86	Sequence 86, Appl	904	7	1.4	129	10	US-09-924-340-74	Sequence 74, Appl
832	7	1.4	115	14	US-10-175-742-86	Sequence 86, Appl	905	7	1.4	129	10	US-09-992-095B-74	Sequence 74, Appl
833	7	1.4	115	14	US-10-175-744-86	Sequence 86, Appl	906	7	1.4	129	10	US-09-999-570-74	Sequence 74, Appl
834	7	1.4	115	14	US-10-175-745-86	Sequence 86, Appl	907	7	1.4	129	14	US-10-000-489-74	Sequence 74, Appl
835	7	1.4	115	14	US-10-175-748-86	Sequence 86, Appl	908	7	1.4	129	14	US-10-000-986-74	Sequence 74, Appl
836	7	1.4	115	14	US-10-175-751-86	Sequence 86, Appl	909	7	1.4	129	14	US-10-154-678-74	Sequence 74, Appl
837	7	1.4	115	14	US-10-175-754-86	Sequence 86, Appl	910	7	1.4	129	16	US-10-437-963-140443	Sequence 140443,
838	7	1.4	115	14	US-10-176-480-86	Sequence 86, Appl	911	7	1.4	129	16	US-10-398-932-46	Sequence 46, Appl
839	7	1.4	115	14	US-10-176-489-86	Sequence 86, Appl	912	7	1.4	130	15	US-10-424-599-210014	Sequence 210014,
840	7	1.4	115	14	US-10-176-754-86	Sequence 86, Appl	913	7	1.4	131	15	US-10-424-599-244554	Sequence 244554,
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842	7	1.4	115	14	US-10-176-759-86	Sequence 86, Appl	915	7	1.4	132	16	US-10-437-963-146985	Sequence 146985,
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848	7	1.4	115	14	US-10-179-512-86	Sequence 86, Appl	921	7	1.4	140	15	US-10-424-599-283542	Sequence 283542,
849	7	1.4	115	14	US-10-179-515-86	Sequence 86, Appl	922	7	1.4	141	15	US-10-131-410-91	Sequence 91, Appl
850	7	1.4	115	14	US-10-173-692-86	Sequence 86, Appl	923	7	1.4	141	15	US-10-131-410-168	Sequence 168, App
851	7	1.4	115	14	US-10-173-702-86	Sequence 86, Appl	924	7	1.4	141	15	US-10-108-260A-2470	Sequence 2470, Ap
852	7	1.4	115	14	US-10-173-703-86	Sequence 86, Appl	925	7	1.4	143	14	US-10-106-698-5159	Sequence 5159, Ap
853	7	1.4	115	14	US-10-173-704-86	Sequence 86, Appl	926	7	1.4	144	15	US-10-425-114-53114	Sequence 53114, A
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855	7	1.4	115	14	US-10-176-486-86	Sequence 86, Appl	928	7	1.4	144	16	US-10-767-701-49797	Sequence 49797, A
856	7	1.4	115	14	US-10-176-490-86	Sequence 86, Appl	929	7	1.4	145	11	US-09-833-245-1978	Sequence 1978, Ap
857	7	1.4	115	14	US-10-176-752-86	Sequence 86, Appl	930	7	1.4	146	11	US-09-833-245-1980	Sequence 1980, Ap
858	7	1.4	115	14	US-10-176-981-86	Sequence 86, Appl	931	7	1.4	147	15	US-10-425-114-42399	Sequence 42399, A
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861	7	1.4	115	14	US-10-179-517-86	Sequence 86, Appl	934	7	1.4	153	16	US-10-437-963-129371	Sequence 129371,
862	7	1.4	115	14	US-10-179-521-86	Sequence 86, Appl	935	7	1.4	153	16	US-10-767-701-41235	Sequence 41235, A
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864	7	1.4	115	15	US-10-195-887-86	Sequence 86, Appl	937	7	1.4	154	15	US-10-424-599-177249	Sequence 177249,
865	7	1.4	115	15	US-10-195-893-86	Sequence 86, Appl	938	7	1.4	154	16	US-10-437-963-105311	Sequence 105311,
866	7	1.4	115	15	US-10-179-509-86	Sequence 86, Appl	939	7	1.4	157	16	US-10-437-963-148046	Sequence 148046,
867	7	1.4	115	15	US-10-194-486-86	Sequence 86, Appl	940	7	1.4	157	16	US-10-398-932-25	Sequence 25, Appl
868	7	1.4	115	15	US-10-195-900-86	Sequence 86, Appl	941	7	1.4	158	16	US-10-398-932-34	Sequence 34, Appl
869	7	1.4	115	15	US-10-198-759-86	Sequence 86, Appl	942	7	1.4	158	16	US-10-398-932-42	Sequence 42, Appl
870	7	1.4	115	15	US-10-205-506-86	Sequence 86, Appl	943	7	1.4	159	15	US-10-424-599-203811	Sequence 203811,
871	7	1.4	115	15	US-10-174-570-86	Sequence 86, Appl	944	7	1.4	160	15	US-10-425-114-62350	Sequence 62350, A
872	7	1.4	115	15	US-10-183-005-86	Sequence 86, Appl	945	7	1.4	160	16	US-10-398-932-27	Sequence 27, Appl
873	7	1.4	115	15	US-10-179-523-86	Sequence 86, Appl	946	7	1.4	161	16	US-10-767-701-36165	Sequence 36165, A
874	7	1.4	115	15	US-10-199-463-86	Sequence 86, Appl	947	7	1.4	163	16	US-10-437-963-177678	Sequence 177678,
875	7	1.4	115	15	US-10-202-471-86	Sequence 86, Appl	948	7	1.4	163	16	US-10-398-932-29	Sequence 29, Appl
876	7	1.4	115	15	US-10-207-915-86	Sequence 86, Appl	949	7	1.4	164	15	US-10-282-122A-71999	Sequence 71999, A
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878	7	1.4	115	15	US-10-197-709-86	Sequence 86, Appl	951	7	1.4	165	16	US-10-398-932-37	Sequence 37, Appl
879	7	1.4	115	15	US-10-206-915-86	Sequence 86, Appl	952	7	1.4	165	16	US-10-767-701-57941	Sequence 57941, A
880	7	1.4	115	15	US-10-424-599-177244	Sequence 177244,	953	7	1.4	166	15	US-10-424-599-161798	Sequence 161798,
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882	7	1.4	115	15	US-10-201-858-86	Sequence 86, Appl	955	7	1.4	169	14	US-10-156-761-10565	Sequence 10565, A
883	7	1.4	115	15	US-10-205-890-86	Sequence 86, Appl	956	7	1.4	169	16	US-10-398-932-35	Sequence 35, Appl
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885	7	1.4	115	15	US-10-201-853-86	Sequence 86, Appl	958	7	1.4	172	13	US-10-109-885-4	Sequence 4, Appli
886	7	1.4	115	15	US-10-206-916-86	Sequence 86, Appl	959	7	1.4	172	14	US-10-205-219-143	Sequence 143, App
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889	7	1.4	115	16	US-10-437-963-159041	Sequence 159041,	962	7	1.4	174	9	US-09-823-038A-12	Sequence 12, Appl

963	7	1.4	174	15	US-10-108-260A-4760	Sequence 4760, Ap	1036	7	1.4	265	16	US-10-437-963-178538,	Sequence 178538,
964	7	1.4	174	15	US-10-389-566-2059	Sequence 2059, Ap	1037	7	1.4	267	16	US-10-437-963-124674	Sequence 124674,
965	7	1.4	174	15	US-10-389-566-2162	Sequence 2162, Ap	1038	7	1.4	268	16	US-10-437-963-149247	Sequence 149247,
966	7	1.4	174	15	US-10-282-122A-52832	Sequence 52832, A	1039	7	1.4	270	15	US-10-168-659-6	Sequence 6, Appli
967	7	1.4	177	15	US-10-389-566-1133	Sequence 1133, Ap	1040	7	1.4	270	15	US-10-282-122A-51152	Sequence 51152, A
968	7	1.4	177	16	US-10-767-701-39332	Sequence 39332, A	1041	7	1.4	270	15	US-10-424-599-273092	Sequence 273092,
969	7	1.4	180	16	US-10-437-963-127587	Sequence 127587,	1042	7	1.4	270	16	US-10-755-889-156	Sequence 156, App
970	7	1.4	180	16	US-10-437-963-180670	Sequence 180670,	1043	7	1.4	272	14	US-10-017-161-1988	Sequence 1988, Ap
971	7	1.4	182	16	US-10-767-701-55772	Sequence 55772, A	1044	7	1.4	272	15	US-10-292-798-1636	Sequence 1636, Ap
972	7	1.4	184	15	US-10-424-599-211626	Sequence 211626,	1045	7	1.4	275	16	US-10-437-963-114707	Sequence 114707,
973	7	1.4	185	15	US-10-264-049-2934	Sequence 2934, Ap	1046	7	1.4	282	15	US-10-369-493-10334	Sequence 10334, A
974	7	1.4	185	15	US-10-282-122A-43835	Sequence 43835, A	1047	7	1.4	282	16	US-10-437-963-130936	Sequence 130936,
975	7	1.4	185	15	US-10-282-122A-60073	Sequence 60073, A	1048	7	1.4	282	15	US-10-425-114-60834	Sequence 60834, A
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977	7	1.4	190	9	US-09-893-737-198	Sequence 198, App	1050	7	1.4	288	15	US-10-425-114-41181	Sequence 41181, A
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981	7	1.4	191	16	US-10-767-701-43769	Sequence 43769, A	1054	7	1.4	297	14	US-10-106-698-4329	Sequence 4329, Ap
982	7	1.4	193	15	US-10-369-493-20191	Sequence 20191, A	1055	7	1.4	298	16	US-10-437-963-169792	Sequence 169792,
983	7	1.4	193	15	US-10-424-599-211506	Sequence 211506,	1056	7	1.4	302	16	US-10-437-963-129372	Sequence 129372,
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ALIGNMENTS

RESULT 1

US-09-963-290-2

Sequence 2, Application US/09963290

Patent No. US20020137713A1

GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: 55054, A No. US20020137713A1e1 Human Metalloprotease and Uses Th

FILE REFERENCE: 10147-47U1

CURRENT APPLICATION NUMBER: US/09/963,290

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SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 507

TYPE: PRT

ORGANISM: Homo sapiens

US-09-963-290-2

Query Match

Best Local Similarity 100.0%; Score 507; DB 9; Length 507;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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; Sequence 57, Application US/09931836  
; Publication No. US20030027249A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3030R1C1  
; CURRENT APPLICATION NUMBER: US/09/931,836  
; CURRENT FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/112514  
; PRIOR FILING DATE: 1998-12-15  
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; PRIOR FILING DATE: 1999-03-31  
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; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
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; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09



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; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-931-836-57

Query Match      100.0%; Score 507; DB 10; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60
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Db 1 MDPKLGMAASLLAVLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60

QY 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120
   |||||
Db 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS 120

QY 121 DPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAF 180
   |||||
Db 121 DPTKGTVCYGHLDVQPADRGDGLWLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAF 180

QY 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240
   |||||
Db 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300
   |||||
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300

QY 301 PLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKBEILMHLWRYPSLSIHGIEGAFDEPG 360
   |||||
Db 301 PLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKBEILMHLWRYPSLSIHGIEGAFDEPG 360

QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420
   |||||
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420

QY 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVD DGEHSQ 480
   |||||
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVD DGEHSQ 480

QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507
   |||||
Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

RESULT 3
US-10-036-342-57
; Sequence 57, Application US/10036342
; Publication No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C5
; CURRENT APPLICATION NUMBER: US/10/036,342
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
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; PRIOR FILING DATE: 1999-04-05
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; PRIOR FILING DATE: 1999-06-08
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; PRIOR APPLICATION NUMBER: 60/146970
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; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
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; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-57

Query Match 100.0%; Score 507; DB 13; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60
Db 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPPALLEKFQYIDLHQDEFVQTLKEWVAIE 60

QY 61 SDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPQLPDGQSLPIPPVILAE LGS 120
Db 61 SDSVQVPFRQELFRMMAVAADTLQRLGARVASVDMGPQLPDGQSLPIPPVILAE LGS 120

QY 121 DPTKGTVCYGHLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAF 180
Db 121 DPTKGTVCYGHLDVQPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAF 180

QY 181 RALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISORKPAIT 240
Db 181 RALEQDLPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISORKPAIT 240

QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMAADLVALLSLVDSGGHILVPGIYDEVV 300
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMAADLVALLSLVDSGGHILVPGIYDEVV 300

QY 301 PLTEEEINTYKAITHLDLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG 360
Db 301 PLTEEEINTYKAITHLDLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPG 360

QY 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA 420
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA 420

QY 421 NIDDTQYLAAKRAIRTVEGTEPDMIRDSGTIPIAKMFQEI VHKS VVLIPLGAVDDGHSQ 480
Db 421 NIDDTQYLAAKRAIRTVEGTEPDMIRDSGTIPIAKMFQEI VHKS VVLIPLGAVDDGHSQ 480

QY 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

RESULT 4
US-10-036-041-57
; Sequence 57, Application US/10036041
; Publication No. US20020192751A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C8
; CURRENT APPLICATION NUMBER: US/10/036,041
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
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; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
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; PRIOR FILING DATE: 1999-07-20





;	PRIOR APPLICATION NUMBER: 60/125826
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;	PRIOR APPLICATION NUMBER: 09/311832
;	PRIOR FILING DATE: 1999-05-14
;	PRIOR APPLICATION NUMBER: 09/380142
;	PRIOR FILING DATE: 1999-08-25
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;	PRIOR FILING DATE: 2000-08-22
;	PRIOR APPLICATION NUMBER: 09/747259
;	PRIOR FILING DATE: 2000-12-20
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;	PRIOR FILING DATE: 2001-05-10
;	PRIOR APPLICATION NUMBER: 09/854280
;	PRIOR FILING DATE: 2001-05-10
;	PRIOR APPLICATION NUMBER: 09/874503
;	PRIOR FILING DATE: 2001-06-05
;	PRIOR APPLICATION NUMBER: 09/869599
;	PRIOR FILING DATE: 2001-06-29
;	PRIOR APPLICATION NUMBER: 09/908,827
;	PRIOR FILING DATE: 2001-07-18
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;	PRIOR FILING DATE: 2000-03-02
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;	PRIOR APPLICATION NUMBER: PCT/US00/34956

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; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-035-855-57

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	Query Match	100.0%;	Score 507;	DB 14;	Length 507;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 507;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDPKLRMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60		
DB	1	MDPKLRMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60		
QY	61	SDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGS	120		
DB	61	SDSVQVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEELGS	120		
QY	121	DPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF	180		
DB	121	DPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF	180		
QY	181	RALEQDLPVNIKFIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT	240		
DB	181	RALEQDLPVNIKFIIEGMEEGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT	240		
QY	241	YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV	300		
DB	241	YGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV	300		
QY	301	PLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKBEILMHLWRYPSLSIHGIEGAFDEPG	360		
DB	301	PLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKBEILMHLWRYPSLSIHGIEGAFDEPG	360		
QY	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIA	420		
DB	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIA	420		
QY	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQ	480		
DB	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIYVHKSVVLIPLGAVDDGEHSQ	480		
QY	481	NEKINRWNYTEGTKLFAAFFLEMAQLH	507		
DB	481	NEKINRWNYTEGTKLFAAFFLEMAQLH	507		

RESULT 6  
US-10-036-214-57  
; Sequence 57, Application US/10036214  
; Publication NO. US20030032061A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.

APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P3030R1C11  
CURRENT APPLICATION NUMBER: US/10/036,214  
CURRENT FILING DATE: 2001-12-26  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/112514  
PRIOR FILING DATE: 1998-12-15  
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PRIOR APPLICATION NUMBER: 60/138166  
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PRIOR APPLICATION NUMBER: 09/644848  
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PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280

PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/869599  
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PRIOR APPLICATION NUMBER: 09/908,827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/28551  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30720  
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PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 57  
LENGTH: 507  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-036-214-57

Query Match 100.0%; Score 507; DB 14; Length 507;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALKEKFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALKEKFQYIDLHQDEFVQTLKEWVAIE 60  
QY 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPPIPVILAE LGS 120  
Db 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPPIPVILAE LGS 120  
QY 121 DPTKGTVCIFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 121 DPTKGTVCIFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
QY 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAIT 240  
Db 181 RALEQDLPVNIKFIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQKPAIT 240  
QY 241 YGTRGNSYFMVEVKCRDQDFHSGTFTGGILHEPMADLVAL LGS LVDSSGHILVPGIYDEVV 300  
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTFTGGILHEPMADLVAL LGS LVDSSGHILVPGIYDEVV 300  
QY 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLDFTKKEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAIHLDLEEYRNSSRVEKFLDFTKKEILMHLWRYPSLSIHGIEGAFDEPG 360





	Query Match	100.0%;	Score 507;	DB 14;	Length 507;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 507;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDPKLRMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60		
Db	1	MDPKLRMAASLLAVLLLLLLERGMFSSPPSPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60		
QY	61	SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS	120		
Db	61	SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS	120		
QY	121	DPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF	180		
Db	121	DPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF	180		
QY	181	RALEQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT	240		
Db	181	RALEQDLPVNIKFIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT	240		
QY	241	YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV	300		
Db	241	YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV	300		
QY	301	PLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360		
Db	301	PLTEEEINTYKAIHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360		
QY	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKNVVMSTLGLHPWIA	420		
Db	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKNVVMSTLGLHPWIA	420		
QY	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQ	480		
Db	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQ	480		
QY	481	NEKINRWNYIEGTKLFAAFFLEMAQLH	507		
Db	481	NEKINRWNYIEGTKLFAAFFLEMAQLH	507		

## RESULT 8

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US-10-036-160-57
; Sequence 57, Application US/10036160
; Publication No. US20030044842A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C3
; CURRENT APPLICATION NUMBER: US/10/036,160
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02

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; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/152664
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/235222
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
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; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/210666
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-036-160-57

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Query Match	100.0%;	Score 507;	DB 14;	Length 507;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 507: Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	

QY	1	MDPKLRMAASLLAVLLLLLGERMFSSPPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60
Db	1	MDPKLRMAASLLAVLLLLLGERMFSSPPALLEKVFQYIDLHQDEFVQTLKEWVAIE	60
QY	61	SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS	120
Db	61	SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGS	120
QY	121	DPTKGTVCFCYGHLDVQPADRGDGLWTDPPVLTVEVDGKLYGRGATDNKGPVLAWINAVSAF	180
Db	121	DPTKGTVCFCYGHLDVQPADRGDGLWTDPPVLTVEVDGKLYGRGATDNKGPVLAWINAVSAF	180
QY	181	RALEQDLPVNIKFIIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT	240
Db	181	RALEQDLPVNIKFIIIEGMEEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT	240
QY	241	YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV	300
Db	241	YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV	300
QY	301	PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360
Db	301	PLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG	360
QY	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIA	420
Db	361	TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSMVMTLGLHPWIA	420
QY	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLLPLGAVD DGEHSQ	480
Db	421	NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLLPLGAVD DGEHSQ	480
QY	481	NEKINRWNYIEGTKLFAAFFLEMAQLH	507
Db	481	NEKINRWNYIEGTKLFAAFFLEMAQLH	507

## RESULT 9

US-10-035-958-57

US 10 035 595  
: Sequence 57, Application US/10035958

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; Publication No. US20030049733A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
;
; FILE REFERENCE: P3030R1C7
;
; CURRENT APPLICATION NUMBER: US/10/035,958
;
; CURRENT FILING DATE: 2001-12-26
;
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/162506
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; PRIOR APPLICATION NUMBER: 09/311832
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; PRIOR FILING DATE: 1999-05-14
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-958-57
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Query Match      100.0%; Score 507; DB 14; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60
Db      1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60

Qy      61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS 120
Db      61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGS 120

Qy      121 DPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180
Db      121 DPTKGTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180
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Qy      181 RALEQDLFVNKFTIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240
Db      181 RALEQDLFVNKFTIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240

Qy      241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300
Db      241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300

Qy      301 PLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360
Db      301 PLTEEEINTYKAHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360

Qy      361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA 420
Db      361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIA 420

Qy      421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSGTIPIAKMFQEIIVHKSVDLPLGAVDDGEHSQ 480
Db      421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSGTIPIAKMFQEIIVHKSVDLPLGAVDDGEHSQ 480

Qy      481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507
Db      481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507
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RESULT 10

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US-10-036-150-57
; Sequence 57, Application US/10036150
; Publication No. US20030049734A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C9
; CURRENT APPLICATION NUMBER: US/10/036,150
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
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; PRIOR FILING DATE: 2000-03-02  
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; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
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; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692

; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 80  
; SEQ ID NO 57  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-036-150-57  
  
Query Match 100.0%; Score 507; DB 14; Length 507;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MDPKLGGRMAASLLAVLLLLLLERGMFSSPPPALKEKYFYQYIDLHQDEFVQTLKEWVAIE 60  
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Db 1 MDPKLGGRMAASLLAVLLLLLLERGMFSSPPPALKEKYFYQYIDLHQDEFVQTLKEWVAIE 60  
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Qy 61 SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGS 120  
|||  
Db 61 SDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGS 120  
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Qy 121 DPTKGTVCYFGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
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Db 121 DPTKGTVCYFGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
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Db 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRKPAIT 240  
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Qy 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
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Db 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
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Qy 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
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Db 301 PLTEEEINTYKAIHLDLEEYRNSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
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Qy 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
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Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIA 420  
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Qy 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVWLIPLGAVDDGHSQ 480  
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Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIHKSVWLIPLGAVDDGHSQ 480  
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Qy 481 NEKINRWNYIEGTKLFAAFPLEMAQLH 507  
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Db 481 NEKINRWNYIEGTKLFAAFPLEMAQLH 507  
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RESULT 11  
US-10-036-063-57  
; Sequence 57, Application US/10036063  
; Publication No. US20030092063A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3030R1C6  
; CURRENT APPLICATION NUMBER: US/10/036,063  
; CURRENT FILING DATE: 2001-12-26

;  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/112514  
; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/113300  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/113430  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113605  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/114140  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/115552  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/116843  
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; PRIOR APPLICATION NUMBER: 60/125774  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125778  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125826  
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; PRIOR APPLICATION NUMBER: 60/131270  
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; PRIOR APPLICATION NUMBER: 60/132383  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: 60/135750  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 60/138166  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/144791  
; PRIOR FILING DATE: 1999-07-20  
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; PRIOR APPLICATION NUMBER: 60/162506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 09/311832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/380142  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/644848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 09/747259  
; PRIOR FILING DATE: 2000-12-20  
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; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 09/854208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/854280  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/874503  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/869599  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/908,827

;  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US99/10733  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30720  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: PCT/US00/05601  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 80  
; SEQ ID NO 57  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-036-063-57

Query Match 100.0%; Score 507; DB 14; Length 507;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
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Db 1 MDPKLGMAASLLAVLLLLLGERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
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Qy 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAE LGS 120  
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Qy 121 DPTKGTVCFYGHLDVQPADRGDWLTDPYVLTTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
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Db 121 DPTKGTVCFYGHLDVQPADRGDWLTDPYVLTTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
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Qy 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
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Db 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
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Qy 241 YGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVAL LGS LVDSSGHILVPGIYDEW 300  
|||  
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTFFGGILHEPMADLVAL LGS LVDSSGHILVPGIYDEW 300  
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Qy 301 PLTEEEINTYKAIHLDLEEYRNSRRVEKFLDFTKKEILMHLWRYP SLSIHGIEGAFDEPG 360  
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Db 301 PLTEEEINTYKAIHLDLEEYRNSRRVEKFLDFTKKEILMHLWRYP SLSIHGIEGAFDEPG 360  
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Qy 361 TKTVIPGRVICKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS SSKMVMVMTLGLHPWIA 420  
|||  
Db 361 TKTVIPGRVICKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNS SSKMVMVMTLGLHPWIA 420  
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Qy 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFEIVHKSV VLIPLGAVDDEHSQ 480

Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDSSTPIAKMFQEI VHKSVVLIPLGAVDDGHSQ 480  
Qy 481 NEKINRWNYIEGTKLF AAFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLF AAFLEMAQLH 507

RESULT 12

US-10-035-977-57  
; Sequence 57, Application US/10035977  
; Publication No. US20030134327A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3030R1C10  
; CURRENT APPLICATION NUMBER: US/10/035,977  
; CURRENT FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/112514  
; PRIOR FILING DATE: 1998-12-15  
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; PRIOR APPLICATION NUMBER: 60/132379  
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; PRIOR APPLICATION NUMBER: 60/132383  
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; PRIOR APPLICATION NUMBER: 60/135750

; PRIOR FILING DATE: 1999-05-25  
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; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/144791  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/146970  
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; PRIOR APPLICATION NUMBER: 09/644848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 09/747259  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/816744  
; PRIOR FILING DATE: 2001-03-22  
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; PRIOR APPLICATION NUMBER: 09/854280  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/874503  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/869599  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/908,827  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US99/10733  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30720  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: PCT/US00/05601  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
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; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 80  
; SEQ ID NO 57  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-035-977-57

Query Match 100.0%; Score 507; DB 14; Length 507;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MDPKIGRMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHQDFVQTLKEWVAIE 60



Db 1 MDPKLGMAASLLAVLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Qy 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
Db 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
Qy 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Qy 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Db 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
Qy 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Db 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Qy 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Qy 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIA 420  
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIA 420  
Qy 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Qy 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

RESULT 13

US-10-275-107-68  
; Sequence 68, Application US/10275107  
; Publication No. US20040063107A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY D.  
; APPLICANT: WHYTE, DAVID  
; APPLICANT: SUDARSANAM, SUCHA  
; APPLICANT: MANNING, GERARD  
; APPLICANT: CAENEPEEL, SEAN R.  
; APPLICANT: PAYNE, VILLA  
; TITLE OF INVENTION: NOVEL PROTEASES  
; FILE REFERENCE: 038602/1479  
; CURRENT APPLICATION NUMBER: US/10/275,107  
; CURRENT FILING DATE: 2003-11-03  
; PRIOR APPLICATION NUMBER: PCT/US01/14431  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/201,879  
; PRIOR FILING DATE: 2000-05-04  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 68  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-275-107-68

Query Match 100.0%; Score 507; DB 15; Length 507;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MDPKLGMAASLLAVLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Db 1 MDPKLGMAASLLAVLLLLERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 60  
Qy 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120

Db 61 SDSVQVPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS 120  
Qy 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
Db 121 DPTKGTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAF 180  
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Db 181 RALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAIT 240  
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Db 241 YGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVV 300  
Qy 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Db 301 PLTEEEINTYKAHLDLEEYRNSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPG 360  
Qy 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIA 420  
Db 361 TKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVSMTLGLHPWIA 420  
Qy 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Db 421 NIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQ 480  
Qy 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507  
Db 481 NEKINRWNYIEGTKLFAAFFLEMAQLH 507

RESULT 14

US-09-731-872-242  
; Sequence 242, Application US/09731872  
; Patent No. US20020102604A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS  
; FILE REFERENCE: 78.US3.REG  
; CURRENT APPLICATION NUMBER: US/09/731,872  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,629  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: US 60/187,470  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 482  
; SOFTWARE: Patent.pm  
; SEQ ID NO 242  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -27...-1  
US-09-731-872-242

Query Match 97.0%; Score 492; DB 9; Length 508;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 LLLLLLGERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 75  
Db 17 LLLLLLGERGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 76  
Qy 76 RMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS DPTKGTVCFYGHLDV 135  
Db 77 RMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAE LGS DPTKGTVCFYGHLDV 136  
Qy 136 QPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI 195  
Db 137 QPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI 196

QY 196 EGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255  
Db 197 EGMEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256  
  
QY 256 RDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHL 315  
Db 257 RDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHL 316  
  
QY 316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375  
Db 317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376  
  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435  
Db 377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436  
  
QY 436 TVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495  
Db 437 TVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496  
  
QY 496 FFAFFLEMAQLH 507  
Db 497 FFAFFLEMAQLH 508

RESULT 15

US-09-948-783-139  
; Sequence 139, Application US/09948783  
; Publication No. US20030100051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P2  
; CURRENT APPLICATION NUMBER: US/09/948,783  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,846  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 09/892,877  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/437,658  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/09847  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: 60/085,093  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,094  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,105  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,180  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,927  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,906  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,924  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,928  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,920  
; PRIOR FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 465  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 139

; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-948-783-139  
  
Query Match 97.0%; Score 492; DB 10; Length 508;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 16 LLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRFRQELF 75  
Db 17 LLLLLLGRGMFSSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPFRFRQELF 76  
  
QY 76 RNMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDV 135  
Db 77 RNMVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDV 136  
  
QY 136 QPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI 195  
Db 137 QPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFI 196  
  
QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255  
Db 197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256  
  
QY 256 RDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHL 315  
Db 257 RDQDFHSGTGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHL 316  
  
QY 316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375  
Db 317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376  
  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435  
Db 377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436  
  
QY 436 TVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495  
Db 437 TVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496  
  
QY 496 FFAFFLEMAQLH 507  
Db 497 FFAFFLEMAQLH 508  
  
RESULT 16  
US-09-876-997-242  
; Sequence 242, Application US/09876997  
; Publication No. US20030152921A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS  
; FILE REFERENCE: 78.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/876,997  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/731,872  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/187,470  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: US 60/169,629  
; PRIOR FILING DATE: 1999-12-08  
; NUMBER OF SEQ ID NOS: 482  
; SOFTWARE: Patent.pm  
; SEQ ID NO 242  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -27...-1

US-09-876-997-242

Query Match 97.0%; Score 492; DB 10; Length 508;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 75  
| | | | |  
Db 17 LLLLLRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 76  
| | | | |  
QY 76 RMMVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEFGSDPTKGTVCYFYGHLDV 135  
| | | | |  
Db 77 RMMVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEFGSDPTKGTVCYFYGHLDV 136  
| | | | |  
QY 136 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195  
| | | | |  
Db 137 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196  
| | | | |  
QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRPKPAITYGTRGNSYFMVEVKC 255  
| | | | |  
Db 197 EGMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRPKPAITYGTRGNSYFMVEVKC 256  
| | | | |  
QY 256 RDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315  
| | | | |  
Db 257 RDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316  
| | | | |  
QY 316 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375  
| | | | |  
Db 317 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376  
| | | | |  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435  
| | | | |  
Db 377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436  
| | | | |  
QY 436 TVFGTEPDMIRGSGTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495  
| | | | |  
Db 437 TVFGTEPDMIRGSGTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496  
| | | | |  
QY 496 FAAFFLEMAQLH 507  
| | | | |  
Db 497 FAAFFLEMAQLH 508  
| | | | |

RESULT 17  
US-09-892-877-137  
; Sequence 137, Application US/09892877  
; Publication No. US20030077809A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: PZ028P1  
; CURRENT APPLICATION NUMBER: US/09/892,877  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 137  
; LENGTH: 509  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (509)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-892-877-137

Query Match 97.0%; Score 492; DB 10; Length 509;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 LLLLLRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 75  
| | | | |

Db 17 LLLLLRGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQVPVPRFRQELF 76  
| | | | |  
QY 76 RMMVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEFGSDPTKGTVCYFYGHLDV 135  
| | | | |  
Db 77 RMMVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEFGSDPTKGTVCYFYGHLDV 136  
| | | | |  
QY 136 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195  
| | | | |  
Db 137 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196  
| | | | |  
QY 196 EGMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRPKPAITYGTRGNSYFMVEVKC 255  
| | | | |  
Db 197 EGMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRPKPAITYGTRGNSYFMVEVKC 256  
| | | | |  
QY 256 RDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315  
| | | | |  
Db 257 RDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316  
| | | | |  
QY 316 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375  
| | | | |  
Db 317 DLEEYRNSSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376  
| | | | |  
QY 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435  
| | | | |  
Db 377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436  
| | | | |  
QY 436 TVFGTEPDMIRGSGTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495  
| | | | |  
Db 437 TVFGTEPDMIRGSGTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496  
| | | | |  
QY 496 FAAFFLEMAQLH 507  
| | | | |  
Db 497 FAAFFLEMAQLH 508  
| | | | |

RESULT 18  
US-09-791-378-674  
; Sequence 674, Application US/09791378  
; Patent No. US20020142303A1  
; GENERAL INFORMATION:  
; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: SCHIZOPHRENIA  
; FILE REFERENCE: 9195-061-999  
; CURRENT APPLICATION NUMBER: US/09/791,378  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 674  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (70)..(70)  
; OTHER INFORMATION: Xaa = Ile or Leu  
US-09-791-378-674

Query Match 84.6%; Score 429; DB 9; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 77 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEFGSDPTKGTVCYFYGHLDVQ 136  
| | | | |  
Db 71 MMAVAADTLQRLGARVASVDMGPPQLPDGQSLPIPPVILAEFGSDPTKGTVCYFYGHLDVQ 130  
| | | | |  
QY 137 PADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196  
| | | | |  
Db 131 PADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 190  
| | | | |  
QY 197 GMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRPKPAITYGTRGNSYFMVEVKCR 256  
| | | | |



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Db      191 GMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250
QY      257 DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 316
Db      251 DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310
QY      317 LEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 376
Db      311 LEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370
QY      377 LVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDDTQYLAAKRAIRT 436
Db      371 LVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDDTQYLAAKRAIRT 430
QY      437 VFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 496
Db      431 VFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490
QY      497 AAFFLEMAQ 505
Db      491 AAFFLEMAQ 499

RESULT 19
US-09-791-393-2
; Sequence 2, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(501)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-791-393-2

Query Match      84.6%; Score 429; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136
Db      71 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 130
QY      137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIE 196
Db      131 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIE 190
QY      197 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 256
Db      191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250
QY      257 DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 316
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Db      251 DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310
QY      317 LEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 376
Db      311 LEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370
QY      377 LVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDDTQYLAAKRAIRT 436
Db      371 LVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVSVMTLGLHPWIANIDDTQYLAAKRAIRT 430
QY      437 VFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 496
Db      431 VFGTEPDMIRDGSTIPIAKMFQEIIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490
QY      497 AAFFLEMAQ 505
Db      491 AAFFLEMAQ 499

RESULT 20
US-09-791-389-2
; Sequence 2, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(501)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-791-389-2

Query Match      84.6%; Score 429; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 136
Db      71 MMAVAADTLQRLGARVASVDMGPPQQLPDGQSLPIPPVILAEGLSDPTKGTVCFYGHLDVQ 130
QY      137 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIE 196
Db      131 PADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIE 190
QY      197 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 256
Db      191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250
QY      257 DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 316
Db      251 DQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310
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QY	317	LEEYRNSSRVEKFLFDTKKEIILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR	376
Db	311	LEEYRNSSRVEKFLFDTKKEIILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR	370
QY	377	LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTGLHPWIANIDDTQYLAAKRAIRT	436
Db	371	LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTGLHPWIANIDDTQYLAAKRAIRT	430
QY	437	VFGTEPDMIRDGSTIPIAKMFOEIVHKSSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF	496
Db	431	VFGTEPDMIRDGSTIPIAKMFOEIVHKSSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF	490
QY	497	AAFFLEMAQ 505	
Db	491	AAFFLEMAQ 499	

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RESULT 21
US-09-791-377-674
; Sequence 674, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 674
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (70)..(70)
; OTHER INFORMATION: Xaa = Ile or Leu
US-09-791-377-674

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Query Match      84.6%; Score 429; DB 11; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	71	MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ	130
QY	137	PADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE	196
Db	131	PADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE	190
QY	197	GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR	256
Db	191	GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR	250
QY	257	DQDFHSGTGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD	316
Db	251	DQDFHSGTGGILHEPMADLVALGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLD	310
QY	317	LEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIR	376
Db	311	LEEYRNSSRVEKFLDFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVPGRVIGKFSIR	370
QY	377	LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKWVSMTLGLHPWIANIDDTQYLAAKRAIRT	436
Db	371	LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKWVSMTLGLHPWIANIDDTQYLAAKRAIRT	430
QY	437	VFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGGEHSQNEKINRWNYIEGTKLF	496

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